

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 150.277 Seconds
(without alignments)
978.085 Million cell updates/sec

Title: US-10-087-631B-9

Perfect score: 28
Sequence: 1 cgtctgggtagtcgcatggtgtt 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

N_Geneseq_23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	75.0	21	9	ADAI13880
2	21	75.0	21	9	ADAI13871
3	21	75.0	21	9	ADAI13872
4	21	75.0	21	9	ADAI13873
5	21	75.0	21	10	ADFS2874
6	21	75.0	21	10	ADFS2876
7	21	75.0	21	10	ADFS2883
8	21	75.0	21	10	ADFS2875
9	20	71.4	21	9	ADAI13879
10	20	71.4	21	9	ADAI13824
11	20	71.4	21	10	ADFS2882
12	20	71.4	21	10	ADFS2848
13	20	71.4	23	10	ADFS2996
14	20	71.4	23	10	ADFS2938
15	19.4	69.3	21	9	ADAI13825
16	19.4	69.3	21	10	ADFS2849
17	19.4	69.3	23	10	ADFS2995
18	19.4	69.3	23	10	ADFS2937
19	19.4	69.3	23	10	ADFS2997
20	19.4	69.3	23	10	ADFS2999
21	19.4	69.3	23	10	ADFS2939

22	19.4	69.3	23	10	ADFS2941	Adf52941 Hepatitis
23	19	67.9	21	9	ADAI13832	Adai13832 Short int
24	19	67.9	21	9	ADAI13878	Adai13878 Short int
25	19	67.9	21	9	ADAI13833	Adai13833 Short int
26	19	67.9	21	9	ADAI13831	Adai13831 Short int
27	19	67.9	21	9	ADAI13826	Adai13826 Short int
28	19	67.9	21	10	ADFS2954	Adf52954 Hepatitis
29	19	67.9	21	10	ADFS3008	Adf53008 Hepatitis
30	19	67.9	21	10	ADFS2857	Adf52857 Hepatitis
31	19	67.9	21	10	ADFS3007	Adf53007 Hepatitis
32	19	67.9	21	10	ADFS2850	Adf52850 Hepatitis
33	19	67.9	21	10	ADFS2949	Adf52949 Hepatitis
34	19	67.9	21	10	ADFS2951	Adf52951 Hepatitis
35	19	67.9	21	10	ADFS2952	Adf52952 Hepatitis
36	19	67.9	21	10	ADFS3011	Adf53011 Hepatitis
37	19	67.9	21	10	ADFS2950	Adf52950 Hepatitis
38	19	67.9	21	10	ADFS3009	Adf53009 Hepatitis
39	19	67.9	21	10	ADFS3010	Adf53010 Hepatitis
40	19	67.9	21	10	ADFS2855	Adf52855 Hepatitis
41	19	67.9	21	10	ADFS3012	Adf53012 Hepatitis
42	19	67.9	21	10	ADFS2881	Adf52881 Hepatitis
43	19	67.9	21	10	ADFS2856	Adf52856 Hepatitis
44	19	67.9	21	10	ADFS2953	Adf52953 Hepatitis
45	19	67.9	23	10	ADFS2938	Adf52938 Hepatitis
46	19	67.9	23	10	ADFS3000	Adf53000 Hepatitis
47	19	67.9	23	10	ADFS2940	Adf52940 Hepatitis
48	19	67.9	23	10	ADFS2942	Adf52942 Hepatitis
49	18	64.3	21	10	ADFS3006	Adf53006 Hepatitis
50	18	64.3	21	10	ADFS2948	Adf52948 Hepatitis
51	18	64.3	23	10	ADFS2934	Adf52934 Hepatitis
52	18	64.3	23	10	ADFS2936	Adf52936 Hepatitis
53	17.4	62.1	23	10	ADFS2943	Adf52943 Hepatitis
54	17.4	62.1	23	10	ADFS3001	Adf53001 Hepatitis
55	17	60.7	21	10	ADFS2955	Adf52955 Hepatitis
56	17	60.7	21	10	ADFS3013	Adf53013 Hepatitis
57	15.8	56.4	34	10	ADK71400	Adk71400 Drug-cole
58	15.8	56.4	47	3	AAZ67333	Aaz67333 Human map
59	15.6	55.0	37	3	AAA12757	Aaal2757 5' PCR pr
60	15.4	55.0	37	12	ADJ98268	Adj98268 Oligonuc1
61	15	53.6	19	8	ADA93661	Ada93661 Murine Ig
62	15	53.6	19	8	ADA93657	Ada93657 Murine Ig
63	15	53.6	23	10	ADFS3002	Adf53002 Hepatitis
64	15	53.6	23	10	ADFS2944	Adf52944 Hepatitis
65	14.6	52.1	21	4	AAF97731	Aaf97731 Human gen
66	14.6	52.1	21	11	ADO69899	Ado69899 Genetical
67	14.6	52.1	22	8	ACA96153	Aca96153 Flavonoid
68	14.6	52.1	23	3	AZ39149	Aaz39149 Antimicro
69	14.6	52.1	37	3	AAA12761	Aaal2761 5' PCR pr
70	14.6	52.1	37	3	AAA12759	Aaal2759 5' PCR pr
71	14.6	52.1	37	10	ADD15049	Add15049 PCR prime
72	14.6	52.1	37	10	ADD15041	Add15041 PCR prime
73	14.6	52.1	38	2	AAV65741	Aav65741 Germin si
74	14.6	52.1	38	8	ABZ70574	Abz70574 Germin si
75	14.6	52.1	40	2	AAQ12193	Aaq12193 ASF-1 bin
76	14.6	52.1	50	3	AAA51885	Aaa51885 Primer Ca
77	14.4	51.4	21	10	ADFS3005	Adf53005 Hepatitis
78	14.4	51.4	25	9	ACK16634	Ack16634 Human mic
79	14.4	51.4	25	9	ACI30300	Act30300 Human mic
80	14.4	51.4	32	2	AAT64665	Aat64665 G-CSF rec
81	14.4	51.4	38	2	AAZ79882	Aaz79882 PCR prime
82	14.4	51.4	38	2	AAZ79862	Aaz79862 PCR prime
83	14.4	51.4	38	2	AAZ35471	Aaz35471 Sense PCR
84	14.4	51.4	38	2	AAZ90592	Aaz90592 Human c-H
85	14.4	51.4	38	2	AAZ60787	Aaz60787 Human c-H
86	14.4	51.4	38	2	AAZ31765	Aaz31765 PCR prime
87	14.4	51.4	38	2	AAZ19533	Aaz19533 Human c-H
88	14.4	51.4	38	2	AAZ79918	Aaz79918 PCR prime
89	14.4	51.4	38	2	AAZ79908	Aaz79908 PCR prime
90	14.4	51.4	38	2	AAZ55505	Aaz55505 Human c-H
91	14.4	51.4	38	2	AAZ26930	Aaz26930 Sense pri
92	14.4	51.4	38	2	AAZ19680	Aaz19680 Human cel
93	14.4	51.4	38	2	AAZ19694	Aaz19694 Human c-H
94	14.4	51.4	38	2	AAZ79872	Aaz79872 PCR prime

c 95	14.4	51.4	38	3	AAZ35481	Aax35481 Human cel	168	13.6	48.6	26	2	AAT36369	Aat36369 Beta-iono
c 96	14.4	51.4	38	3	AAZ35482	Aax35482 Primer fo	169	13.6	48.6	27	6	ABL99556	ABL99556 Canine BR
c 97	14.4	51.4	38	3	AAZ35462	Aax35462 Human C-H	170	13.6	48.6	27	10	ABZ83650	ABZ83650 Toxicolog
c 98	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	171	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 99	14.4	51.4	38	3	AAZ53489	Aax53489 Human C-H	c 172	13.6	48.6	36	2	AAV45199	AAV45199 Vectorial
c 100	14.4	51.4	38	3	AAZ54427	Aax54427 Human C-H	c 173	13.6	48.6	39	2	AAV45198	AAV45198 Vectorial
c 101	14.4	51.4	38	3	AAZ59809	Aax59809 C-H-ras-L	c 174	13.6	48.6	39	8	ADQ29011	ADQ29011 Human GPC
c 102	14.4	51.4	38	3	AAZ60502	Aax60502 Sense PCR	c 175	13.6	48.6	39	12	ADQ98172	ADQ98172 Human GPC
c 103	14.4	51.4	38	3	AAZ38803	Aax38803 Human C-H	c 176	13.6	48.6	42	2	AAV30729	AAV30729 Telomeras
c 104	14.4	51.4	38	3	AAZ58857	Aax58857 Human H-r	c 177	13.6	48.6	43	3	AAZ94862	AAZ94862 Primer #1
c 105	14.4	51.4	38	3	AAZ599553	Aax599553 C-H-ras-L	c 178	13.6	48.6	50	2	AAZ52203	AAZ52203 Synthetic
c 106	14.4	51.4	38	3	AAZ63345	Aax63345 Human C-H	c 179	13.4	47.9	24	12	ADIO3810	ADIO3810 Mouse Ly6
c 107	14.4	51.4	38	3	AAZ13784	Aax13784 Human C-H	c 180	13.4	47.9	25	9	ACI42015	ACI42015 Human mic
c 108	14.4	51.4	38	3	AAZ59933	Aax59933 Human C-H	c 181	13.4	47.9	25	9	ACK23752	ACK23752 Human mic
c 109	14.4	51.4	38	3	AAZ13703	Aax13703 Human C-H	c 182	13.4	47.9	25	9	ACI15213	ACI15213 Human mic
c 110	14.4	51.4	38	3	AAZ28751	Aax28751 Sense pri	c 183	13.4	47.9	25	9	ACI15212	ACI15212 Human mic
c 111	14.4	51.4	38	3	AAZ599572	Aax599572 C-H-ras-L	c 184	13.4	47.9	25	9	ACI17058	ACI17058 Human mic
c 112	14.4	51.4	38	3	AAZ599591	Aax599591 C-H-ras-L	c 185	13.4	47.9	29	6	ABS61287	ABS61287 Human pol
c 113	14.4	51.4	38	4	AAZ82131	Aax82131 Human cel	c 186	13.4	47.9	39	6	ABS61277	ABS61277 Human pol
c 114	14.4	51.4	38	4	AAZ13518	Aax13518 Human C-H	c 187	13.4	47.9	48	2	AAZ81453	AAZ81453 PCR prime
c 115	14.4	51.4	38	4	AAZ47349	Aax47349 Human C-H	c 188	13.4	47.9	48	12	ADD16920	ADD16920 Pseudomon
c 116	14.4	51.4	38	4	AAZ514711	Aax514711 Sense str	c 189	13.4	47.9	50	10	ADD16920	ADD16920 Pseudomon
c 117	14.4	51.4	38	4	AAZ57900	Aax57900 Human cel	c 190	13.2	47.1	20	10	ADD16920	ADD16920 Pseudomon
c 118	14.4	51.4	38	4	AAZ74851	Aax74851 PCR prime	c 191	13.2	47.1	24	10	ADD16920	ADD16920 Pseudomon
c 119	14.4	51.4	38	4	AAZ15415	Aax15415 Human cel	c 192	13.2	47.1	25	9	ACK16104	ACK16104 Human mic
c 120	14.4	51.4	38	4	AAZ47368	Aax47368 Human C-H	c 193	13.2	47.1	25	9	ACK16104	ACK16104 Human mic
c 121	14.4	51.4	38	4	AAZ43817	Aax43817 Cellular-	c 194	13.2	47.1	25	9	ACK16105	ACK16105 Human mic
c 122	14.4	51.4	38	4	AAZ87103	Aax87103 PCR prime	c 195	13.2	47.1	25	9	ACK16105	ACK16105 Human mic
c 123	14.4	51.4	38	4	AAZ37979	Aax37979 PCR prime	c 196	13.2	47.1	25	9	ACK16105	ACK16105 Human mic
c 124	14.4	51.4	38	4	AAZ47330	Aax47330 Human C-H	c 197	13.2	47.1	26	2	AAV38206	AAV38206 Human mic
c 125	14.4	51.4	38	4	AAZ59708	Aax59708 Human C-H	c 198	13.2	47.1	29	3	AAQ78185	AAQ78185 PCR prime
c 126	14.4	51.4	38	4	AAZ47483	Aax47483 PCR prime	c 199	13.2	47.1	29	3	AAQ78185	AAQ78185 PCR prime
c 127	14.4	51.4	38	5	AAZ23761	Aax23761 Human C-H	c 200	13.2	47.1	34	12	AAQ77909	AAQ77909 PA gene S
c 128	14.4	51.4	38	5	AAZ18798	Aax18798 Human C-H	c 201	13.2	47.1	35	2	AAQ77909	AAQ77909 PA gene S
c 129	14.4	51.4	38	5	AAZ77231	Aax77231 PCR prime	c 202	13.2	47.1	37	3	AAZ27779	AAZ27779 Mutagenic
c 130	14.4	51.4	38	5	AAZ74781	Aax74781 PCR prime	c 203	13.2	47.1	39	6	AAZ69384	AAZ69384 Anti-huma
c 131	14.4	51.4	38	5	AAZ52784	Aax52784 H-ras PCR	c 204	13.2	47.1	43	2	AAZ2994	AAZ2994 M. tuberc
c 132	14.4	51.4	38	6	AAZ42034	Aax42034 Sense PCR	c 205	13.2	47.1	43	6	ABK89090	ABK89090 Mutant PC
c 133	14.4	51.4	38	6	AAZ88797	Aax88797 Human cel	c 206	13.2	47.1	45	3	AAZ81274	AAZ81274 Human/mou
c 134	14.4	51.4	38	6	ABK10023	Abk10023 Expressio	c 207	13.2	47.1	47	3	AAZ72095	AAZ72095 SCET anti
c 135	14.4	51.4	38	6	AAZ25643	Aax25643 Human cel	c 208	13.2	47.1	49	2	AAQ88989	AAQ88989 VEGF 2'-N
c 136	14.4	51.4	38	6	AAZ14384	Aax14384 Sense PCR	c 209	13.2	47.1	50	6	ABZ03835	ABZ03835 Human leu
c 137	14.4	51.4	38	8	AAZ51903	Aax51903 Human C-H	c 210	13	46.4	21	6	ABT04622	ABT04622 Human lli
c 138	14.4	51.4	38	10	AAZ54110	Aax54110 Prenyl-pr	c 211	13	46.4	23	4	AAZ19868	AAZ19868 TYDV LIR
c 139	14.2	50.7	20	2	AAZ29692	Aax29692 beta-acti	c 212	13	46.4	23	5	AAH47146	AAH47146 B1466 gen
c 140	14.2	50.7	24	10	AAZ59541	Aax59541 Mouse bet	c 213	13	46.4	24	12	ADN59638	ADN59638 Beta-gluc
c 141	14.2	50.7	46	2	AAZ22928	Aax22928 DE1973659	c 214	13	46.4	25	6	ABV80911	ABV80911 Human HTP
c 142	14.2	50.7	48	3	AAZ64783	Aax64783 C. tracho	c 215	13	46.4	25	6	ABV80912	ABV80912 Human HTP
c 143	14.2	50.7	48	4	AAZ56286	Aax56286 Chlamydia	c 216	13	46.4	25	6	ABV80913	ABV80913 Human HTP
c 144	14.2	50.7	48	6	ABZ192515	Abz192515 Chlamydia	c 217	13	46.4	25	6	ABV80910	ABV80910 Human HTP
c 145	14.2	50.7	49	12	ADZ180447	Adz180447 Anti-tumo	c 218	13	46.4	25	6	ABV80909	ABV80909 Human HTP
c 146	14	50.0	21	10	ADZ53014	Adz53014 Hepatitis	c 219	13	46.4	25	9	ACK03003	ACK03003 Human mic
c 147	14	50.0	21	10	ADZ52956	Adz52956 Hepatitis	c 220	13	46.4	25	9	ACK22303	ACK22303 Human mic
c 148	14	50.0	23	10	ADZ52993	Adz52993 Hepatitis	c 221	13	46.4	25	9	ACK22302	ACK22302 Human mic
c 149	14	50.0	25	9	ADZ51585	Adz51585 DNA targe	c 222	13	46.4	25	9	ACK22303	ACK22303 Human mic
c 150	14	50.0	27	6	ABA99194	Abz99194 Human HCC	c 223	13	46.4	25	9	ACK22013	ACK22013 Human mic
c 151	14	50.0	30	12	ADO79804	Ado79804 CENPC1 PC	c 224	13	46.4	25	9	ACK22013	ACK22013 Human mic
c 152	13.8	49.3	25	9	ACI95823	AcI95823 Human mic	c 225	13	46.4	25	9	ACK22938	ACK22938 Human mic
c 153	13.8	49.3	25	12	ADQ30807	Adq30807 A fumigat	c 226	13	46.4	25	9	ACH58547	ACH58547 DNA targe
c 154	13.8	49.3	26	5	AAI62009	Aai62009 Soybean 2	c 227	13	46.4	25	9	ACH52471	ACH52471 DNA targe
c 155	13.8	49.3	30	12	ADE85726	Ade85726 Human Eph	c 228	13	46.4	26	2	AAZ40806	AAZ40806 Oligonuc1
c 156	13.8	49.3	40	2	AAZ44878	Aat44878 HPV linke	c 229	13	46.4	30	2	ABA99190	ABA99190 Human HCC
c 157	13.8	49.3	40	2	AAZ78099	Aat78099 Human pap	c 230	13	46.4	30	2	AAZ39272	AAZ39272 Human bet
c 158	13.8	49.3	41	8	ABZ25604	Abz25604 Human pre	c 231	13	46.4	30	2	AAV26823	AAV26823 3'RACE Hu
c 159	13.8	49.3	41	8	ABZ25603	Abz25603 Human pre	c 232	13	46.4	30	10	ADC55441	ADC55441 Oligonuc1
c 160	13.6	48.6	20	3	AAZ86971	Aaz86971 35S promo	c 233	13	46.4	30	12	ADO79802	ADO79802 CENPC1 PC
c 161	13.6	48.6	20	3	AAZ93200	Aaz93200 35S promo	c 234	13	46.4	36	4	AAV99646	AAV99646 Human tis
c 162	13.6	48.6	20	8	ACD45238	Acd45238 Molecular	c 235	13	46.4	36	4	AAZ03473	AAZ03473 Human t-p
c 163	13.6	48.6	25	9	ACI61431	AcI61431 Cauliflow	c 236	13	46.4	36	4	AAZ03471	AAZ03471 Human t-p
c 164	13.6	48.6	25	9	ACK27910	Ack27910 Human mic	c 237	13	46.4	38	2	AAZ73348	AAZ73348 Probe for
c 165	13.6	48.6	25	9	ACK27910	Ack27910 Human mic	c 238	13	46.4	40	10	AAQ12194	AAQ12194 as-1b mut
c 166	13.6	48.6	25	9	ACI07358	AcI07358 Human mic	c 239	13	46.4	40	10	ADH11033	ADH11033 Human bet
c 167	13.6	48.6	25	9	ACI32629	AcI32629 Human mic	c 240	13	46.4	43	2	AAZ01306	AAZ01306 PCR prime

241	13	46.4	45	2	AAx88768	AAx88768 SV40 olig	C 314	12.8	45.7	38	3	AAA9597	AAa9597 C-K-ras-V
242	13	46.4	45	2	AAx88772	AAx88772 SV40 olig	C 315	12.8	45.7	38	4	AAF82137	Aaf82137 Human C-K
243	13	46.4	47	8	ABT1441	ABt1441 HCV envel	C 316	12.8	45.7	38	4	AAF82140	Aaf82140 Human C-K
244	13	46.4	47	8	AD50591	pGENTE1sh	C 317	12.8	45.7	38	4	RAH13524	Rah13524 Human C-K
245	13	46.4	47	10	ABQ84199	Abq84199 HCV EI-H6	C 318	12.8	45.7	38	4	RAH47355	Rah47355 Human C-K
246	12.8	45.7	20	3	AA229852	AAa229852 Human jun	C 319	12.8	45.7	38	4	RAA14717	Raa14717 Sense str
247	12.8	45.7	20	6	AB194656	ABi94656 Capture o	C 320	12.8	45.7	38	4	RAA14720	Raa14720 Sense str
248	12.8	45.7	20	11	ADP75359	ADp75359 Human ADA	C 321	12.8	45.7	38	4	AAF58372	Aaf58372 Human cel
249	12.8	45.7	21	3	AAZ44473	AAa44473 H. pylori	C 322	12.8	45.7	38	4	RAH74857	Rah74857 PCR prime
250	12.8	45.7	24	4	AA506943	AAa06943 PCR prime	C 323	12.8	45.7	38	4	RAH74855	Rah74855 PCR prime
251	12.8	45.7	24	6	AB185882	ABi85882 Capture o	C 324	12.8	45.7	38	4	RAH74855	Rah74855 PCR prime
252	12.8	45.7	24	6	AB185883	ABi85883 Capture o	C 325	12.8	45.7	38	4	RAH74855	Rah74855 PCR prime
253	12.8	45.7	25	9	ACK13357	ACK13357 Human mic	C 326	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
254	12.8	45.7	25	9	ACI29108	ACi29108 Human mic	C 327	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
255	12.8	45.7	25	9	ACI66658	ACi66658 Human mic	C 328	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
256	12.8	45.7	25	9	ACI66658	ACi66658 Human mic	C 329	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
257	12.8	45.7	25	9	ACI78480	ACi78480 Human mic	C 330	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
258	12.8	45.7	25	9	ACI30301	ACi30301 Human mic	C 331	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
259	12.8	45.7	25	9	ACI66659	ACi66659 Human mic	C 332	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
260	12.8	45.7	25	9	ACI26855	ACi26855 Human mic	C 333	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
261	12.8	45.7	25	9	ACI51673	ACi51673 Human mic	C 334	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
262	12.8	45.7	25	9	ACK16635	ACK16635 Human mic	C 335	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
263	12.8	45.7	25	9	ADAL14320	ADa14320 Human Skp	C 336	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
264	12.8	45.7	26	12	ADP12302	ADp12302 Taqman pr	C 337	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
265	12.8	45.7	27	6	ABK27861	ABk27861 Corn male	C 338	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
266	12.8	45.7	31	12	ADO58802	ADo58802 Human CAR	C 339	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
267	12.8	45.7	33	12	ADK67297	ADk67297 RT-PCR pr	C 340	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
268	12.8	45.7	34	4	AAF58375	Aaf58375 Human cel	C 341	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
269	12.8	45.7	34	4	AAF59717	Aaf59717 Human C-K	C 342	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
270	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 343	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
271	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 344	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
272	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 345	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
273	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 346	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
274	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 347	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
275	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 348	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
276	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 349	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
277	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 350	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
278	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 351	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
279	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 352	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
280	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 353	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
281	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 354	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
282	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 355	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
283	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 356	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
284	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 357	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
285	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 358	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
286	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 359	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
287	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 360	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
288	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 361	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
289	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 362	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
290	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 363	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
291	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 364	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
292	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 365	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
293	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 366	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
294	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 367	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
295	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 368	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
296	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 369	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
297	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 370	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
298	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 371	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
299	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 372	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
300	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 373	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
301	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 374	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
302	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 375	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
303	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 376	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
304	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 377	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
305	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 378	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
306	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 379	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
307	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 380	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
308	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 381	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
309	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 382	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
310	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 383	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
311	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 384	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
312	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 385	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K
313	12.8	45.7	38	2	AAH43984	Aat43984 Octopine	C 386	12.8	45.7	38	4	RAH47374	Rah47374 Human C-K

387	12.6	45.0	35	5	AD04347	Aad04347	Complemen	460	12.4	44.3	40	2	AA87164	Aat87164	IFN-gamma
388	12.6	45.0	36	2	AAV33725	Aav33725	Human thy	c 461	12.4	44.3	40	12	ADI82369	Adi82369	Amorpha-4
C 389	12.6	45.0	36	5	AA04341	Aad04341	MLV parti	c 462	12.4	44.3	41	6	ABZ49616	Abz49616	Human sul
C 390	12.6	45.0	36	12	ADM82777	Adm82777	Extracell	c 463	12.4	44.3	41	5	AAF16714	Aaf16714	dGMP-spec
C 391	12.6	45.0	38	2	AAQ34772	Aaq34772	URR3 gene	c 464	12.4	44.3	44	10	ADG17428	Adg17428	PCR prime
C 392	12.6	45.0	38	2	AAQ37233	Aaq37233	PCR prime	c 465	12.4	44.3	44	10	ADG17428	Adg17427	PCR prime
C 393	12.6	45.0	38	2	AA81856	Aat81856	Human c-m	c 466	12.4	44.3	47	3	AAZ68897	Aaz68897	Human map
C 394	12.6	45.0	38	4	AAH02081	Aah02081	Candida d	c 467	12.4	44.3	50	4	AAH45612	Aah45612	Human SNP
C 395	12.6	45.0	38	6	ACN25781	Acn25781	WNV minus	c 468	12.4	44.3	50	4	AAH45612	Aah45612	Human cys
C 396	12.6	45.0	39	2	AA04347	Aad04347	Complemen	c 469	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 397	12.6	45.0	39	6	ABZ45799	Abz45799	Human car	c 470	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 398	12.6	45.0	41	3	AA000548	Aad00548	Human ade	c 471	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 399	12.6	45.0	41	3	AA000548	Aad00548	Human ade	c 472	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 400	12.6	45.0	42	2	AA000546	Aad00546	Human ade	c 473	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 401	12.6	45.0	42	3	AA000546	Aad00546	Human ade	c 474	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 402	12.6	45.0	42	3	AA000546	Aad00546	Human ade	c 475	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 403	12.6	45.0	42	6	ABU51760	Abu51760	Hydroxypr	c 476	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 404	12.6	45.0	42	6	AA000546	Aad00546	Human ade	c 477	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 405	12.6	45.0	42	6	AA000546	Aad00546	Human ade	c 478	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 406	12.6	45.0	42	6	AA000546	Aad00546	Human ade	c 479	12.4	44.3	50	6	AAH45612	Aah45612	Human cys
C 407	12.6	45.0	47	3	AA266826	Aaz66826	Human map	c 480	12.4	44.3	50	8	ABZ55681	Abz55681	Cystic fi
C 408	12.6	45.0	47	3	AA266826	Aaz66826	Human map	c 481	12.4	44.3	50	8	ABZ55681	Abz55681	Cystic fi
C 409	12.6	45.0	48	6	ACN36134	Acn36134	WNV minus	c 482	12.4	44.3	50	8	ABZ55681	Abz55681	Cystic fi
C 410	12.6	45.0	50	6	ABZ04744	Abz04744	Human leu	c 483	12.4	44.3	50	8	ABZ55681	Abz55681	Cystic fi
C 411	12.4	44.3	20	2	AA0206189	Aa0206189	PCR prime	c 484	12.4	44.3	50	9	ACD28516	Acd28516	Human cys
C 412	12.4	44.3	24	6	AB185306	Ab185306	Capture o	c 485	12.4	44.3	50	9	ACD28516	Acd28516	Human cys
C 413	12.4	44.3	24	6	AB185307	Ab185307	Capture o	c 486	12.4	44.3	50	9	ACD28516	Acd28516	Human cys
C 414	12.4	44.3	24	6	AB185307	Ab185307	Capture o	c 487	12.4	44.3	50	9	ACD28516	Acd28516	Human cys
C 415	12.4	44.3	24	6	AB185307	Ab185307	Capture o	c 488	12.4	44.3	50	9	ACD28516	Acd28516	Human cys
C 416	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 489	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 417	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 490	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 418	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 491	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 419	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 492	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 420	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 493	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 421	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 494	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 422	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 495	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 423	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 496	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 424	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 497	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 425	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 498	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 426	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 499	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 427	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 500	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 428	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 501	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 429	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 502	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 430	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 503	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 431	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 504	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 432	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 505	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 433	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 506	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 434	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 507	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 435	12.4	44.3	25	9	ACI18660	Ac118660	Human mic	c 508	12.4	44.3	50	10	ADD29363	Add29363	Human cys
C 436	12.4	44.3	25	12	ADP15504	Adp15504	Renal cel	c 509	12.2	43.6	18	10	ADP15504	Adp15504	Renal cel
C 437	12.4	44.3	26	4	AAH01109	Aah01109	vanC1/2/3	c 510	12.2	43.6	18	10	ADP15504	Adp15504	Renal cel
C 438	12.4	44.3	27	4	AAH4525	Aah4525	Human Her	c 511	12.2	43.6	19	2	AAH4525	Aah4525	Human Her
C 439	12.4	44.3	30	2	AAQ99481	Aaq99481	Oligonuc1	c 512	12.2	43.6	20	6	ABZ08829	Abz08829	Human CMV
C 440	12.4	44.3	30	2	AAQ99481	Aaq99481	Oligonuc1	c 513	12.2	43.6	20	6	ABZ08829	Abz08829	Human CMV
C 441	12.4	44.3	30	5	AA084633	Aa084633	Mouse LD7	c 514	12.2	43.6	21	4	AAH16687	Aah16687	Cucumis m
C 442	12.4	44.3	30	6	ABK91124	Abk91124	IRE5 muta	c 515	12.2	43.6	21	4	AAH16687	Aah16687	Cucumis m
C 443	12.4	44.3	31	12	ADP46285	Adp46285	PCR prime	c 516	12.2	43.6	22	6	ABZ08829	Abz08829	Human CMV
C 444	12.4	44.3	31	2	AAH30195	Aah30195	p53 gene	c 517	12.2	43.6	22	6	ABZ08829	Abz08829	Human CMV
C 445	12.4	44.3	31	2	AAH30195	Aah30195	p53 gene	c 518	12.2	43.6	22	6	ABZ08829	Abz08829	Human CMV
C 446	12.4	44.3	32	2	AAQ80042	Aaq80042	5' flanki	c 519	12.2	43.6	23	3	AAH78361	Aah78361	Humanised
C 447	12.4	44.3	32	2	AAQ80042	Aaq80042	5' flanki	c 520	12.2	43.6	23	3	AAH78361	Aah78361	Humanised
C 448	12.4	44.3	32	2	AAQ80042	Aaq80042	5' flanki	c 521	12.2	43.6	23	3	AAH78361	Aah78361	Humanised
C 449	12.4	44.3	33	10	ADP75325	Adp75325	PCR prime	c 522	12.2	43.6	24	10	ADP75325	Adp75325	PCR prime
C 450	12.4	44.3	36	3	AAH30642	Aah30642	Human HDG	c 523	12.2	43.6	24	10	ADP75325	Adp75325	PCR prime
C 451	12.4	44.3	36	4	AAH11479	Aah11479	Anti-Her-	c 524	12.2	43.6	25	4	AAH11479	Aah11479	Anti-Her-
C 452	12.4	44.3	37	3	AAH96800	Aah96800	Nucleotid	c 525	12.2	43.6	25	4	AAH11479	Aah11479	Anti-Her-
C 453	12.4	44.3	37	3	AAH96800	Aah96800	Nucleotid	c 526	12.2	43.6	25	4	AAH11479	Aah11479	Anti-Her-
C 454	12.4	44.3	37	3	AAH96800	Aah96800	Nucleotid	c 527	12.2	43.6	25	4	AAH11479	Aah11479	Anti-Her-
C 455	12.4	44.3	37	4	AAH43906	Aah43906	Human apc	c 528	12.2	43.6	25	4	AAH11479	Aah11479	Anti-Her-
C 456	12.4	44.3	37	4	AAH43906	Aah43906	Human apc	c 529	12.2	43.6	25	4	AAH11479	Aah11479	Anti-Her-
C 457	12.4	44.3	37	5	AAH43985	Aah43985	Human apc	c 530	12.2	43.6	26	2	AAH43985	Aah43985	Human apc
C 458	12.4	44.3	38	6	ABU57116	Abu57116	S100 calc	c 531	12.2	43.6	26	6	ADH47822	Adh47822	NOV10 pro
C 459	12.4	44.3	39	4	AAH21383	Aah21383	Human his	c 532	12.2	43.6	26	6	ADH47822	Adh47822	NOV10 pro

C 533	12.2	43.6	26	11	ADP68350	Adp68350 DNA probe	606	12.2	43.6	50	6	ABZ05683	Abz05683 Human leu
C 534	12.2	43.6	26	11	ADP68353	Adp68353 DNA probe	C 607	12	42.9	20	2	AAQ50842	AAQ50842 HTLV-1 de
C 535	12.2	43.6	26	12	ADL25704	Adl25704 Human NOV	608	12	42.9	20	2	AAT63653	Aat63653 Anti-HTLV
C 536	12.2	43.6	26	12	ADL25701	Adl25701 Human NOV	609	12	42.9	20	2	AAV63222	AAV63222 Reverse p
C 537	12.2	43.6	27	10	ADF50351	Adf50351 PCR prime	C 610	12	42.9	20	2	AZ020208	Az020208 PCR prime
C 538	12.2	43.6	28	6	ABK66286	Abk66286 Human gen	611	12	42.9	20	3	RAC93194	Rac93194 Human STA
C 539	12.2	43.6	28	10	ABS58319	Abs58319 Baees 380	612	12	42.9	20	6	AAS96811	Aas96811 Human STA
540	12.2	43.6	29	3	AAA04442	Aaa04442 Polymorph	C 613	12	42.9	20	10	ABZ86199	Abz86199 Human oli
C 541	12.2	43.6	29	6	ABA99925	Ab99925 NDV HN PC	C 614	12	42.9	20	11	ABD22429	Abd22429 Human cat
C 542	12.2	43.6	30	2	AAT31857	Aat31857 Primer fo	C 615	12	42.9	20	12	ADI37414	Adi37414 M. tuberc
C 543	12.2	43.6	30	6	ABT03850	Abt03850 Human RFC	C 616	12	42.9	20	12	ADK96487	Adk96487 Primer of
C 544	12.2	43.6	30	9	ADA19166	Ada19166 Human koh	C 617	12	42.9	20	12	ADL22948	Adl22948 Human gra
C 545	12.2	43.6	31	2	AAT80047	Aat80047 Primer IG	618	12	42.9	20	12	ADK73270	Adk73270 Chimeric
C 546	12.2	43.6	31	2	AAx06483	Aax06483 Human bin	619	12	42.9	20	12	ADK73535	Adk73535 Chimeric
C 547	12.2	43.6	31	4	AAI29870	Aai29870 Human sia	620	12	42.9	21	10	ADF39601	Adf39601 EST gene
C 548	12.2	43.6	33	2	AAQ63306	Aaq63306 Canine ho	C 621	12	42.9	21	10	ACC43493	Acc43493 PCR prime
C 549	12.2	43.6	33	2	AAQ69065	Aaq69065 Primer fo	622	12	42.9	21	11	ADL70122	Adl70122 Human GIP
C 550	12.2	43.6	33	2	AAx85502	Aax85502 PCR prime	623	12	42.9	21	11	ADL70130	Adl70130 Human GIP
C 551	12.2	43.6	33	2	AAx26918	Aax26918 5' PCR pr	624	12	42.9	21	11	ADL70138	Adl70138 Human GIP
C 552	12.2	43.6	33	3	AAA48956	Aaa48956 PCR prime	625	12	42.9	22	2	AAx36858	Aax36858 Human Xli
C 553	12.2	43.6	33	3	AAA48955	Aaa48955 PCR prime	626	12	42.9	22	8	AAAD56067	AAad56067 Primer #2
C 554	12.2	43.6	33	6	ABA92442	Ab92442 Human per	627	12	42.9	22	9	ADA09280	Ada09280 Mouse 14-
C 555	12.2	43.6	35	10	ABV74520	Abv74520 Human G p	628	12	42.9	22	10	ADC23485	Adc23485 Human imm
C 556	12.2	43.6	35	12	ADN11790	Adn11790 PCR prime	C 629	12	42.9	23	12	ADM74245	Adm74245 Human NOV
C 557	12.2	43.6	36	5	AAH78962	Aah78962 Antisense	630	12	42.9	24	5	AAF85529	Aaf85529 Salmonell
C 558	12.2	43.6	36	5	AAH78961	Aah78961 Antisense	631	12	42.9	24	6	ABI83975	Abi83975 Capture o
C 559	12.2	43.6	37	10	ADF50463	Adf50463 PCR prime	C 632	12	42.9	24	6	ABI83974	Abi83974 Capture o
C 560	12.2	43.6	38	3	AAA62474	Aaa62474 Human SEC	633	12	42.9	24	8	ABZ69862	Abz69862 Human gly
C 561	12.2	43.6	38	4	AAH22717	Aah22717 Human sec	634	12	42.9	24	10	ADG17439	Adg17439 PCR prime
C 562	12.2	43.6	38	6	AD303054	Ad303054 Human B7-	635	12	42.9	24	10	ADG17440	Adg17440 PCR prime
C 563	12.2	43.6	38	6	AAAL50540	Aal50540 Human B7-	C 636	12	42.9	25	6	AD37476	Ad37476 Interleuk
C 564	12.2	43.6	40	5	AAF31477	Aaf31477 Primer #3	C 637	12	42.9	25	6	ABV80908	Abv80908 Human HTP
C 565	12.2	43.6	40	5	AAAL40251	Aal40251 Isoprenoi	C 638	12	42.9	25	6	ABV80914	Abv80914 Human HTP
C 566	12.2	43.6	40	10	ADF18589	Adf18589 Mouse zal	639	12	42.9	25	9	ACI07359	Act07359 Human mic
C 567	12.2	43.6	40	10	ADG63342	Adg63342 Human wil	640	12	42.9	25	9	ACI85532	Act85532 Human mic
C 568	12.2	43.6	41	2	AAQ53758	Aaq53758 Ligand fo	641	12	42.9	25	9	ACI85862	Act85862 Human mic
C 569	12.2	43.6	41	2	AAQ7959	Aaq7959 Bacteriop	642	12	42.9	25	9	ACI39290	Act39290 Human mic
C 570	12.2	43.6	41	2	AAV00975	Aav00975 SELEX lig	643	12	42.9	25	9	ACI84993	Act84993 Human mic
C 571	12.2	43.6	41	2	AAV14760	Aav14760 Clone 5,	644	12	42.9	25	9	ACK27911	Ack27911 Human mic
C 572	12.2	43.6	41	2	AAV79835	Aav79835 RNA ligan	645	12	42.9	25	9	ACI56843	Act56843 Human mic
C 573	12.2	43.6	41	3	AAA92935	Aaa92935 High-affi	646	12	42.9	25	9	ACI61430	Act61430 Human mic
C 574	12.2	43.6	41	4	AAH78919	Aah78919 Human spe	647	12	42.9	25	9	ACI56215	Act56215 Human mic
C 575	12.2	43.6	41	4	AAH78920	Aah78920 Human spe	648	12	42.9	25	9	ACK08450	Ack08450 Human mic
C 576	12.2	43.6	41	6	ABK61311	Abk61311 SELEX pro	C 649	12	42.9	25	9	ACI32628	Act32628 Human mic
C 577	12.2	43.6	41	6	ABL61505	Ab161505 Vector pG	650	12	42.9	25	9	ACI37287	Act37287 Human mic
C 578	12.2	43.6	41	6	ABZ44662	Abz44662 Human ATP	C 651	12	42.9	25	9	ACI43865	Act43865 Human mic
C 579	12.2	43.6	41	6	ABZ47159	Abz47159 Human ATP	C 652	12	42.9	25	9	ACI25083	Act25083 Human mic
C 580	12.2	43.6	41	10	ADF67699	Adf67699 Bacteriop	C 653	12	42.9	25	9	ACI76831	Act76831 Human mic
C 581	12.2	43.6	41	12	ADG39247	Adg39247 RNA clone	654	12	42.9	25	9	ACK30936	Ack30936 Human mic
C 582	12.2	43.6	42	6	AAAD41168	Aad41168 Human HGP	655	12	42.9	25	9	ACI38282	Act38282 Human mic
C 583	12.2	43.6	42	9	ACC58890	Acc58890 Human G-p	656	12	42.9	25	9	ACK08451	Ack08451 Human mic
C 584	12.2	43.6	43	2	AAQ53769	Aaq53769 Ligand fo	C 657	12	42.9	25	12	ADP15850	Adp15850 Renal cel
C 585	12.2	43.6	43	2	AAQ53769	Aaq53769 Bacteriop	C 658	12	42.9	25	12	ADP17205	Adp17205 Renal cel
C 586	12.2	43.6	43	2	AAV00986	Aav00986 SELEX lig	C 659	12	42.9	25	12	ADP17204	Adp17204 Renal cel
C 587	12.2	43.6	43	2	AAV14771	Aav14771 Clone 16,	C 660	12	42.9	26	2	AAA70661	Aaa70661 Comamonas
C 588	12.2	43.6	43	2	AAV79846	Aav79846 RNA ligan	C 661	12	42.9	26	12	ADN01584	Adn01584 Enterococ
C 589	12.2	43.6	43	3	AAA92946	Aaa92946 High-affi	C 662	12	42.9	27	10	ACC43497	Acc43497 PCR prime
C 590	12.2	43.6	43	6	ABK61322	Abk61322 SELEX pro	663	12	42.9	27	10	ABZ84245	Abz84245 Toxicolog
C 591	12.2	43.6	43	9	ACD07848	Act07848 Human con	664	12	42.9	27	10	ADO31399	Ado31399 Human CFT
C 592	12.2	43.6	43	9	ACD07849	Act07849 Human con	665	12	42.9	29	3	AAA16766	Aaa16766 Human sec
C 593	12.2	43.6	43	10	ADF67710	Adf67710 Bacteriop	666	12	42.9	29	10	ADDA0784	Add40784 Human ten
C 594	12.2	43.6	43	12	ADG39258	Adg39258 RNA clone	667	12	42.9	30	4	AHA20232	Aha20232 Human ADA
C 595	12.2	43.6	44	2	AAV66743	Aav66743 PCR prime	C 668	12	42.9	30	4	AAH41475	Aah41475 Trichosan
C 596	12.2	43.6	44	6	ADG69920	Adg69920 Aspergill	C 669	12	42.9	30	6	ABA95173	Ab95173 Trichosan
C 597	12.2	43.6	44	10	AAD64573	Aad64573 N-vp16-78	C 670	12	42.9	30	10	ADC77570	Adc77570 Zebrafish
C 598	12.2	43.6	44	11	ADN88854	Adn88854 FAE-N5 pr	671	12	42.9	30	12	ADP08887	Adp08887 PCR prime
C 599	12.2	43.6	45	6	ABK70067	Abk70067 Antibody	672	12	42.9	30	12	ADP45978	Adp45978 PCR prime
C 600	12.2	43.6	45	6	ABK70067	Abk70067 Probe der	C 673	12	42.9	31	3	AAA40389	Aaa40389 A. thalia
C 601	12.2	43.6	45	10	ADL18019	Adl18019 Anti-Ilect	C 674	12	42.9	32	10	ADC03036	Adc03036 Ex vivo s
C 602	12.2	43.6	45	11	ADL35283	Adl35283 Anti-Pcga	C 675	12	42.9	32	12	ADI58711	Adi58711 Human int
C 603	12.2	43.6	48	2	AAV24496	Aav24496 CC49/218	676	12	42.9	33	2	AAT47659	Aat47659 Primer fo
C 604	12.2	43.6	50	2	AAV66651	Aav66651 Anti-huma	677	12	42.9	33	2	AAT45437	Aat45437 Human tra
605	12.2	43.6	50	3	AAA78342	Aaa78342 Humanised	678	12	42.9	33	2	AAT45431	Aat45431 Human tra

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679	12	42.9	33	2	AAx25991	Aax25991 Reverse pr	C 752	12	42.9	49	9	ADAL13269	Adal13269 Human sec
680	12	42.9	33	3	AAZ87136	Aaz87136 Human TRA	C 753	12	42.9	49	9	ADAL13127	Adal13127 Human sec
681	12	42.9	34	3	AAZ57969	Aaz57969 D-JH and	C 754	12	42.9	49	9	ADAL13137	Adal13137 Human sec
682	12	42.9	34	6	AAAL43729	AAal43729 Immunoglo	C 755	12	42.9	49	9	ADAL19955	Adal19955 Human sec
683	12	42.9	34	9	ADA24367	Ada24367 Murine th	C 756	12	42.9	49	9	ADAL17342	Adal17342 Human sec
684	12	42.9	35	2	ADA24367	Ada24367 Murine th	C 757	12	42.9	49	9	ADAL17484	Adal17484 Human sec
685	12	42.9	35	2	AAT63640	Aat63640 Anti-HrLV	C 758	12	42.9	49	9	ADA42987	Ada42987 Human sec
686	12	42.9	35	2	AAx78011	Aax78011 ChimERIC	C 759	12	42.9	49	9	ADA42845	Ada42845 Human sec
687	12	42.9	35	2	AAx23288	Aax23288 TRYI PCR	C 760	12	42.9	49	9	ACD23687	Acd23687 Human PRO
688	12	42.9	36	2	AAAT35381	Aa63544 Oligonuc1	C 761	12	42.9	49	9	ACD23810	Acd23810 Human PRO
689	12	42.9	36	2	AAAT4063	Aat4063 5' primer	C 762	12	42.9	49	10	ADB77905	Adb77905 Human sec
690	12	42.9	36	2	AAV11587	Aav11587 Human che	C 763	12	42.9	49	10	ADB77764	Adb77764 Human sec
691	12	42.9	37	10	ADC03037	Adc03037 Ex vivo s	C 764	12	42.9	49	10	ADB74900	Adb74900 Human sec
692	12	42.9	37	12	ADI58712	Adi58712 Human int	C 765	12	42.9	49	10	ADB75041	Adb75041 Human sec
693	12	42.9	38	3	AAAS1708	Aaa51708 Primer TO	C 766	12	42.9	49	10	ADC28688	Adc28688 Human sec
694	12	42.9	38	6	AAAD2840	Aad2840 TOPP PCR	C 767	12	42.9	49	10	ADC28546	Adc28546 Human sec
695	12	42.9	39	2	AAV64569	Aad2840 TOPP PCR	C 768	12	42.9	49	10	ADC39888	Adc39888 Human sec
696	12	42.9	39	2	AAV64569	Aad2840 TOPP PCR	C 769	12	42.9	49	10	ADC39746	Adc39746 Human sec
697	12	42.9	39	2	AAV64569	Aad2840 TOPP PCR	C 770	12	42.9	49	10	ADC40402	Adc40402 Human sec
698	12	42.9	39	2	AAV64569	Aad2840 TOPP PCR	C 771	12	42.9	49	10	ADC40260	Adc40260 Human sec
699	12	42.9	40	1	AAV71093	Aat71093 Mouse his	C 772	12	42.9	49	10	ADC19226	Adc19226 Human sec
700	12	42.9	40	2	AAV71243	Aat71243 Recombina	C 773	12	42.9	49	10	ADC19084	Adc19084 Human sec
701	12	42.9	40	2	AAV71243	Aat71243 Recombina	C 774	12	42.9	49	10	ADC34526	Adc34526 Human sec
702	12	42.9	41	5	AAAF80122	Aaf80122 PCR prime	C 775	12	42.9	49	10	ADC34384	Adc34384 Human sec
703	12	42.9	41	6	ABN73159	Abn73159 Bovine em	C 776	12	42.9	49	10	ADC29439	Adc29439 Human sec
704	12	42.9	44	2	AAAT00584	Aat00584 Phosphogl	C 777	12	42.9	49	10	ADC29581	Adc29581 Human sec
705	12	42.9	45	2	AAO7609	Aat07609 RT-PCR pr	C 778	12	42.9	49	10	ADC29112	Adc29112 Human sec
706	12	42.9	45	2	AAO91319	Aaq91319 Primer #2	C 779	12	42.9	49	10	ADC28970	Adc28970 Human sec
707	12	42.9	45	2	AAO91318	Aaq91318 Primer #2	C 780	12	42.9	49	10	ADC40855	Adc40855 Human sec
708	12	42.9	45	2	AAO0677	Aat00677 Primer #2	C 781	12	42.9	49	10	ADC40997	Adc40997 Human sec
709	12	42.9	47	2	AAQ91320	Aaq91320 Primer #2	C 782	12	42.9	49	10	ADC19512	Adc19512 Human sec
710	12	42.9	48	2	AAQ91317	Aaq91317 Primer #2	C 783	12	42.9	49	10	ADC19654	Adc19654 Human sec
711	12	42.9	48	3	AAAF7332	Aaf7332 Human clo	C 784	12	42.9	49	10	ADC34102	Adc34102 Human sec
712	12	42.9	48	4	AAAF26385	Aaf26385 Covalenti	C 785	12	42.9	49	10	ADC33960	Adc33960 Human sec
713	12	42.9	48	6	ABK23388	Abk23388 Human ERG	C 786	12	42.9	49	10	ADC13030	Adc13030 Human sec
714	12	42.9	48	6	ACN36973	Acn36973 WNV minus	C 787	12	42.9	49	10	ADC13172	Adc13172 Human sec
715	12	42.9	49	3	AAx52504	Aax52504 Probe 309	C 788	12	42.9	49	10	ADC12482	Adc12482 Human sec
716	12	42.9	49	3	AAx78692	Aaf78692 Human PRO	C 789	12	42.9	49	10	ADC12624	Adc12624 Human sec
717	12	42.9	49	4	AAAF72662	Aaf72662 Human PRO	C 790	12	42.9	49	10	ADD05037	Add05037 Human sec
718	12	42.9	49	8	ACA60196	Aca60196 Human sec	C 791	12	42.9	49	10	ADD05179	Add05179 Human sec
719	12	42.9	49	8	ACA60319	Aca60319 Human sec	C 792	12	42.9	49	10	ADD04185	Add04185 Human sec
720	12	42.9	49	8	ACD07720	Acd07720 Novel hum	C 793	12	42.9	49	10	ADD04043	Add04043 Human sec
721	12	42.9	49	8	ACD07596	Acd07596 Novel hum	C 794	12	42.9	49	10	ADD03619	Add03619 Human sec
722	12	42.9	49	8	ABX71768	Abx71768 Human sec	C 795	12	42.9	49	10	ADD03761	Add03761 Human sec
723	12	42.9	49	8	ABX71644	Abx71644 Human sec	C 796	12	42.9	49	10	ADJ26401	Adj26401 Human sec
724	12	42.9	49	8	ACH07099	Ach07099 Human sec	C 797	12	42.9	49	10	ADJ26543	Adj26543 Human sec
725	12	42.9	49	8	ACH06976	Ach06976 Human sec	C 798	12	42.9	49	10	ADJ26543	Adj26543 Human sec
726	12	42.9	49	8	ABX96336	Abx96336 Human sec	C 799	12	42.9	49	10	ADJ26543	Adj26543 Human sec
727	12	42.9	49	8	ACA05657	Aca05657 Human sec	C 800	12	42.9	49	10	ADJ26543	Adj26543 Human sec
728	12	42.9	49	8	ACA05534	Aca05534 Human sec	C 801	12	42.9	49	10	ADJ26543	Adj26543 Human sec
729	12	42.9	49	8	ACD20201	Acd20201 Human sec	C 802	12	42.9	49	10	ADJ26543	Adj26543 Human sec
730	12	42.9	49	8	ACD20201	Acd20201 Human sec	C 803	12	42.9	49	10	ADJ26543	Adj26543 Human sec
731	12	42.9	49	8	ACA55004	Aca55004 Novel sec	C 804	12	42.9	49	10	ADJ26543	Adj26543 Human sec
732	12	42.9	49	8	ACA55128	Aca55128 Novel sec	C 805	12	42.9	49	10	ADJ26543	Adj26543 Human sec
733	12	42.9	49	8	ACD19839	Acd19839 Human sec	C 806	12	42.9	49	10	ADJ26543	Adj26543 Human sec
734	12	42.9	49	9	ACD19839	Acd19839 Human sec	C 807	12	42.9	49	10	ADJ26543	Adj26543 Human sec
735	12	42.9	49	9	ADB29443	Adb29443 Human sec	C 808	12	42.9	49	10	ADJ26543	Adj26543 Human sec
736	12	42.9	49	9	ADB29443	Adb29443 Human sec	C 809	12	42.9	49	10	ADJ26543	Adj26543 Human sec
737	12	42.9	49	9	ADA18441	Ada18441 Human sec	C 810	12	42.9	49	10	ADJ26543	Adj26543 Human sec
738	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 811	12	42.9	49	10	ADJ26543	Adj26543 Human sec
739	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 812	12	42.9	49	10	ADJ26543	Adj26543 Human sec
740	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 813	12	42.9	49	10	ADJ26543	Adj26543 Human sec
741	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 814	12	42.9	49	10	ADJ26543	Adj26543 Human sec
742	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 815	12	42.9	49	10	ADJ26543	Adj26543 Human sec
743	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 816	12	42.9	49	10	ADJ26543	Adj26543 Human sec
744	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 817	12	42.9	49	10	ADJ26543	Adj26543 Human sec
745	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 818	12	42.9	49	10	ADJ26543	Adj26543 Human sec
746	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 819	12	42.9	49	10	ADJ26543	Adj26543 Human sec
747	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 820	12	42.9	49	10	ADJ26543	Adj26543 Human sec
748	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 821	12	42.9	49	10	ADJ26543	Adj26543 Human sec
749	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 822	12	42.9	49	10	ADJ26543	Adj26543 Human sec
750	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 823	12	42.9	49	10	ADJ26543	Adj26543 Human sec
751	12	42.9	49	9	ADA18299	Ada18299 Human sec	C 824	12	42.9	49	10	ADJ26543	Adj26543 Human sec

C 825	12	42.9	49	12	ADF74057	Adf74057 Human sec	898	11.8	42.1	23	6	ABK97004	Abk97004 Synthetic
C 826	12	42.9	49	12	ADF73633	Adf73633 Human sec	899	11.8	42.1	23	6	ABK97020	Abk97020 Synthetic
C 827	12	42.9	49	12	ADF73491	Adf73491 Human sec	900	11.8	42.1	23	6	ABK96988	Abk96988 Synthetic
C 828	12	42.9	49	12	ADG92334	Adg92334 Human sec	901	11.8	42.1	23	6	ABK97032	Abk97032 Synthetic
C 829	12	42.9	49	12	ADG92476	Adg92476 Human sec	902	11.8	42.1	23	12	ADJ95881	Adj95881 Cell prol
C 830	12	42.9	49	12	ADG92903	Adg92903 Human sec	903	11.8	42.1	23	12	ADJ95791	Adj95791 Cell prol
C 831	12	42.9	49	12	ADG92761	Adg92761 Human sec	904	11.8	42.1	23	12	ADJ95803	Adj95803 Cell prol
C 832	12	42.9	49	12	ADH20692	Adh20692 Human sec	905	11.8	42.1	23	12	ADJ95839	Adj95839 Cell prol
C 833	12	42.9	49	12	ADH20550	Adh20550 Human sec	906	11.8	42.1	23	12	ADJ95759	Adj95759 Cell prol
C 834	12	42.9	49	12	ADH07547	Adh07547 Human sec	907	11.8	42.1	23	12	ADJ95775	Adj95775 Cell prol
C 835	12	42.9	49	12	ADH07405	Adh07405 Human sec	908	11.8	42.1	24	2	AAT43346	Aat43346 Primer GS
C 836	12	42.9	49	12	ADH60092	Adh60092 Human sec	C 909	11.8	42.1	24	2	AAT95061	Aat95061 Primer fo
C 837	12	42.9	49	12	ADH59950	Adh59950 Human sec	910	11.8	42.1	24	2	AAX90069	Aax90069 Fervidoba
C 838	12	42.9	49	12	ADH06978	Adh06978 Human sec	911	11.8	42.1	24	6	ABK97006	Abk97006 Synthetic
C 839	12	42.9	49	12	ADH07120	Adh07120 Human sec	912	11.8	42.1	24	6	ABK97022	Abk97022 Synthetic
C 840	12	42.9	49	12	ADI18720	Adi18720 Human sec	913	11.8	42.1	24	6	ABK96990	Abk96990 Synthetic
C 841	12	42.9	49	12	ADI18862	Adi18862 Human sec	914	11.8	42.1	24	6	ABK97112	Abk97112 Synthetic
C 842	12	42.9	49	12	ADI65582	Adi65582 Human sec	915	11.8	42.1	24	6	ABK97034	Abk97034 Synthetic
C 843	12	42.9	49	12	ADI65440	Adi65440 Human sec	916	11.8	42.1	24	6	ABK97070	Abk97070 Synthetic
C 844	12	42.9	49	12	ADI37841	Adi37841 Human sec	C 917	11.8	42.1	24	6	ABI89312	Abi89312 Capture o
C 845	12	42.9	49	12	ADI37699	Adi37699 Human sec	918	11.8	42.1	24	6	ABI89313	Abi89313 Capture o
C 846	12	42.9	49	12	ADH37499	Adh37499 Human sec	919	11.8	42.1	24	12	ADJ95761	Adj95761 Cell prol
C 847	12	42.9	49	12	ADH97641	Adh97641 Human sec	920	11.8	42.1	24	12	ADJ95805	Adj95805 Cell prol
C 848	12	42.9	49	12	ADI65867	Adi65867 Human sec	921	11.8	42.1	24	12	ADJ95883	Adj95883 Cell prol
C 849	12	42.9	49	12	ADI66009	Adi66009 Human sec	922	11.8	42.1	24	12	ADJ95777	Adj95777 Cell prol
C 850	12	42.9	49	12	ADH60610	Adh60610 Human sec	923	11.8	42.1	24	12	ADJ95841	Adj95841 Cell prol
C 851	12	42.9	49	12	ADH60752	Adh60752 Human sec	924	11.8	42.1	24	12	ADJ95793	Adj95793 Cell prol
C 852	12	42.9	49	12	ADJ99667	Adj99667 Human sec	C 925	11.8	42.1	25	2	AAT65132	Aat65132 Primer 31
C 853	12	42.9	49	12	ADJ99809	Adj99809 Human sec	C 926	11.8	42.1	25	2	AAH74103	Aah74103 Oligonucl
C 854	12	42.9	49	12	ADL08860	Adl08860 Human sec	927	11.8	42.1	25	6	ABK89633	Abk89633 Chimeric
C 855	12	42.9	49	12	ADL09002	Adl09002 Human sec	928	11.8	42.1	25	6	ABNI13636	Abni13636 Human GDM
C 856	12	42.9	49	12	ADM25201	Adm25201 Human sec	929	11.8	42.1	25	6	ABNI13635	Abni13635 Human GDM
C 857	12	42.9	49	12	ADM25343	Adm25343 Human sec	930	11.8	42.1	25	6	ABNI13634	Abni13634 Human GDM
C 858	12	42.9	49	12	ADM29951	Adm29951 Human sec	931	11.8	42.1	25	6	ABK96992	Abk96992 Synthetic
C 859	12	42.9	49	12	ADM30093	Adm30093 Human sec	C 932	11.8	42.1	25	6	ABK97037	Abk97037 Synthetic
C 860	12	42.9	49	12	ADO06415	Ado06415 Human PRO	933	11.8	42.1	25	6	ABK97036	Abk97036 Synthetic
C 861	12	42.9	49	12	ADO06273	Ado06273 Human PRO	934	11.8	42.1	25	6	ABK97072	Abk97072 Synthetic
C 862	12	42.9	50	4	AAL31007	Aal31007 Human SNP	C 935	11.8	42.1	25	6	ABK97115	Abk97115 Synthetic
C 863	12	42.9	50	6	ABZ06873	Abz06873 Human leu	936	11.8	42.1	25	6	ABK97008	Abk97008 Synthetic
C 864	12	42.9	50	6	ABZ04772	Abz04772 Human leu	937	11.8	42.1	25	6	ABK97024	Abk97024 Synthetic
C 865	12	42.9	50	6	ABZ06483	Abz06483 Human leu	938	11.8	42.1	25	6	ABK97114	Abk97114 Synthetic
C 866	12	42.9	50	6	ABZ01039	Abz01039 Human leu	939	11.8	42.1	25	8	ACD00055	Acdo0055 G-protein
C 867	12	42.9	50	6	ABZ00259	Abz00259 Human leu	940	11.8	42.1	25	8	ACD00056	Acdo0056 G-protein
C 868	12	42.9	50	6	ABZ03066	Abz03066 Human leu	941	11.8	42.1	25	8	ACD00057	Acdo0057 G-protein
C 869	12	42.9	50	6	ABZ02986	Abz02986 Human leu	942	11.8	42.1	25	9	ACI15692	Acti15692 Human mic
C 870	12	42.9	50	10	ADD31791	Add31791 Anti-CEA	C 943	11.8	42.1	25	9	ACI17719	Acti17719 Human mic
C 871	12	42.9	50	12	ADP10275	Adp10275 50-mer ol	C 944	11.8	42.1	25	9	ACI56965	Acti56965 Human mic
C 872	11.8	42.1	17	8	ACD59071	Acd59071 HCV DNaz	945	11.8	42.1	25	9	ACI09842	Acti09842 Human mic
C 873	11.8	42.1	17	8	ACD63598	Acd63598 HCV minus	946	11.8	42.1	25	9	ACI73063	Acti73063 Human mic
C 874	11.8	42.1	17	12	ADI86156	Adi86156 HCV DNaz	947	11.8	42.1	25	9	ACK25403	Actk25403 Human mic
C 875	11.8	42.1	17	12	ADI83907	Adi83907 HCV DNaz	948	11.8	42.1	25	9	ACK05762	Actk05762 Human mic
C 876	11.8	42.1	18	2	AAZ41099	Aaz41099 Human G-a	C 949	11.8	42.1	25	9	ACI37838	Acti37838 Human mic
C 877	11.8	42.1	18	2	AAZ19470	Aaz19470 Human G-a	C 950	11.8	42.1	25	9	ACI38426	Acti38426 Human mic
C 878	11.8	42.1	19	5	AAF26278	Aaf26278 Human egf	C 951	11.8	42.1	25	9	ACK00994	Actk00994 Human mic
C 879	11.8	42.1	19	5	AAF26269	Aaf26269 Human egf	C 952	11.8	42.1	25	9	ACK20213	Actk20213 Human mic
C 880	11.8	42.1	19	12	ADQ27840	Adq27840 RNA inter	C 953	11.8	42.1	25	9	ACI50116	Acti50116 Human mic
C 881	11.8	42.1	20	2	AAQ53932	Aaq53932 Synthetic	C 954	11.8	42.1	25	9	ACI17059	Acti17059 Human mic
C 882	11.8	42.1	20	3	AAAS1711	Aas1711 R17 ligan	C 955	11.8	42.1	25	9	ACI32119	Acti32119 Human mic
C 883	11.8	42.1	20	5	AAF90588	Aaf90588 Human zap	C 956	11.8	42.1	25	9	ACI12041	Acti12041 Human mic
C 884	11.8	42.1	20	6	ADQ36758	Adq36758 Human RIN	C 957	11.8	42.1	25	9	ACI45908	Acti45908 Human mic
C 885	11.8	42.1	20	6	ADQ28215	Adq28215 Alphaviru	C 958	11.8	42.1	25	9	ACI56964	Acti56964 Human mic
C 886	11.8	42.1	20	11	ABZ32478	Abz32478 Human oli	C 959	11.8	42.1	25	9	ACI88756	Acti88756 Human mic
C 887	11.8	42.1	20	11	ABD28708	Abd28708 AA48261-	C 960	11.8	42.1	25	9	ACI43709	Acti43709 Human mic
C 888	11.8	42.1	20	12	ADK96098	Adk96098 Primer of	C 961	11.8	42.1	25	9	ACK23753	Actk23753 Human mic
C 889	11.8	42.1	21	3	AAAL6736	Aaal6736 Human sec	C 962	11.8	42.1	25	9	ACI09566	Acti09566 Human mic
C 890	11.8	42.1	21	8	ABZ81891	Abz81891 Primer Ba	C 963	11.8	42.1	25	9	ACI79116	Acti79116 Human mic
C 891	11.8	42.1	21	12	ADG64974	Adg64974 Primer #5	C 964	11.8	42.1	25	9	ACI42014	Acti42014 Human mic
C 892	11.8	42.1	21	12	ADK96320	Adk96320 Primer of	C 965	11.8	42.1	25	9	ACI78057	Acti78057 Human mic
C 893	11.8	42.1	22	2	AAQ88191	Aaq88191 C1 inhibi	C 966	11.8	42.1	25	9	ACK04749	Actk04749 Human mic
C 894	11.8	42.1	22	2	AAQ90141	Aaq90141 Transthyr	C 967	11.8	42.1	25	9	ACK05136	Actk05136 Human mic
C 895	11.8	42.1	22	10	ADA43545	Ada43545 Mouse PAP	C 968	11.8	42.1	25	9	ACI08930	Acti08930 Human mic
C 896	11.8	42.1	23	6	ABK97110	Abk97110 Synthetic	C 969	11.8	42.1	25	9	ACI39054	Acti39054 Human mic
C 897	11.8	42.1	23	6	ABK97068	Abk97068 Synthetic	970	11.8	42.1	25	9	ACI47841	Acti47841 Human mic

c	971	11.8	42.1	25	9	ACI89056	AcI89056 Human mic
c	972	11.8	42.1	25	9	ACI91715	AcI91715 Human mic
c	973	11.8	42.1	25	9	ACI23114	AcI23114 Human mic
c	974	11.8	42.1	25	9	ACI39682	AcI39682 Human mic
c	975	11.8	42.1	25	9	ACH64079	ACH64079 DNA targe
c	976	11.8	42.1	25	10	ADF63356	ADF63356 Human PCC
c	977	11.8	42.1	25	10	ADF63357	ADF63357 Human PCC
c	978	11.8	42.1	25	10	ADF63358	ADF63358 Human PCC
c	979	11.8	42.1	25	12	ADJ95808	ADJ95808 Cell prol
c	980	11.8	42.1	25	12	ADJ95808	ADJ95808 Cell prol
c	981	11.8	42.1	25	12	ADJ95886	ADJ95886 Cell prol
c	982	11.8	42.1	25	12	ADJ95795	ADJ95795 Cell prol
c	983	11.8	42.1	25	12	ADJ95763	ADJ95763 Cell prol
c	984	11.8	42.1	25	12	ADJ95885	ADJ95885 Cell prol
c	985	11.8	42.1	25	12	ADJ95779	ADJ95779 Cell prol
c	986	11.8	42.1	25	12	ADJ95807	ADJ95807 Cell prol
c	987	11.8	42.1	25	12	ADJ95843	ADJ95843 Cell prol
c	988	11.8	42.1	26	6	AA147432	AA147432 Human Slo
c	989	11.8	42.1	26	6	AD117407	AD117407 PCR prime
c	990	11.8	42.1	26	12	ADN42496	ADN42496 Human NOV
c	991	11.8	42.1	27	2	AAQ53402	AAQ53402 Mouse bet
c	992	11.8	42.1	28	3	AAA98365	AAA98365 D. vulgar
c	993	11.8	42.1	28	8	ABL35176	ABL35176 Immunosti
c	994	11.8	42.1	28	8	AD53890	AD53890 PCR prime
c	995	11.8	42.1	28	8	AD53889	AD53889 PCR prime
c	996	11.8	42.1	28	10	ADB89206	ADB89206 Human Gal
c	997	11.8	42.1	28	10	ADC24553	ADC24553 Human Gal
c	998	11.8	42.1	28	10	AD67823	AD67823 Human Gia
c	999	11.8	42.1	28	10	AD810536	AD810536 Minicell
c	1000	11.8	42.1	28	10	AD811458	AD811458 Human Gal
c				28	10	AD812636	AD812636 Human Gal

ALIGNMENTS

RESULT 1	ADAI3880/c	
ID	ADAI3880 standard; RNA; 21 BP.	
XX		
AC	ADAI3880;	
XX		
DT	20-NOV-2003 (first entry)	
XX		
DE	Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:217.	
XX		
KW	double-stranded short interfering nucleic acid;	
KW	short interfering nucleic acid; siNA; expression; replication;	
KW	inhibition; RNA interference; virucide; anti-HIV; hepatotropic;	
KW	antiinflammatory; plant; antiviral; vasotropic; neuroprotective;	
KW	cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;	
KW	endocrine; viral infection; hepatitis B; hepatitis C; HIV;	
KW	herpes simplex; cytomegalovirus; human papillomavirus;	
KW	respiratory syncytial virus; influenza virus; restenosis;	
KW	neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;	
KW	pulmonary; renal; liver; mitochondrial; reproductive disease;	
KW	chemical modification; ss.	
OS	Synthetic.	
XX		
PN	WO2003070918-A2.	
XX		
PD	28-AUG-2003.	
XX		
PF	20-FEB-2003; 2003WO-US005346.	
XX		
PR	20-FEB-2002; 2002US-0358580P.	
PR	11-MAR-2002; 2002US-0363124P.	
PR	06-JUN-2002; 2002US-0386782P.	
PR	29-AUG-2002; 2002US-0406784P.	
PR	03-SEP-2002; 2002US-0408378P.	
PR	03-SEP-2002; 2002US-0409293P.	
PR	15-JAN-2003; 2003US-0440129P.	
XX		

PA	(RIBO-) RIBOZYME PHARM INC.	
XX		
PI	Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;	
PI	Morrissey D, Fornaugh K, Mokler V, Jamison S;	
XX		
DR	WPI; 2003-689785/65.	
XX		
PT	New short interfering nucleic acid containing no ribonucleotides, useful	
PT	e.g. for treating viral infection, downregulates expression of target	
PT	gene or RNA.	
XX		
PS	Example 4; Page 139; 20app; English.	
XX		
CC	The present invention describes a double-stranded short interfering	
CC	nucleic acid (siNA) that downregulates expression of a target gene, where	
CC	the siNA molecule comprises no ribonucleotides and each strand of the	
CC	double-stranded siNA comprises about 21 nucleotides. Also described: (1)	
CC	a siNA molecule that inhibits expression of target RNA; (2) a siNA	
CC	molecule that inhibits replication of a virus and optionally does not	
CC	require presence of a ribonucleotide for inhibition; (3) a siNA molecule	
CC	that inhibits expression of a target gene and does not require presence	
CC	of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits	
CC	expression of a target gene by mediating RNA interference; and (5) a	
CC	method for modulating expression of a gene in a cell using siNA	
CC	molecules. siNA's can have virucide, anti-HIV, hepatotropic,	
CC	antiinflammatory, plant antiviral, vasotropic, neuroprotective,	
CC	cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic	
CC	and endocrine activities. The siNA's are useful for downregulating	
CC	expression of target genes, inhibiting expression of target RNA, and	
CC	inhibiting replication of a virus. siNA molecules can be used: (a) for	
CC	therapy of any disorder that responds to modulation of gene expression,	
CC	especially animal and plant viral infections, specifically hepatitis B or	
CC	C; HIV; herpes simplex; cytomegalo; human papilloma; respiratory	
CC	syntical or influenza viruses, and also many other diseases such as	
CC	restenosis, neurodegeneration, cancers, and cardiovascular, neurological,	
CC	prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,	
CC	endocrine or reproductive diseases; and (b) for diagnosis, target	
CC	validation, genomic discovery, genetic engineering, pharmacogenomics and	
CC	analysis of gene function. Chemical modification of siNA molecules	
CC	improves interfering activity; stability; cellular uptake; binding	
CC	affinity and/or mediates increased polymerase activity. siNA may be	
CC	designed to target many related genes containing a conserved sequence.	
CC	The present sequence represents a siNA oligonucleotide sequence, which is	
CC	used in the exemplification of the present invention.	
XX		
SQ	Sequence 21 BP; 7 A; 8 C; 3 G; 0 T; 3 U; 0 Other;	

Query Match	75.0%;	Score 21;	DB 9;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 3.4;		
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	8	GGGATAGTCCGTCATGGGTT	28
Db	21	GGGATAGTCCGTCATGGGTT	1

RESULT 2	
ADAI3871	
ID	ADAI3871 standard; RNA; 21 BP.
XX	
AC	ADAI3871;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:208.
XX	
KW	double-stranded short interfering nucleic acid;
KW	short interfering nucleic acid; siNA; expression; replication;
KW	inhibition; RNA interference; virucide; anti-HIV; hepatotropic;
KW	antiinflammatory; plant; antiviral; vasotropic; neuroprotective;
KW	cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;
KW	endocrine; viral infection; hepatitis B; hepatitis C; HIV;
KW	herpes simplex; cytomegalovirus; human papillomavirus;

KW respiratory syncytial virus; influenza virus; restenosis;
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;
KW pulmonary; renal; liver; mitochondrial; reproductive disease;
KW chemical modification; ss.
OS Synthetic.
XX
PN WO2003070918-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005346.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;
XX
XX WPI; 2003-689785/65.
XX
XX New short interfering nucleic acid containing no ribonucleotides, useful
PT e.g. for treating viral infection, downregulates expression of target
PT gene or RNA.
XX
XX Example 4; Page 138; 204pp; English.
XX
XX The present invention describes a double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of a target gene, where
CC the siNA molecule comprises no ribonucleotides and each strand of the
CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)
CC a siNA molecule that inhibits expression of target RNA; (2) a siNA
CC molecule that inhibits replication of a virus and optionally does not
CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule
CC that inhibits expression of a target gene and does not require presence
CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits
CC expression of a target gene by mediating RNA interference; and (5) a
CC method for modulating expression of a gene in a cell using siNA
CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,
CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,
CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic
CC expression of target genes, inhibiting expression of target RNA, and
CC inhibiting replication of a virus. siNA molecules can be used: (a) for
CC therapy of any disorder that responds to modulation of gene expression,
CC especially animal and plant viral infections, specifically hepatitis B or
CC C; HIV; herpes simplex; cytomegalo; human papilloma; respiratory
CC syncytial or influenza viruses, and also many other diseases such as
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
CC endocrine or reproductive diseases; and (b) for diagnosis, target
CC validation, genomic discovery, genetic engineering, pharmacogenomics and
CC analysis of gene function. Chemical modification of siNA molecules
CC improves interfering activity; stability; cellular uptake; binding
CC affinity and/or mediates increased polymerase activity. siNA may be
CC designed to target many related genes containing a conserved sequence.
CC The present sequence represents a siNA oligonucleotide sequence, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;
Query Match 75.0%; Score 21; DB 9; Length 21;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Oy 8 GGGATAGTCGCTCATGGTGT 28

||||:||||:||||:||||:||||:
Db 1 GCGAUGACGCCGCAUGGUGUU 21
RESULT 3
ADA13872
ID ADA13872 standard; RNA; 21 BP.
XX
XX ADA13872;
XX
XX 20-NOV-2003 (first entry)
XX
XX Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:209.
XX
XX double-stranded short interfering nucleic acid;
KW short interfering nucleic acid; siNA; expression; replication;
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;
KW cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;
KW herpes simplex; cytomegalovirus; human papillomavirus;
KW respiratory syncytial virus; influenza virus; restenosis;
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;
KW pulmonary; renal; liver; mitochondrial; reproductive disease;
KW chemical modification; ss.
XX
XX Synthetic.
XX
XX WO2003070918-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005346.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;
XX
XX WPI; 2003-689785/65.
XX
XX New short interfering nucleic acid containing no ribonucleotides, useful
PT e.g. for treating viral infection, downregulates expression of target
PT gene or RNA.
XX
XX Example 4; Page 138; 204pp; English.
XX
XX The present invention describes a double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of a target gene, where
CC the siNA molecule comprises no ribonucleotides and each strand of the
CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)
CC a siNA molecule that inhibits expression of target RNA; (2) a siNA
CC molecule that inhibits replication of a virus and optionally does not
CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule
CC that inhibits expression of a target gene and does not require presence
CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits
CC expression of a target gene by mediating RNA interference; and (5) a
CC method for modulating expression of a gene in a cell using siNA
CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,
CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,
CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic
CC expression of target genes, inhibiting expression of target RNA, and
CC inhibiting replication of a virus. siNA molecules can be used: (a) for
CC therapy of any disorder that responds to modulation of gene expression,
CC especially animal and plant viral infections, specifically hepatitis B or
CC C; HIV; herpes simplex; cytomegalo; human papilloma; respiratory
CC syncytial or influenza viruses, and also many other diseases such as
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
CC endocrine or reproductive diseases; and (b) for diagnosis, target
CC validation, genomic discovery, genetic engineering, pharmacogenomics and
CC analysis of gene function. Chemical modification of siNA molecules
CC improves interfering activity; stability; cellular uptake; binding
CC affinity and/or mediates increased polymerase activity. siNA may be
CC designed to target many related genes containing a conserved sequence.
CC The present sequence represents a siNA oligonucleotide sequence, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;
Query Match 75.0%; Score 21; DB 9; Length 21;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Oy 8 GGGATAGTCGCTCATGGTGT 28

Wed Nov 24 08:46:11 2004

CC especially animal and plant viral infections, specifically hepatitis B or
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory
 CC syncytial or influenza viruses, and also many other diseases such as
 CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
 CC endocrine or reproductive diseases; and (b) for diagnosis, target
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and
 CC analysis of gene function. Chemical modification of siRNA molecules
 CC improves interfering activity; stability; cellular uptake; binding
 CC affinity and/or mediates increased polymerase activity. siRNA may be
 CC designed to target many related genes containing a conserved sequence.
 CC The present sequence represents a siRNA oligonucleotide sequence, which is
 CC used in the exemplification of the present invention.

XX SQ Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;
 Query Match 75.0%; Score 21; DB 9; Length 21;
 Best Local Similarity 66.7%; Pred. No. 3.4;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 7 TGGGATAGTCCGTCATGGTGT 27
 Db 1 UGGGAUAGUCCGCAUGGUGU 21

RESULT 4
 ADAL13873
 ID ADAL13873 standard; RNA; 21 BP.
 XX AC ADAL13873;
 XX DT 20-NOV-2003 (first entry)
 XX DE Short interfering nucleic acid (siRNA) oligonucleotide SEQ ID NO:210.
 XX KW double-stranded short interfering nucleic acid;
 KW short interfering nucleic acid; siRNA; expression; replication;
 KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;
 KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;
 KW cystostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;
 KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;
 KW herpes simplex; cytomegalovirus; human papillomavirus;
 KW respiratory syncytial virus; influenza virus; restenosis;
 KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;
 KW pulmonary; renal; liver; mitochondrial; reproductive disease;
 KW chemical modification; ss.
 XX OS Synthetic.
 XX PN WO2003070918-A2.
 XX PD 28-AUG-2003.
 XX PF 20-FEB-2003; 2003WO-US005346.
 XX PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX PA Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;
 XX PI Morrissey D, Fosnaugh K, Mokier V, Jamison S;
 XX WI; 2003-689785/65.
 XX New short interfering nucleic acid containing no ribonucleotides, useful
 XX e.g. for treating viral infection, downregulates expression of target
 XX gene or RNA.
 XX PT

XX Example 4; Page 138; 204pp; English.
 XX The present invention describes a double-stranded short interfering
 CC nucleic acid (siRNA) that downregulates expression of a target gene, where
 CC the siRNA molecule comprises no ribonucleotides and each strand of the
 CC double-stranded siRNA comprises about 21 nucleotides. Also described: (1)
 CC a siRNA molecule that inhibits expression of target RNA; (2) a siRNA
 CC molecule that inhibits replication of a virus and optionally does not
 CC require presence of a ribonucleotide for inhibition; (3) a siRNA molecule
 CC that inhibits expression of a target gene and does not require presence
 CC of a ribonucleotide for inhibition; (4) a siRNA molecule that inhibits
 CC expression of a target gene by mediating RNA interference; and (5) a
 CC method for modulating expression of a gene in a cell using siRNA
 CC molecules. siRNA's can have virucide, anti-HIV, hepatotropic,
 CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,
 CC cystostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic
 CC and endocrine activities. The siRNA's are useful for downregulating
 CC expression of target genes, inhibiting expression of target RNA, and
 CC inhibiting replication of a virus. siRNA molecules can be used: (a) for
 CC therapy of any disorder that responds to modulation of gene expression,
 CC especially animal and plant viral infections, specifically hepatitis B or
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory
 CC syncytial or influenza viruses, and also many other diseases such as
 CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
 CC endocrine or reproductive diseases; and (b) for diagnosis, target
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and
 CC analysis of gene function. Chemical modification of siRNA molecules
 CC improves interfering activity; stability; cellular uptake; binding
 CC affinity and/or mediates increased polymerase activity. siRNA may be
 CC designed to target many related genes containing a conserved sequence.
 CC The present sequence represents a siRNA oligonucleotide sequence, which is
 CC used in the exemplification of the present invention.

XX SQ Sequence 21 BP; 3 A; 3 C; 9 G; 0 T; 6 U; 0 Other;
 Query Match 75.0%; Score 21; DB 9; Length 21;
 Best Local Similarity 71.4%; Pred. No. 3.4;
 Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 6 GTGGGATAGTCCGTCATGGTGT 26
 Db 1 GUGGAUAGUCCGCAUGGUG 21

RESULT 5
 ADF52874
 ID ADF52874 standard; RNA; 21 BP.
 XX AC ADF52874;
 XX DT 12-FEB-2004 (first entry)
 XX DE Hepatitis C virus modified siRNA sense strand SeqID1465.
 XX KW short interfering nucleic acid; siRNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cystostatic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.
 XX OS Synthetic.
 XX OS Hepatitis C virus.
 XX PN WO2003070750-A2.
 XX PD 28-AUG-2003.
 XX PF 20-FEB-2003; 2003WO-US005043.
 XX PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002WO-US009187.
 XX PT

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PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 1465; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure, diagnosis, target
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains. NOTE: This sequence may contain one or more of several
XX modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
XX (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
XX base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
XX modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 75.0%; Score 21; DB 10; Length 21;
XX Best Local Similarity 66.7%; Pred. No. 3.4;
XX Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX
QY 8 GGGATAGTCCTCATGGTGT 28
DB 1 GGGGAUAGUCCGCAUGGUGU 21
XX
RESULT 6
ADF52876
ID ADF52876 standard; RNA; 21 BP.
XX
XX ADF52876;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus modified siNA sense strand SeqID1467.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Synthetic.
XX
XX Hepatitis C virus.
XX
XX WO2003070750-A2.

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XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 1467; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure, diagnosis, target
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains. NOTE: This sequence may contain one or more of several
XX modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
XX (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
XX base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
XX modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX Sequence 21 BP; 3 A; 3 C; 9 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 75.0%; Score 21; DB 10; Length 21;
XX Best Local Similarity 71.4%; Pred. No. 3.4;
XX Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GTGGGATAGTCCTCATGGTGT 26
DB 1 GUGGAUAGUCCGCAUGGUG 21
XX
RESULT 7
ADF52883/c
ID ADF52883 standard; RNA; 21 BP.
XX
XX ADF52883;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus modified siNA sense strand SeqID1474.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX

```

KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.
OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 26-MAR-2002; 2002WO-US009187.

XX 06-JUN-2002; 2002US-0386782P.

XX 05-AUG-2002; 2002US-0401104P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.

XX Example 3; SEQ ID NO 1474; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).

XX Sequence 21 BP; 7 A; 8 C; 3 G; 0 T; 3 U; 0 Other;

XX Query Match 75.0%; Score 21; DB 10; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 3.4;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGGATAGTCGTCATGGTGT 28

Db 21 GGGATAGTCGTCATGGTGT 1

RESULT 8

ADF52875

.ID ADF52875 standard; RNA; 21 BP.

XX ADF52875;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siRNA sense strand SeqID1466.

XX short interfering nucleic acid; siRNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 26-MAR-2002; 2002WO-US009187.

XX 06-JUN-2002; 2002US-0386782P.

XX 05-AUG-2002; 2002US-0401104P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.

XX Example 3; SEQ ID NO 1466; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).

XX Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;

XX Query Match 75.0%; Score 21; DB 10; Length 21;

XX Best Local Similarity 66.7%; Pred. No. 3.4;

XX Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCCGTCATGGTGT 27
Db :||||:||||:||||:||||:
1 UGGGAUAGUCCGCAUGGUGU 21

RESULT 9
ID ADA13879 standard; RNA; 21 BP.
XX AC ADA13879;
XX DT 20-NOV-2003 (first entry)
XX Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:216.
XX double-stranded short interfering nucleic acid;
KW short interfering nucleic acid; siNA; expression; replication;
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;
KW cytosolic; cardiovascular; immunosuppressive; respiratory; nephrotropic;
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;
KW herpes simplex; cytomegalovirus; human papillomavirus;
KW respiratory syncytial virus; influenza virus; restenosis;
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;
KW pulmonary; renal; liver; mitochondrial; reproductive disease;
KW chemical modification; ss.
XX OS Synthetic.
XX WO2003070918-A2.
XX DT 28-AUG-2003.
XX DT 20-FEB-2003; 2003WO-US005346.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;
XX WPI; 2003-689785/65.
XX New short interfering nucleic acid containing no ribonucleotides, useful
XX e.g. for treating viral infection, downregulates expression of target
XX gene or RNA.
XX Example 4; Page 139; 204pp; English.
XX The present invention describes a double-stranded short interfering
XX nucleic acid (siNA) that downregulates expression of a target gene, where
XX the siNA molecule comprises no ribonucleotides and each strand of the
XX double-stranded siNA comprises about 21 nucleotides. Also described: (1)
XX a siNA molecule that inhibits expression of target RNA; (2) a siNA
XX molecule that inhibits replication of a virus and optionally does not
XX require presence of a ribonucleotide for inhibition; (3) a siNA molecule
XX that inhibits expression of a target gene and does not require presence
XX of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits
XX expression of a target gene by mediating RNA interference; and (5) a
XX method for modulating expression of a gene in a cell using siNA
XX molecules. siNA's can have virucide, anti-HIV, hepatotropic,
XX antiinflammatory, plant antiviral, vasotropic, neuroprotective,
XX cytosolic, cardiovascular, immunosuppressive, respiratory, nephrotropic
XX and endocrine activities. The siNA's are useful for downregulating
XX expression of target genes, inhibiting expression of target RNA, and
XX inhibiting replication of a virus. siNA molecules can be used: (a) for

CC therapy of any disorder that responds to modulation of gene expression,
CC especially animal and plant viral infections, specifically hepatitis B or
CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory
CC syncytial or influenza viruses, and also many other diseases such as
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
CC endocrine or reproductive diseases; and (b) for diagnosis, target
CC validation, genomic discovery, genetic engineering, pharmacogenomics and
CC analysis of gene function. Chemical modification of siNA molecules
CC improves interfering activity; stability; cellular uptake; binding
CC affinity and/or mediates increased polymerase activity. siNA may be
CC designed to target many related genes containing a conserved sequence.
CC The present sequence represents a siNA oligonucleotide sequence, which is
XX used in the exemplification of the present invention.
XX SQ Sequence 21 BP; 7 A; 7 C; 4 G; 0 T; 3 U; 0 Other;
Query Match 71.4%; Score 20; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GGATAGTCCGTCATGGTGT 28
Db :||||:||||:||||:||||:
21 GGATAGTCCGTCATGGTGT 2

RESULT 10
ADA13824
ID ADA13824 standard; RNA; 21 BP.
XX AC ADA13824;
XX DT 20-NOV-2003 (first entry)
XX Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:161.
XX double-stranded short interfering nucleic acid;
KW short interfering nucleic acid; siNA; expression; replication;
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;
KW cytosolic; cardiovascular; immunosuppressive; respiratory; nephrotropic;
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;
KW herpes simplex; cytomegalovirus; human papillomavirus;
KW respiratory syncytial virus; influenza virus; restenosis;
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;
KW pulmonary; renal; liver; mitochondrial; reproductive disease;
KW chemical modification; ss.
XX OS Synthetic.
XX WO2003070918-A2.
XX DT 28-AUG-2003.
XX DT 20-FEB-2003; 2003WO-US005346.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;
XX WPI; 2003-689785/65.
XX New short interfering nucleic acid containing no ribonucleotides, useful
XX e.g. for treating viral infection, downregulates expression of target

PT Gene or RNA.
XX
PS Example 4; Page 136; 20app; English.
XX
CC The present invention describes a double-stranded short interfering
CC nucleic acid (siRNA) that downregulates expression of a target gene, where
CC the siRNA molecule comprises no ribonucleotides and each strand of the
CC double-stranded siRNA comprises about 21 nucleotides. Also described: (1)
CC a siRNA molecule that inhibits expression of a virus and optionally does not
CC require presence of a ribonucleotide for inhibition; (3) a siRNA molecule
CC that inhibits expression of a target gene and does not require presence
CC of a ribonucleotide for inhibition; (4) a siRNA molecule that inhibits
CC expression of a target gene by mediating RNA interference; and (5) a
CC method for modulating expression of a gene in a cell using siRNA
CC molecules. siRNA's can have virucide, anti-HIV, hepatotropic,
CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,
CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic
CC and endocrine activities. The siRNA's are useful for downregulating
CC expression of target genes, inhibiting expression of target RNA, and
CC inhibiting replication of a virus. siRNA molecules can be used: (a) for
CC therapy of any disorder that responds to modulation of gene expression,
CC especially animal and plant viral infections, specifically hepatitis B or
CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory
CC syncytial or influenza viruses, and also many other diseases such as
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
CC endocrine or reproductive diseases; and (b) for diagnosis, target
CC validation, genomic discovery, genetic engineering, pharmacogenomics, and
CC analysis of gene function. Chemical modification of siRNA molecules
CC improves interfering activity; stability; cellular uptake; binding
CC affinity and/or mediates increased polymerase activity. siRNA may be
CC assigned to target many related genes containing a conserved sequence.
CC The present sequence represents a siRNA oligonucleotide sequence, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 21 BP; 3 A; 3 C; 8 G; 2 T; 5 U; 0 Other;
Query Match 71.4%; Score 20; DB 9; Length 21;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 7 TGGGATAGTCCGTCATGGTGT 26
DB 2 TGGGAUAGUCCGUAUGGUG 21
RESULT 11
ADF52882/c
ID ADF52882 standard; RNA; 21 BP.
XX ADF52882;
AC ADF52882;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus modified siRNA sense strand SeqID1473.
XX short interfering nucleic acid; siRNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
XX
FN WO2003070750-A2.
XX 28-AUG-2003.
PD
XX 20-FEB-2003; 2003WO-US005043.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR

26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 23-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
FI WPI; 2003-689778/65.
XX
DR New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1473; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: this sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX Sequence 21 BP; 7 A; 7 C; 4 G; 0 T; 3 U; 0 Other;
SQ
Query Match 71.4%; Score 20; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GGATAGTCCGTCATGGTGT 28
DB 21 GGATAGTCCGTCATGGTGT 2
RESULT 12
ADF52848
ID ADF52848 standard; RNA; 21 BP.
XX
AC ADF52848;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus modified siRNA sense strand SeqID1439.
XX short interfering nucleic acid; siRNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
XX

PN WO2003070750-A2.
 XX 28-AUG-2003.
 XX 20-FEB-2003; 2003WO-US005043.
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002WO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 05-AUG-2002; 2002US-0401104P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
 PI WPI; 2003-689778/65.
 XX New double-stranded short interfering nucleic acid comprises sugar-
 PT modified pyrimidine bases useful for treating infection with hepatitis C
 PT virus.
 XX Example 3; SEQ ID NO 1439; 183pp; English.
 XX This invention relates to novel double-stranded short interfering nucleic
 CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
 CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
 CC interference. The siRNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identifying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siRNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 CC 158).
 XX Sequence 21 BP; 3 A; 3 C; 8 G; 2 T; 5 U; 0 Other;
 SQ Query Match 71.4%; Score 20; DB 10; Length 21;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TGGGATAGTCGTCATGGT 26
 |||||:||||:||||:||||:
 Db 2 TGGGAUAGUCCGCAUGGUG 21
 RESULT 13
 ADF52996
 ID ADF52996 standard; RNA; 23 BP.
 XX ADF52996;
 AC ADF52996;
 XX 12-FEB-2004 (first entry)
 DT Hepatitis C virus modified siRNA sense strand SeqID1587.
 DE
 XX

KW short interfering nucleic acid; siRNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.
 XX Synthetic.
 OS Hepatitis C virus.
 XX WO2003070750-A2.
 XX 28-AUG-2003.
 XX 20-FEB-2003; 2003WO-US005043.
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002WO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 05-AUG-2002; 2002US-0401104P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
 PI WPI; 2003-689778/65.
 XX New double-stranded short interfering nucleic acid comprises sugar-
 PT modified pyrimidine bases useful for treating infection with hepatitis C
 PT virus.
 XX Example 3; SEQ ID NO 1587; 183pp; English.
 XX This invention relates to novel double-stranded short interfering nucleic
 CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
 CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
 CC interference. The siRNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identifying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siRNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 CC 158).
 XX Sequence 23 BP; 3 A; 3 C; 8 G; 2 T; 5 U; 2 Other;
 SQ Query Match 71.4%; Score 20; DB 10; Length 23;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GTGGATAGTCGTCATGGT 25
 |||||:||||:||||:||||:
 Db 2 GUGGAUAGUCCGCAUGGT 21
 RESULT 14
 ADF52938

QY	Db	6 GTGGGATAGTCCGTCATGGT 25 : : : : 2 GUGGGAUAGUCGUGCAUGGT 21
ADFS2938 standard; RNA; 23 BP.	ADFS2938;	12-FEB-2004 (first entry)
Hepatitis C virus modified siNA sense strand SeqID1529.	XX	XX
short interfering nucleic acid; siNA; virus replication inhibition;	XX	XX
hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;	KW	KW
hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;	KW	KW
hepatocellular cancer; cirrhosis; ss.	KW	KW
Synthetic.	OS	OS
Hepatitis C virus.	OS	OS
WO2003070750-A2.	PN	PN
28-AUG-2003.	PD	PD
20-FEB-2003; 2003WO-US005043.	XX	XX
20-FEB-2002; 2002US-0358580P.	XX	XX
11-MAR-2002; 2002US-0363124P.	PR	PR
26-MAR-2002; 2002WO-US009187.	PR	PR
06-JUN-2002; 2002US-0386782P.	PR	PR
03-AUG-2002; 2002US-0401104P.	PR	PR
29-AUG-2002; 2002US-0406784P.	PR	PR
05-SEP-2002; 2002US-0408378P.	PR	PR
09-SEP-2002; 2002US-0409293P.	PR	PR
15-JAN-2003; 2003US-0440129P.	PR	PR
(SIRN-) SIRNA THERAPEUTICS INC.	XX	XX
Mcswiggen J, Beigelman L, Macejak D, Morrissey D;	PI	PI
WPI; 2003-689778/65.	XX	XX
New double-stranded short interfering nucleic acid comprises sugar-	XX	XX
modified pyrimidine bases useful for treating infection with hepatitis C	XX	XX
virus.	XX	XX
Example 3; SEQ ID NO 1529; 183pp; English.	XX	XX
This invention relates to novel double-stranded short interfering nucleic	XX	XX
acids (siNA) that inhibits replication of hepatitis C virus (HCV), where	XX	XX
one strand is an antisense strand (ASS) that is complementary to (part	XX	XX
of) an HCV RNA (portion) and a sense strand (SS) that is complementary to	XX	XX
ASS, and where most of the pyrimidine nucleotides comprise a sugar	XX	XX
modification. The invention may allow development of compounds with	XX	XX
virucide, antiinflammatory, hepatotropic or cytostatic activities by	XX	XX
modulation (inhibition) of expression or activity of HCV RNA, by RNA	XX	XX
interference. The siNA's of the invention may be used to inhibit	XX	XX
replication of HCV, in cells, tissue explants or organisms, for treating	XX	XX
HCV infection and its consequences (liver failure; hepatocellular cancer	XX	XX
and cirrhosis), and also for drug screening, diagnosis, target	XX	XX
identification and validation, genetic engineering, pharmacogenomics,	XX	XX
studying gene function and gene mapping (for example of single-nucleotide	XX	XX
polymorphisms). The chemical modification improves stability, activity,	XX	XX
cellular uptake and/or binding affinity. The siNA can be directed to	XX	XX
conserved regions of HCV genes, so are active against many different	XX	XX
strains. NOTE: This sequence may contain one or more of several	XX	XX
modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine	XX	XX
(T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal	XX	XX
base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These	XX	XX
modifications are specified in table 3 of the specification (pages 150-	XX	XX
158).	XX	XX
Sequence 23 BP; 3 A; 3 C; 8 G; 2 T; 5 U; 2 Other;	XX	XX
Query Match 71.4%; Score 20; DB 10; Length 23;	XX	XX
Best Local Similarity 75.0%; Pred. No. 10;	XX	XX
Conservative 15.0%; Mismatches 5; Indels 0; Gaps 0;	XX	XX

DR WPI; 2003-689778/65.
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1586; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, anti-inflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
XX Sequence 23 BP; 3 A; 3 C; 7 G; 2 T; 6 U; 2 Other;
SQ
Query Match 69.3%; Score 19.4; DB 10; Length 23;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 7 TGGGATAGTCGTCATCGTGT 27
:||||:||||:||||:|
Db 2 UGGGAUAGUCCGCAUGGUTT 22
RESULT 18
ADFS2937
ID ADFS2937 standard; RNA; 23 BP.
AC ADFS2937;
XX 12-FEB-2004 (first entry)
XX Hepatitis C virus modified siRNA sense strand SeqID1528.
XX short interfering nucleic acid; siRNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; anti-inflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
XX WO2003070750-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005043.
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
PI WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1528; 183pp; English.
PS
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, anti-inflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
XX Sequence 23 BP; 3 A; 3 C; 7 G; 2 T; 6 U; 2 Other;
SQ
Query Match 69.3%; Score 19.4; DB 10; Length 23;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 7 TGGGATAGTCGTCATCGTGT 27
:||||:||||:||||:|
Db 2 UGGGAUAGUCCGCAUGGUTT 22
RESULT 19
ADFS2997
ID ADFS2997 standard; RNA; 23 BP.
XX ADFS2997;
AC ADFS2997;
XX 12-FEB-2004 (first entry)
XX Hepatitis C virus modified siRNA sense strand SeqID1588.
XX short interfering nucleic acid; siRNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; anti-inflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
XX WO2003070750-A2.
XX 28-AUG-2003.
XX

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DT 12-FEB-2004 (first entry)
XX Hepatitis C virus modified siNA sense strand SeqID1530.
DE short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
XX WO2003070750-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005043.
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 23-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX Example 3; SEQ ID NO 1530; 183pp; English.
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains. NOTE: This sequence may contain one or more of several
XX modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
XX (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
XX base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
XX modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX Sequence 23 BP; 3 A; 4 C; 7 G; 2 T; 5 U; 2 Other;
XX Query Match 69.3%; Score 19.4; DB 10; Length 23;
XX Best Local Similarity 71.4%; Pred. NO. 20;
XX Matches 15; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
OY 5 CGTGGGATAGTCGTCATGGT 25
DB 2 CGUGGAUGAUGCCGUGAUGTT 22
```

```
RESULT 22
ADF52941
ID ADF52941 standard; RNA; 23 BP.
XX
AC ADF52941;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus modified siNA sense strand SeqID1532.
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
XX WO2003070750-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005043.
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX Example 3; SEQ ID NO 1532; 183pp; English.
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains. NOTE: This sequence may contain one or more of several
XX modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
XX (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
XX base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
XX modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX Sequence 23 BP; 2 A; 4 C; 7 G; 2 T; 6 U; 2 Other;
```


Query Match 69.3%; Score 19.4; DB 10; Length 23;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTCTGGGATAGTCGTCAT 22
Db 2 GUUCGUGGUAUCCGUCTT 22

RESULT 23
ADA13832/C
ID ADA13832 standard; RNA; 21 BP.
XX
AC ADA13832;
XX
DT 20-NOV-2003 (first entry)
XX
DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:169.
XX
KW double-stranded short interfering nucleic acid;
KW short interfering nucleic acid; siNA; expression; replication;
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;
KW cytosstatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;
KW herpes simplex; cytomegalovirus; human papillomavirus;
KW respiratory syncytial virus; influenza virus; restenosis;
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;
KW pulmonary; renal; liver; mitochondrial; reproductive disease;
KW chemical modification; ss.
XX
OS Synthetic.
XX
PN WO2003070918-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005346.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
FA (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;
XX
XX WPI; 2003-689785/65.
XX
XX New short interfering nucleic acid containing no ribonucleotides, useful
PT e.g. for treating viral infection, downregulates expression of target
PT gene or RNA.
XX
XX Example 4; Page 137; 204pp; English.
PS
XX
CC The present invention describes a double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of a target gene, where
CC the siNA molecule comprises no ribonucleotides and each strand of the
CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)
CC a siNA molecule that inhibits expression of target RNA; (2) a siNA
CC molecule that inhibits replication of a virus and optionally does not
CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule
CC that inhibits expression of a target gene and does not require presence
CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits
CC expression of a target gene by mediating RNA interference; and (5) a
CC method for modulating expression of a gene in a cell using siNA
CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,

CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,
CC cytosstatic, cardiovascular, immunosuppressive, respiratory, nephrotropic
CC and endocrine activities. The siNA's are useful for downregulating
CC expression of target genes, inhibiting expression of target RNA, and
CC inhibiting replication of a virus. siNA molecules can be used: (a) for
CC therapy of any disorder that responds to modulation of gene expression,
CC especially animal and plant viral infections, specifically hepatitis B or
CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory
CC syncytial or influenza viruses, and also many other diseases such as
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
CC endocrine or reproductive diseases; and (b) for diagnosis, target
CC validation, genomic discovery, genetic engineering, pharmacogenomics and
CC analysis of gene function. Chemical modification of siNA molecules
CC improves interfering activity; stability; cellular uptake; binding
CC affinity and/or mediates increased polymerase activity. siNA may be
CC designed to target many related genes containing a conserved sequence.
CC The present sequence represents a siNA oligonucleotide sequence, which is
CC used in the exemplification of the present invention.

XX SQ Sequence 21 BP; 6 A; 7 C; 3 G; 2 T; 3 U; 0 Other;

Query Match 67.9%; Score 19; DB 9; Length 21;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATAGTCCGTCATGGTGT 27

Db 21 GGATAGTCCGTCATGGTGT 3

RESULT 24

ADA13878/C

ID ADA13878 standard; RNA; 21 BP.

XX AC ADA13878;

XX DT 20-NOV-2003 (first entry)

XX DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:215.

XX KW double-stranded short interfering nucleic acid;

XX KW short interfering nucleic acid; siNA; expression; replication;

XX KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;

XX KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;

XX KW cytosstatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;

XX KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;

XX KW herpes simplex; cytomegalovirus; human papillomavirus;

XX KW respiratory syncytial virus; influenza virus; restenosis;

XX KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;

XX KW pulmonary; renal; liver; mitochondrial; reproductive disease;

XX KW chemical modification; ss.

XX OS Synthetic.

XX PN WO2003070918-A2.

XX PD 28-AUG-2003.

XX PF 20-FEB-2003; 2003WO-US005346.

XX PR 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;

PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;

XX OS Synthetic.

XX PN WO2003070918-A2.

XX PD 28-AUG-2003.

XX PF 20-FEB-2003; 2003WO-US005346.

XX PR 20-FEB-2002; 2002US-0359580P.

XX PR 11-MAR-2002; 2002US-0363124P.

XX PR 06-JUN-2002; 2002US-0386782P.

XX PR 29-AUG-2002; 2002US-0406784P.

XX PR 05-SEP-2002; 2002US-0408378P.

XX PR 09-SEP-2002; 2002US-0409293P.

XX PR 15-JAN-2003; 2003US-0440129P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI McSwiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;

XX PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;

XX WPI; 2003-689785/65.

XX New short interfering nucleic acid containing no ribonucleotides, useful

XX e.g. for treating viral infection, downregulates expression of target

XX gene or RNA.

XX Example 4; Page 137; 204pp; English.

XX The present invention describes a double-stranded short interfering

XX nucleic acid (siRNA) that downregulates expression of a target gene, where

XX the siRNA molecule comprises no ribonucleotides and each strand of the

XX double-stranded siRNA comprises about 21 nucleotides. Also described: (1)

XX a siRNA molecule that inhibits expression of target RNA; (2) a siRNA

XX molecule that inhibits replication of a virus and optionally does not

XX require presence of a ribonucleotide for inhibition; (3) a siRNA molecule

XX that inhibits expression of a target gene and does not require presence

XX of a ribonucleotide for inhibition; (4) a siRNA molecule that inhibits

XX expression of a target gene by mediating RNA interference; and (5) a

XX method for modulating expression of a gene in a cell using siRNA

XX molecules. siRNA's can have virucide, anti-HIV, hepatotropic,

XX antiinflammatory, plant antiviral, vasotrophic, neuroprotective,

XX cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic

XX and endocrine activities. The siRNA's are useful for downregulating

XX expression of target genes, inhibiting expression of target RNA, and

XX inhibiting replication of a virus. siRNA molecules can be used: (a) for

XX therapy of any disorder that responds to modulation of gene expression,

XX especially animal and plant viral infections, specifically hepatitis B or

XX C; HIV; herpes simplex; cytomegalo; human papilloma; respiratory

XX restenosis, neurodegeneration, cancers, and also many other diseases such as

XX prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,

XX endocrine or reproductive diseases; and (b) for diagnosis, target

XX validation, genomic discovery, genetic engineering, pharmacogenomics and

XX analysis of gene function. Chemical modification of siRNA molecules

XX improves interfering activity; stability; cellular uptake; binding

XX affinity and/or mediates increased polymerase activity. siRNA may be

XX designed to target many related genes containing a conserved sequence.

XX The present sequence represents a siRNA oligonucleotide sequence, which is

XX used in the exemplification of the present invention.

XX Sequence 21 BP; 7 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

XX Query Match 67.9%; Score 19; DB 9; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 30;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCGTCATGCTGTT 28

DB 21 GATAGTCGTCATGCTGTT 3

RESULT 25

ADAI13833/c

ID ADAI13833 standard; RNA; 21 BP.

AC ADAI13833;

XX 20-NOV-2003 (first entry)

XX Short interfering nucleic acid (siRNA) oligonucleotide SEQ ID NO:170.

XX double-stranded short interfering nucleic acid;

XX short interfering nucleic acid; siRNA; expression; replication;

XX inhibition; RNA interference; virucide; anti-HIV; hepatotropic;

XX antiinflammatory; plant; antiviral; vasotrophic; neuroprotective;

XX cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;

XX endocrine; viral infection; hepatitis B; hepatitis C; HIV;

XX herpes simplex; cytomegalovirus; human papillomavirus;

XX respiratory syncytial virus; influenza virus; restenosis;

XX neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;

XX pulmonary; renal; liver; mitochondrial; reproductive disease;

XX chemical modification; ss.

CC nucleic acid (siRNA) that downregulates expression of a target gene, where
 CC the siRNA molecule comprises no ribonucleotides and each strand of the
 CC double-stranded siRNA comprises about 21 nucleotides. Also described: (1)
 CC a siRNA molecule that inhibits expression of target RNA; (2) a siRNA
 CC molecule that inhibits replication of a virus and optionally does not
 CC require presence of a ribonucleotide for inhibition; (3) a siRNA molecule
 CC that inhibits expression of a target gene and does not require presence
 CC of a ribonucleotide for inhibition; (4) a siRNA molecule that inhibits
 CC expression of a target gene by mediating RNA interference; and (5) a
 CC method for modulating expression of a gene in a cell using siRNA
 CC molecules. siRNA's can have virucide, anti-HIV, hepatotropic,
 CC antiinflammatory, plant antiviral, vasotrophic, neuroprotective,
 CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic
 CC and endocrine activities. The siRNA's are useful for downregulating
 CC expression of target genes, inhibiting expression of target RNA, and
 CC inhibiting replication of a virus. siRNA molecules can be used: (a) for
 CC therapy of any disorder that responds to modulation of gene expression,
 CC especially animal and plant viral infections, specifically hepatitis B or
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory
 CC syncytial or influenza viruses, and also many other diseases such as
 CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,
 CC endocrine or reproductive diseases; and (b) for diagnosis, target
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and
 CC analysis of gene function. Chemical modification of siRNA molecules
 CC improves interfering activity; stability; cellular uptake; binding
 CC affinity and/or mediates increased polymerase activity. siRNA may be
 CC designed to target many related genes containing a conserved sequence.
 CC The present sequence represents a siRNA oligonucleotide sequence, which is
 CC used in the exemplification of the present invention.

XX Sequence 21 BP; 3 A; 3 C; 6 G; 2 T; 7 U; 0 Other;
 CC Query Match 67.9%; Score 19; DB 9; Length 21;
 CC Best Local Similarity 63.2%; Pred. No. 30;
 CC Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCCGTCATGGTGT 28
 DB 3 GAUAGUCCGUCAUGGUUU 21

RESULT 28
 ADF52954/c
 ID ADF52954 standard; RNA; 21 BP.
 XX ADF52954;
 AC ADF52954;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siRNA antisense strand SeqID1545.

XX short interfering nucleic acid; siRNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.
 OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (STRN-) SIRNA THERAPEUTICS INC.
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
 XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-
 PT modified pyrimidine bases useful for treating infection with hepatitis C
 PT virus.

XX Example 3; SEQ ID NO 1545; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic
 CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
 CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA by RNA
 CC interference. The siRNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siRNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 CC 158).

XX Sequence 21 BP; 6 A; 7 C; 4 G; 2 T; 2 U; 0 Other;

XX Query Match 67.9%; Score 19; DB 10; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 30;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCGTGGGATAGTCCGT 19

DB 19 CGTTCGTGGGATAGTCCGT 1

RESULT 29

ADP53008/c

ID ADF53008 standard; RNA; 21 BP.

XX ADF53008;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siRNA antisense strand SeqID1599.

XX short interfering nucleic acid; siRNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

```
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1599; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
SQ Sequence 21 BP; 5 A; 8 C; 3 G; 2 T; 3 U; 0 Other;
Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GTGGGATAGTCGTCATCG 24
Db 19 GTGGGATAGTCGTCATCG 1
RESULT 30
ADF52857/c
ID ADF52857 standard; RNA; 21 BP.
XX
AC ADF52857;
XX
XX 12-FEB-2004 (first entry)
DT
DE Hepatitis C virus modified siNA sense strand SeqID1448.
XX
KW short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
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OS Synthetic.
OS Hepatitis C virus.
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2002; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1448; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
SQ Sequence 21 BP; 7 A; 6 C; 3 G; 2 T; 3 U; 0 Other;
Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 GATAGTCGTCATCGTGT 28
Db 21 GATAGTCGTCATCGTGT 3
RESULT 31
ADF53007/c
ID ADF53007 standard; RNA; 21 BP.
XX
AC ADF53007;
XX
XX 12-FEB-2004 (first entry)
DT
```

XX Hepatitis C virus modified siNA antisense strand SeqID1598.
DE short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
OS WO2003070750-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005043.
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX Example 3; SEQ ID NO 1598; 183pp; English.
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX Sequence 21 BP; 6 A; 7 C; 3 G; 2 T; 3 U; 0 Other;
SQ Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 TGGGATAGTCGTCATGGT 25
DB 19 TGGGATAGTCGTCATGGT 1

RESULT 32
ADF52850
ID ADF52850 standard; RNA; 21 BP.
XX ADF52850;
XX 12-FEB-2004 (first entry)
XX Hepatitis C virus modified siNA sense strand SeqID1441.
DE short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
OS WO2003070750-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005043.
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX Example 3; SEQ ID NO 1441; 183pp; English.
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX Sequence 21 BP; 3 A; 3 C; 6 G; 2 T; 7 U; 0 Other;
SQ

Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 63.2%; Pred. No. 30;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 10 GATAGTCGTCATGCTGTT 28
||:||||:||||:||||:|
Db 3 GAUAGUCGUCAGGUGUU 21

RESULT 33
ID ADF52949/c
XX ADF52949 standard; RNA; 21 BP.
AC ADF52949;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus modified siNA antisense strand SeqID1540.
XX
KW short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
FN WO2003070750-A2.
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1540; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytosstatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several

CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
SQ Sequence 21 BP; 6 A; 7 C; 3 G; 2 T; 3 U; 0 Other;

Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TGGGATAGTCGTCATGCT 25
|||||||
Db 19 TGGGATAGTCGTCATGCT 1

RESULT 34
ID ADF52951/c
XX ADF52951 standard; RNA; 21 BP.
AC ADF52951;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus modified siNA antisense strand SeqID1542.
XX
KW short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
FN WO2003070750-A2.
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1542; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytosstatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating

CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 CC 158).

XX SQ Sequence 21 BP; 5 A; 7 C; 4 G; 2 T; 3 U; 0 Other;
 Query Match 67.9%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGTGGGATAGTCGTCATG 23
 DB 19 CGTGGGATAGTCGTCATG 1

RESULT 35
 ADF52952/c
 ID ADF52952 standard; RNA; 21 BP.
 XX AC ADF52952;
 XX DT 12-FEB-2004 (first entry)
 XX DE Hepatitis C virus modified siNA antisense strand SeqID1543.
 XX short interfering nucleic acid; siNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.
 XX OS Synthetic.
 OS Hepatitis C virus.
 XX WO2003070750-A2.
 XX PD 28-AUG-2003.
 XX PF 20-FEB-2003; 2003WO-US005043.
 XX PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002WO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 05-AUG-2002; 2002US-0401104P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 XX PA Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
 XX PI WPI; 2003-689778/65.
 XX DR New double-stranded short interfering nucleic acid comprises sugar-
 XX modified pyrimidine bases useful for treating infection with hepatitis C
 XX virus.
 XX Example 3; SEQ ID NO 1543; 183pp; English.
 XX This invention relates to novel double-stranded short interfering nucleic
 XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
 CC

CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
 CC interference. The siNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 CC 158).

XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 2 T; 3 U; 0 Other;
 Query Match 67.9%; Score 19; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGTGGGATAGTCGTCAT 22
 DB 19 TCGTGGGATAGTCGTCAT 1

RESULT 36
 ADF53011/c
 ID ADF53011 standard; RNA; 21 BP.
 XX AC ADF53011;
 XX DT 12-FEB-2004 (first entry)
 XX DE Hepatitis C virus modified siNA antisense strand SeqID1602.
 XX short interfering nucleic acid; siNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.
 XX OS Synthetic.
 OS Hepatitis C virus.
 XX WO2003070750-A2.
 XX PD 28-AUG-2003.
 XX PF 20-FEB-2003; 2003WO-US005043.
 XX PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 26-MAR-2002; 2002WO-US009187.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 05-AUG-2002; 2002US-0401104P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 XX PA Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
 XX PI WPI; 2003-689778/65.
 XX DR

PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 1602; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX Sequence 21 BP; 6 A; 7 C; 4 G; 2 T; 2 U; 0 Other;
XX
XX Query Match 67.9%; Score 19; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 30;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 GTTCGTGGGATAGTCGTC 20
XX |||||
XX Db 19 GTTCGTGGGATAGTCGTC 1
XX
XX RESULT 37
XX ADF52950/c
XX ID ADF52950 standard; RNA; 21 BP.
XX AC ADF52950;
XX XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Hepatitis C virus modified siNA antisense strand SeqID1541.
XX
XX KW short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX OS Synthetic.
XX OS Hepatitis C virus.
XX
XX PN WO2003070750-A2.
XX
XX PD 28-AUG-2003.
XX
XX PF 20-FEB-2003; 2003WO-US005043.
XX
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 26-MAR-2002; 2002WO-US009187.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 05-AUG-2002; 2002US-0401104P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.
XX
XX PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
XX DR New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX PS Example 3; SEQ ID NO 1541; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX SQ Sequence 21 BP; 5 A; 8 C; 3 G; 2 T; 3 U; 0 Other;
XX
XX Query Match 67.9%; Score 19; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 30;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 GTGGGATAGTCGTCATGG 24
XX |||||
XX Db 19 GTGGGATAGTCGTCATGG 1
XX
XX RESULT 38
XX ADF53009/c
XX ID ADF53009 standard; RNA; 21 BP.
XX AC ADF53009;
XX XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Hepatitis C virus modified siNA antisense strand SeqID1600.
XX
XX KW short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX OS Synthetic.
XX OS Hepatitis C virus.
XX
XX PN WO2003070750-A2.
XX
XX PD 28-AUG-2003.
XX
XX PF 20-FEB-2003; 2003WO-US005043.
XX
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 26-MAR-2002; 2002WO-US009187.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 05-AUG-2002; 2002US-0401104P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.

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PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1600; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX Sequence 21 BP; 5 A; 7 C; 4 G; 2 T; 3 U; 0 Other;
XX
XX Query Match 67.9%; Score 19; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 30;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 CGTGGGATAGTCGTCATG 23
DB 19 CGTGGGATAGTCGTCATG 1
XX
RESULT 39
ADF53010/c
ID ADF53010 standard; RNA; 21 BP.
XX
XX ADF53010;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus modified siNA antisense strand SeqID1601.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Synthetic.
XX

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OS Hepatitis C virus.
XX
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1601; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX Sequence 21 BP; 6 A; 6 C; 4 G; 2 T; 3 U; 0 Other;
XX
XX Query Match 67.9%; Score 19; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 30;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4 TCGTGGGATAGTCGTCAT 22
DB 19 TCGTGGGATAGTCGTCAT 1
XX
RESULT 40
ADF52855/c
ID ADF52855 standard; RNA; 21 BP.
XX
XX ADF52855;
XX
XX 12-FEB-2004 (first entry)
XX

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Search completed: November 23, 2004, 17:30:09
Job time : 168.277 secs

DE Hepatitis C virus modified siNA sense strand SeqID1446.
XX short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
XX 28-AUG-2003.
PD
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
PI
XX
XX WPI; 2003-689778/65.
DR
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1446; 183pp; English.
PS
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
SQ Sequence 21 BP; 5 A; 8 C; 3 G; 2 T; 3 U; 0 Other;
Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GGGATAGTCCGTCATGGTG 26
|||||
DB 21 GGGATAGTCCGTCATGGTG 3

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 32.4045 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631B-9

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Sequence: 1 cgttcgtggatgcgcgtcatgtgtt 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	60.7	47	4	US-09-422-978-1680
2	15	53.6	15	4	US-09-153-242-37
3	14.6	52.1	21	4	US-09-657-472-2496
4	14.6	52.1	38	3	US-08-821-827C-25
5	14.6	52.1	38	3	US-09-290-202B-25
6	14.6	52.1	50	4	US-09-469-211A-14
7	14.4	51.4	32	3	US-08-833-167-78
8	14.4	51.4	32	3	US-09-344-837A-78
9	14.4	51.4	38	2	US-08-985-337A-6
10	14.4	51.4	38	2	US-08-985-124A-6
11	14.4	51.4	38	2	US-08-985-320A-6
12	14.4	51.4	38	3	US-08-984-732A-6
13	14.4	51.4	38	3	US-09-195-578-18
14	14.4	51.4	38	3	US-09-170-951-18
15	14.4	51.4	38	3	US-09-164-482-18
16	14.4	51.4	38	3	US-09-332-769-13
17	14.4	51.4	38	3	US-09-456-153-13
18	14.4	51.4	38	3	US-09-167-180-18
19	14.4	51.4	38	3	US-09-455-627-13
20	14.4	51.4	38	3	US-09-426-533-13
21	14.4	51.4	38	3	US-09-609-205-14
22	14.4	51.4	38	3	US-09-516-945-13
23	14.4	51.4	38	3	US-09-757-218-14
24	14.4	51.4	38	3	US-09-516-757-13
25	14.4	51.4	38	3	US-09-516-750-13
26	14.4	51.4	38	3	US-09-342-577-14
27	14.4	51.4	38	3	US-09-516-756-13

14.4	51.4	38	3	US-09-828-061A-14	Sequence 14, Appl
14.4	51.4	38	3	US-09-463-917-13	Sequence 13, Appl
14.4	51.4	38	4	US-09-347-673-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-757-213-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-656-653-13	Sequence 13, Appl
14.4	51.4	38	4	US-09-757-251-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-828-259A-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-719-878-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-757-217A-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-828-325A-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-756-248-13	Sequence 13, Appl
14.2	50.7	20	1	US-08-333-565-58	Sequence 58, Appl
14.2	50.7	20	2	US-08-661-479-58	Sequence 58, Appl
14.2	50.7	46	4	US-09-486-241-20	Sequence 20, Appl
14.2	50.7	48	4	US-09-556-877-215	Sequence 215, Appl
14.2	50.7	48	4	US-09-620-412C-215	Sequence 215, Appl
14.2	50.7	48	4	US-09-598-419-215	Sequence 215, Appl
13.8	49.3	40	1	US-08-474-542A-235	Sequence 235, Appl
13.6	48.6	40	1	US-08-457-648-235	Sequence 235, Appl
13.6	48.6	20	3	US-09-358-972-182	Sequence 182, Appl
13.6	48.6	20	3	US-09-406-147-44	Sequence 44, Appl
13.6	48.6	20	4	US-09-790-417-182	Sequence 182, Appl
13.6	48.6	26	2	US-08-632-434-10	Sequence 10, Appl
13.6	48.6	35	2	US-08-353-372A-29	Sequence 29, Appl
13.6	48.6	35	3	US-08-057-430A-20	Sequence 20, Appl
13.6	48.6	36	3	US-09-331-362-9	Sequence 9, Appl
13.6	48.6	42	3	US-08-974-549A-505	Sequence 505, Appl
13.6	48.6	42	3	US-09-311-362-7	Sequence 7, Appl
13.6	48.6	42	4	US-08-912-951-272	Sequence 272, Appl
13.6	48.6	42	4	US-09-402-181B-505	Sequence 505, Appl
13.6	48.6	42	4	US-09-721-456-505	Sequence 505, Appl
13.6	48.6	50	4	US-09-554-929-184	Sequence 184, Appl
13.4	47.9	48	3	US-09-486-356-20	Sequence 20, Appl
13.4	47.9	48	4	US-09-577-528B-20	Sequence 20, Appl
13.2	47.1	18	1	US-08-328-592-13	Sequence 13, Appl
13.2	47.1	18	1	US-08-328-592-14	Sequence 14, Appl
13.2	47.1	18	1	US-08-328-592-14	Sequence 14, Appl
13.2	47.1	20	4	US-09-332-522E-36	Sequence 36, Appl
13.2	47.1	29	3	US-08-713-569-7	Sequence 7, Appl
13.2	47.1	29	3	US-09-304-232-11	Sequence 11, Appl
13.2	47.1	43	1	US-08-640-378-1	Sequence 1, Appl
13.2	47.1	45	4	US-09-561-490E-37	Sequence 37, Appl
13	46.4	30	1	US-08-381-572-24	Sequence 24, Appl
13	46.4	30	1	US-08-592-820-24	Sequence 24, Appl
13	46.4	36	3	US-09-411-977-13	Sequence 13, Appl
13	46.4	36	3	US-09-411-977-13	Sequence 13, Appl
13	46.4	36	3	US-08-846-338-16	Sequence 16, Appl
13	46.4	43	2	US-08-846-338-16	Sequence 16, Appl
13	46.4	45	2	US-08-882-756-6	Sequence 6, Appl
12.8	45.7	20	3	US-09-344-001-37	Sequence 37, Appl
12.8	45.7	34	3	US-09-609-205-23	Sequence 23, Appl
12.8	45.7	38	2	US-08-985-337A-12	Sequence 12, Appl
12.8	45.7	38	2	US-08-985-124A-12	Sequence 12, Appl
12.8	45.7	38	2	US-08-985-320A-12	Sequence 12, Appl
12.8	45.7	38	3	US-08-984-732A-12	Sequence 12, Appl
12.8	45.7	38	3	US-08-195-578-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-170-951-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-164-482-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-332-769-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-456-153-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-167-180-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-455-627-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-426-533-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-609-205-20	Sequence 20, Appl
12.8	45.7	38	3	US-09-516-945-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-757-218-20	Sequence 20, Appl
12.8	45.7	38	3	US-08-757-218-23	Sequence 23, Appl
12.8	45.7	38	3	US-09-516-757-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-516-750-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-342-577-20	Sequence 20, Appl
12.8	45.7	38	3	US-09-342-577-23	Sequence 23, Appl
12.8	45.7	38	3	US-09-516-756-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-828-061A-20	Sequence 20, Appl
12.8	45.7	38	3	US-09-828-061A-23	Sequence 23, Appl
12.8	45.7	38	3	US-09-463-917-19	Sequence 19, Appl

c 101	12.8	45.7	38	4	US-09-347-673-20	Sequence 20, Appl	c 174	12.2	43.6	19	4	US-09-064-935-2	Sequence 2, Appl
c 102	12.8	45.7	38	4	US-09-347-673-23	Sequence 23, Appl	c 175	12.2	43.6	20	4	US-09-517-467B-131	Sequence 131, App
c 103	12.8	45.7	38	4	US-09-757-213-20	Sequence 20, Appl	c 176	12.2	43.6	23	4	US-09-305-856B-110	Sequence 110, App
c 104	12.8	45.7	38	4	US-09-757-213-23	Sequence 23, Appl	c 177	12.2	43.6	25	4	US-08-887-497A-52	Sequence 52, Appl
c 105	12.8	45.7	38	4	US-09-656-663-19	Sequence 19, Appl	c 178	12.2	43.6	26	3	US-09-155-427-12	Sequence 12, Appl
c 106	12.8	45.7	38	4	US-09-656-663-22	Sequence 22, Appl	c 179	12.2	43.6	28	2	US-08-859-998-374	Sequence 374, App
c 107	12.8	45.7	38	4	US-09-757-231-20	Sequence 20, Appl	c 180	12.2	43.6	28	3	US-09-225-928-374	Sequence 374, App
c 108	12.8	45.7	38	4	US-09-757-251-23	Sequence 23, Appl	c 181	12.2	43.6	28	4	US-09-225-201B-374	Sequence 374, App
c 109	12.8	45.7	38	4	US-09-828-259A-20	Sequence 20, Appl	c 182	12.2	43.6	29	3	US-09-304-232-642	Sequence 642, App
c 110	12.8	45.7	38	4	US-09-828-259A-23	Sequence 23, Appl	c 183	12.2	43.6	30	4	US-08-960-656B-5	Sequence 5, Appl
c 111	12.8	45.7	38	4	US-09-719-878-20	Sequence 20, Appl	c 184	12.2	43.6	33	1	US-08-173-510B-11	Sequence 11, Appl
c 112	12.8	45.7	38	4	US-09-719-878-23	Sequence 23, Appl	c 185	12.2	43.6	33	1	US-08-458-218-11	Sequence 11, Appl
c 113	12.8	45.7	38	4	US-09-757-217A-20	Sequence 20, Appl	c 186	12.2	43.6	33	2	US-08-450-497-11	Sequence 11, Appl
c 114	12.8	45.7	38	4	US-09-757-217A-23	Sequence 23, Appl	c 187	12.2	43.6	33	3	US-09-167-796-5	Sequence 5, Appl
c 115	12.8	45.7	38	4	US-09-828-325A-20	Sequence 20, Appl	c 188	12.2	43.6	35	3	US-08-060-433C-8	Sequence 8, Appl
c 116	12.8	45.7	38	4	US-09-828-325A-23	Sequence 23, Appl	c 189	12.2	43.6	35	3	US-08-840-767-28	Sequence 28, Appl
c 117	12.8	45.7	38	4	US-09-756-248-19	Sequence 19, Appl	c 190	12.2	43.6	38	4	US-09-910-174B-25	Sequence 25, Appl
c 118	12.8	45.7	43	3	US-09-281-481A-13	Sequence 13, Appl	c 191	12.2	43.6	38	4	US-09-620-461-25	Sequence 25, App
c 119	12.8	45.7	43	2	US-08-406-855A-13	Sequence 13, Appl	c 192	12.2	43.6	41	1	US-07-931-473B-235	Sequence 235, App
c 120	12.8	45.7	45	2	US-09-206-899-13	Sequence 13, Appl	c 193	12.2	43.6	41	1	US-07-931-473B-235	Sequence 235, App
c 121	12.8	45.7	45	3	US-09-206-899-13	Sequence 13, Appl	c 194	12.2	43.6	41	1	US-08-412-110-235	Sequence 235, App
c 122	12.8	45.7	45	4	US-09-688-415-18	Sequence 18, Appl	c 195	12.2	43.6	41	1	US-08-409-442A-235	Sequence 235, App
c 123	12.6	45.0	20	2	US-08-669-536-3	Sequence 3, Appl	c 196	12.2	43.6	41	2	US-08-469-609A-235	Sequence 235, App
c 124	12.6	45.0	22	4	US-09-600-848-3	Sequence 3, Appl	c 197	12.2	43.6	41	3	US-09-143-190-235	Sequence 235, App
c 125	12.6	45.0	30	4	US-09-359-301A-11	Sequence 11, Appl	c 198	12.2	43.6	41	3	US-09-502-344-235	Sequence 235, App
c 126	12.6	45.0	38	1	US-09-640-304-12	Sequence 12, Appl	c 199	12.2	43.6	43	1	US-07-931-473B-246	Sequence 246, App
c 127	12.6	45.0	38	1	US-08-150-103-12	Sequence 12, Appl	c 200	12.2	43.6	43	1	US-07-931-473B-246	Sequence 246, App
c 128	12.6	45.0	38	1	US-08-454-778-4	Sequence 4, Appl	c 201	12.2	43.6	43	1	US-08-412-110-246	Sequence 246, App
c 129	12.6	45.0	38	1	US-08-373-124A-501	Sequence 501, App	c 202	12.2	43.6	43	1	US-08-409-442A-246	Sequence 246, App
c 130	12.6	45.0	38	1	US-08-373-124A-2388	Sequence 2388, Ap	c 203	12.2	43.6	43	2	US-08-469-609A-246	Sequence 246, App
c 131	12.6	45.0	38	1	US-08-435-628-501	Sequence 501, App	c 204	12.2	43.6	43	3	US-09-143-190-246	Sequence 246, App
c 132	12.6	45.0	38	1	US-08-435-628-2388	Sequence 2388, Ap	c 205	12.2	43.6	43	3	US-09-502-344-246	Sequence 246, App
c 133	12.6	45.0	41	4	US-09-434-354-31	Sequence 31, Appl	c 206	12.2	43.6	45	1	US-08-446-822-11	Sequence 11, Appl
c 134	12.6	45.0	41	4	US-09-709-785-31	Sequence 31, Appl	c 207	12.2	43.6	45	3	US-09-328-314-11	Sequence 11, Appl
c 135	12.6	45.0	41	4	US-09-119-507B-63	Sequence 63, Appl	c 208	12.2	43.6	45	5	PCT-US93-12586-11	Sequence 11, Appl
c 136	12.6	45.0	42	4	US-09-434-354-28	Sequence 28, Appl	c 209	12.2	43.6	48	3	US-09-069-821-32	Sequence 32, Appl
c 137	12.6	45.0	42	4	US-08-897-556A-63	Sequence 63, Appl	c 210	12.2	43.6	48	3	US-09-956-086-32	Sequence 32, Appl
c 138	12.6	45.0	42	4	US-09-547-693-63	Sequence 63, Appl	c 211	12.2	43.6	48	4	US-09-956-087-32	Sequence 32, Appl
c 139	12.6	45.0	42	4	US-09-709-785-28	Sequence 28, Appl	c 212	12.2	43.6	48	4	US-09-288-461-45	Sequence 45, Appl
c 140	12.6	45.0	45	3	US-09-217-228-4	Sequence 4, Appl	c 213	12.2	42.9	20	3	US-09-380-662-13	Sequence 13, Appl
c 141	12.6	45.0	47	3	US-09-422-978-1173	Sequence 1173, Ap	c 214	12.2	42.9	20	4	US-09-758-881-45	Sequence 45, Appl
c 142	12.4	44.3	27	3	US-09-630-706-4	Sequence 4, Appl	c 215	12.2	42.9	20	4	US-08-465-615-3	Sequence 3, Appl
c 143	12.4	44.3	31	3	US-09-161-466-5	Sequence 5, Appl	c 216	12.2	42.9	27	1	US-08-411-796-496	Sequence 496, App
c 144	12.4	44.3	31	3	US-09-161-466-21	Sequence 21, Appl	c 217	12.2	42.9	32	1	US-08-411-039-496	Sequence 496, App
c 145	12.4	44.3	32	2	US-08-454-028-18	Sequence 18, Appl	c 218	12.2	42.9	32	3	US-08-535-057A-14	Sequence 14, Appl
c 146	12.4	44.3	32	2	US-08-454-028-19	Sequence 19, Appl	c 219	12.2	42.9	32	4	US-08-559-390-496	Sequence 496, App
c 147	12.4	44.3	32	5	PCT-US94-05388-18	Sequence 18, Appl	c 220	12.2	42.9	32	4	US-09-503-252-14	Sequence 14, Appl
c 148	12.4	44.3	32	5	PCT-US94-05388-19	Sequence 19, Appl	c 221	12.2	42.9	32	5	PCT-US93-11198-496	Sequence 9, Appl
c 149	12.4	44.3	32	5	PCT-US96-07496-18	Sequence 18, Appl	c 222	12.2	42.9	33	3	US-08-468-846-9	Sequence 38, Appl
c 150	12.4	44.3	36	1	US-08-435-480-2	Sequence 2, Appl	c 223	12.2	42.9	33	3	US-09-110-517-38	Sequence 9, Appl
c 151	12.4	44.3	36	4	US-09-675-016-11	Sequence 3, Appl	c 224	12.2	42.9	33	3	US-08-915-086A-9	Sequence 5, Appl
c 152	12.4	44.3	37	3	US-09-277-016-3	Sequence 3, Appl	c 225	12.2	42.9	33	4	US-09-227-853A-11	Sequence 11, Appl
c 153	12.4	44.3	37	4	US-09-455-950-3	Sequence 5, Appl	c 226	12.2	42.9	33	4	US-09-227-853A-11	Sequence 11, Appl
c 154	12.4	44.3	42	2	US-08-716-284-3	Sequence 3, Appl	c 227	12.2	42.9	33	5	PCT-US95-06385-5	Sequence 5, Appl
c 155	12.4	44.3	42	4	US-09-578-634A-58	Sequence 58, Appl	c 228	12.2	42.9	34	3	PCT-US95-06385-11	Sequence 12, Appl
c 156	12.4	44.3	47	4	US-09-422-978-2307	Sequence 2307, Ap	c 229	12.2	42.9	35	3	US-09-343-634-12	Sequence 1, Appl
c 157	12.4	44.3	50	4	US-09-613-263-5	Sequence 5, Appl	c 230	12.2	42.9	35	3	US-09-197-801-1	Sequence 1, Appl
c 158	12.4	44.3	50	4	US-09-613-263-6	Sequence 6, Appl	c 231	12.2	42.9	35	4	US-09-463-282D-23	Sequence 23, Appl
c 159	12.4	44.3	50	4	US-09-613-263-9	Sequence 9, Appl	c 232	12.2	42.9	35	4	US-09-664-595A-1	Sequence 1, Appl
c 160	12.4	44.3	50	4	US-09-613-263-10	Sequence 10, Appl	c 233	12.2	42.9	36	3	US-08-943-336A-13	Sequence 13, Appl
c 161	12.4	44.3	50	4	US-09-613-263-10	Sequence 10, Appl	c 234	12.2	42.9	36	3	US-09-635-899-13	Sequence 13, Appl
c 162	12.4	44.3	50	4	US-09-998-155B-2	Sequence 2, Appl	c 235	12.2	42.9	36	4	US-09-479-005A-950	Sequence 950, App
c 163	12.4	44.3	50	4	US-09-909-496-5	Sequence 5, Appl	c 236	12.2	42.9	36	5	PCT-US95-01780-13	Sequence 13, Appl
c 164	12.4	44.3	50	4	US-09-909-496-7	Sequence 7, Appl	c 237	12.2	42.9	37	1	US-08-411-796-497	Sequence 497, App
c 165	12.4	44.3	50	4	US-09-909-496-11	Sequence 11, Appl	c 238	12.2	42.9	37	3	US-08-471-039-497	Sequence 497, App
c 166	12.2	43.6	18	1	US-08-152-313-90	Sequence 90, Appl	c 239	12.2	42.9	37	4	US-08-559-390-497	Sequence 497, App
c 167	12.2	43.6	18	5	PCT-US94-12947A-90	Sequence 90, Appl	c 240	12.2	42.9	37	4	US-09-479-005A-1159	Sequence 1159, Ap
c 168	12.2	43.6	18	5	PCT-US94-12947A-90	Sequence 90, Appl	c 241	12.2	42.9	37	5	PCT-US93-11198-497	Sequence 497, App
c 169	12.2	43.6	19	1	US-08-379-081B-136	Sequence 136, App	c 242	12.2	42.9	38	3	US-09-476-298-48	Sequence 48, Appl
c 170	12.2	43.6	19	1	US-08-379-081B-137	Sequence 137, App	c 243	12.2	42.9	38	3	US-09-609-154-48	Sequence 48, Appl
c 171	12.2	43.6	19	1	US-08-379-078-136	Sequence 136, App	c 244	12.2	42.9	38	3	US-09-608-730B-28	Sequence 28, Appl
c 172	12.2	43.6	19	1	US-08-379-078-137	Sequence 137, App	c 245	12.2	42.9	38	4	US-09-371-772B-7157	Sequence 7157, Ap
c 173	12.2	43.6	19	2	US-08-741-327E-2	Sequence 2, Appl	c 246	12.2	42.9	38	4		

247	12	42.9	45	1	US-08-078-683A-27	Sequence 27, Appl	c 320	11.8	42.1	38	4	US-09-656-653-16	Sequence 16, Appl
248	12	42.9	45	1	US-08-078-683A-28	Sequence 28, Appl	c 321	11.8	42.1	38	4	US-09-757-251-17	Sequence 17, Appl
c 249	12	42.9	45	1	US-08-233-009-44	Sequence 44, Appl	c 322	11.8	42.1	38	4	US-09-828-259A-17	Sequence 17, Appl
250	12	42.9	45	4	US-08-471-970A-27	Sequence 27, Appl	c 323	11.8	42.1	38	4	US-09-719-878-17	Sequence 17, Appl
251	12	42.9	45	4	US-08-471-970A-28	Sequence 28, Appl	c 324	11.8	42.1	38	4	US-09-757-217A-17	Sequence 17, Appl
252	12	42.9	45	4	US-09-723-677B-27	Sequence 27, Appl	c 325	11.8	42.1	38	4	US-09-828-325A-17	Sequence 17, Appl
253	12	42.9	45	4	US-09-723-677B-28	Sequence 28, Appl	c 326	11.8	42.1	38	4	US-09-756-248-16	Sequence 16, Appl
254	12	42.9	47	1	US-08-078-683A-29	Sequence 29, Appl	c 327	11.8	42.1	40	4	US-09-348-930A-28	Sequence 28, Appl
255	12	42.9	47	4	US-08-471-970A-29	Sequence 29, Appl	c 328	11.8	42.1	41	2	US-08-985-337A-4	Sequence 4, Appl
c 256	12	42.9	47	4	US-09-422-978-697	Sequence 697, Appl	c 329	11.8	42.1	41	2	US-08-761-277A-66	Sequence 66, Appl
c 257	12	42.9	47	4	US-09-422-978-3251	Sequence 3251, Ap	c 330	11.8	42.1	41	2	US-08-985-124A-4	Sequence 4, Appl
258	12	42.9	47	4	US-09-723-677B-29	Sequence 29, Appl	c 331	11.8	42.1	41	2	US-08-985-320A-4	Sequence 4, Appl
259	12	42.9	48	1	US-08-078-683A-26	Sequence 26, Appl	c 332	11.8	42.1	41	3	US-08-984-732A-4	Sequence 4, Appl
260	12	42.9	48	4	US-08-471-970A-26	Sequence 26, Appl	c 333	11.8	42.1	41	3	US-09-195-578-16	Sequence 16, Appl
c 261	12	42.9	48	4	US-09-443-139C-1075	Sequence 1075, Ap	c 334	11.8	42.1	41	3	US-09-170-951-16	Sequence 16, Appl
262	12	42.9	48	4	US-09-723-677B-26	Sequence 26, Appl	c 335	11.8	42.1	41	3	US-09-164-482-16	Sequence 16, Appl
c 263	12	42.9	48	4	US-09-723-677A-238	Sequence 238, App	c 336	11.8	42.1	41	3	US-09-332-769-11	Sequence 11, Appl
c 264	12	42.9	49	4	US-09-907-794A-380	Sequence 380, App	c 337	11.8	42.1	41	3	US-09-456-153-11	Sequence 11, Appl
c 265	12	42.9	49	4	US-09-905-125A-238	Sequence 238, App	c 338	11.8	42.1	41	3	US-09-167-180-16	Sequence 16, Appl
c 266	12	42.9	49	4	US-09-905-125A-380	Sequence 380, App	c 339	11.8	42.1	41	3	US-09-455-627-11	Sequence 11, Appl
c 267	12	42.9	49	4	US-09-902-775A-238	Sequence 238, App	c 340	11.8	42.1	41	3	US-09-426-533-11	Sequence 11, Appl
c 268	12	42.9	49	4	US-09-902-775A-380	Sequence 380, App	c 341	11.8	42.1	41	3	US-09-609-205-12	Sequence 12, Appl
c 269	12	42.9	49	4	US-09-906-700-238	Sequence 238, App	c 342	11.8	42.1	41	3	US-09-516-945-11	Sequence 11, Appl
c 270	12	42.9	49	4	US-09-906-700-380	Sequence 380, App	c 343	11.8	42.1	41	3	US-09-757-218-12	Sequence 12, Appl
c 271	12	42.9	49	4	US-09-903-603A-238	Sequence 238, App	c 344	11.8	42.1	41	3	US-09-516-757-11	Sequence 11, Appl
c 272	12	42.9	49	4	US-09-903-603A-380	Sequence 380, App	c 345	11.8	42.1	41	3	US-09-516-750-11	Sequence 11, Appl
c 273	11.8	42.1	18	2	US-09-205-922-10	Sequence 10, Appl	c 346	11.8	42.1	41	3	US-09-342-577-12	Sequence 12, Appl
c 274	11.8	42.1	19	4	US-09-627-132-11	Sequence 1, Appl	c 347	11.8	42.1	41	3	US-09-516-756-11	Sequence 11, Appl
c 275	11.8	42.1	19	4	US-09-627-132-10	Sequence 10, Appl	c 348	11.8	42.1	41	3	US-09-828-061A-12	Sequence 12, Appl
c 276	11.8	42.1	20	2	US-08-193-039B-10	Sequence 10, Appl	c 349	11.8	42.1	41	3	US-09-463-317-11	Sequence 11, Appl
c 277	11.8	42.1	20	3	US-09-476-299-51	Sequence 51, Appl	c 350	11.8	42.1	41	4	US-09-347-673-12	Sequence 12, Appl
c 278	11.8	42.1	20	3	US-09-608-154-51	Sequence 51, Appl	c 351	11.8	42.1	41	4	US-09-757-213-12	Sequence 12, Appl
c 279	11.8	42.1	20	4	US-09-608-730B-3	Sequence 3, Appl	c 352	11.8	42.1	41	4	US-09-656-653-11	Sequence 11, Appl
c 280	11.8	42.1	20	4	US-09-860-761-10	Sequence 10, Appl	c 353	11.8	42.1	41	4	US-09-757-251-12	Sequence 12, Appl
281	11.8	42.1	22	1	US-08-148-117A-5	Sequence 5, Appl	c 354	11.8	42.1	41	4	US-09-828-259A-12	Sequence 12, Appl
c 282	11.8	42.1	22	2	US-08-603-163-2	Sequence 2, Appl	c 355	11.8	42.1	41	4	US-09-719-878-12	Sequence 12, Appl
c 283	11.8	42.1	24	1	US-08-323-910-9	Sequence 9, Appl	c 356	11.8	42.1	41	4	US-09-757-217A-12	Sequence 12, Appl
284	11.8	42.1	25	4	US-09-866-108A-13626	Sequence 13626, A	c 357	11.8	42.1	41	4	US-09-828-325A-12	Sequence 12, Appl
285	11.8	42.1	25	4	US-09-866-108A-13627	Sequence 13627, A	c 358	11.8	42.1	41	4	US-09-756-248-11	Sequence 11, Appl
286	11.8	42.1	25	4	US-09-866-108A-13628	Sequence 13628, A	c 359	11.8	42.1	44	4	US-10-001-051B-8	Sequence 8, Appl
287	11.8	42.1	27	5	PCT-US93-05224-1	Sequence 1, Appl	c 360	11.8	42.1	47	3	US-09-306-405-14	Sequence 14, Appl
288	11.8	42.1	37	1	US-08-049-264C-36	Sequence 36, Appl	c 361	11.8	42.1	47	3	US-09-306-405-30	Sequence 30, Appl
289	11.8	42.1	37	1	US-08-476-562-36	Sequence 36, Appl	c 362	11.8	42.1	47	4	US-09-671-317-804	Sequence 804, App
290	11.8	42.1	37	1	US-08-479-723A-36	Sequence 36, Appl	c 363	11.8	42.1	47	4	US-09-422-978-786	Sequence 786, App
291	11.8	42.1	37	3	US-09-476-299-49	Sequence 49, Appl	c 364	11.8	42.1	50	4	US-09-613-263-7	Sequence 7, Appl
292	11.8	42.1	37	3	US-09-609-154-49	Sequence 49, Appl	c 365	11.8	42.1	50	4	US-09-613-263-8	Sequence 8, Appl
293	11.8	42.1	37	3	US-09-210-748A-16	Sequence 16, Appl	c 366	11.8	42.1	50	4	US-09-613-263-11	Sequence 11, Appl
294	11.8	42.1	37	4	US-09-608-730B-29	Sequence 29, Appl	c 367	11.8	42.1	50	4	US-09-909-496-6	Sequence 6, Appl
295	11.8	42.1	37	4	US-09-939-581A-16	Sequence 16, Appl	c 368	11.8	42.1	50	4	US-09-909-496-8	Sequence 8, Appl
296	11.8	42.1	37	5	PCT-US94-04310-36	Sequence 36, Appl	c 369	11.8	42.1	50	4	US-09-909-496-10	Sequence 10, Appl
c 297	11.8	42.1	38	2	US-08-985-337A-9	Sequence 9, Appl	c 370	11.6	41.4	18	4	US-09-527-058-12	Sequence 12, Appl
c 298	11.8	42.1	38	2	US-08-985-124A-9	Sequence 9, Appl	c 371	11.6	41.4	18	4	US-09-527-058-14	Sequence 14, Appl
c 299	11.8	42.1	38	2	US-08-985-320A-9	Sequence 9, Appl	c 372	11.6	41.4	19	3	US-08-803-346-51	Sequence 51, Appl
c 300	11.8	42.1	38	3	US-08-984-732A-9	Sequence 9, Appl	c 373	11.6	41.4	19	4	US-09-725-752A-11	Sequence 11, Appl
c 301	11.8	42.1	38	3	US-09-195-578-21	Sequence 21, Appl	c 374	11.6	41.4	20	4	US-09-198-452A-1394	Sequence 1394, Ap
c 302	11.8	42.1	38	3	US-09-170-951-21	Sequence 21, Appl	c 375	11.6	41.4	21	4	US-09-676-610B-14	Sequence 14, Appl
c 303	11.8	42.1	38	3	US-09-164-482-21	Sequence 21, Appl	c 376	11.6	41.4	21	4	US-09-657-472-1914	Sequence 1914, Ap
c 304	11.8	42.1	38	3	US-09-332-769-16	Sequence 16, Appl	c 377	11.6	41.4	22	4	US-08-192-943-27	Sequence 27, Appl
c 305	11.8	42.1	38	3	US-09-456-153-16	Sequence 16, Appl	c 378	11.6	41.4	23	3	US-09-266-409-4	Sequence 4, Appl
c 306	11.8	42.1	38	3	US-09-167-180-21	Sequence 21, Appl	c 379	11.6	41.4	23	3	US-09-172-045-10	Sequence 10, Appl
c 307	11.8	42.1	38	3	US-09-455-627-16	Sequence 16, Appl	c 380	11.6	41.4	23	3	US-09-304-452-4	Sequence 4, Appl
c 308	11.8	42.1	38	3	US-09-426-533-16	Sequence 16, Appl	c 381	11.6	41.4	23	4	US-09-636-735A-18	Sequence 18, Appl
c 309	11.8	42.1	38	3	US-09-609-205-17	Sequence 17, Appl	c 382	11.6	41.4	23	4	US-09-678-620-4	Sequence 4, Appl
c 310	11.8	42.1	38	3	US-09-516-945-16	Sequence 16, Appl	c 383	11.6	41.4	23	4	US-09-342-325C-10	Sequence 10, Appl
c 311	11.8	42.1	38	3	US-09-757-218-17	Sequence 17, Appl	c 384	11.6	41.4	23	4	US-09-688-188B-48	Sequence 48, Appl
c 312	11.8	42.1	38	3	US-09-516-757-16	Sequence 16, Appl	c 385	11.6	41.4	23	4	US-09-291-417D-48	Sequence 48, Appl
c 313	11.8	42.1	38	3	US-09-516-750-16	Sequence 16, Appl	c 386	11.6	41.4	24	2	US-08-442-010-9	Sequence 9, Appl
c 314	11.8	42.1	38	3	US-09-342-577-17	Sequence 17, Appl	c 387	11.6	41.4	24	3	US-08-680-116-11	Sequence 11, Appl
c 315	11.8	42.1	38	3	US-09-516-756-16	Sequence 16, Appl	c 388	11.6	41.4	25	4	US-09-866-108A-4555	Sequence 4555, Ap
c 316	11.8	42.1	38	3	US-09-828-061A-17	Sequence 17, Appl	c 389	11.6	41.4	25	4	US-09-866-108A-4556	Sequence 4556, Ap
c 317	11.8	42.1	38	3	US-09-463-917-17	Sequence 17, Appl	c 390	11.6	41.4	25	4	US-09-866-108A-4557	Sequence 4557, Ap
c 318	11.8	42.1	38	4	US-09-347-673-17	Sequence 17, Appl	c 391	11.6	41.4	25	4	US-09-866-108A-4558	Sequence 4558, Ap
c 319	11.8	42.1	38	4	US-09-757-213-17	Sequence 17, Appl	c 392	11.6	41.4	25	4	US-09-866-108A-4559	Sequence 4559, Ap

C 393	11.6	41.4	25	4	US-09-866-108A-4560	Sequence 4560, Ap	C 466	11.4	40.7	32	1	US-08-591-070A-30	Sequence 30, Appl
C 394	11.6	41.4	25	4	US-09-866-108A-4561	Sequence 4561, Ap	C 467	11.4	40.7	32	2	US-08-927-855-30	Sequence 30, Appl
C 395	11.6	41.4	25	4	US-09-866-108A-4562	Sequence 4562, Ap	C 468	11.4	40.7	33	3	US-09-477-392-23	Sequence 23, Appl
C 396	11.6	41.4	28	4	US-09-559-306-12	Sequence 12, Appl	C 469	11.4	40.7	35	3	US-09-023-173-15	Sequence 15, Appl
C 397	11.6	41.4	28	4	US-09-877-476-46	Sequence 46, Appl	C 470	11.4	40.7	35	3	US-09-023-339-12	Sequence 12, Appl
C 398	11.6	41.4	30	3	US-09-092-317-3	Sequence 3, Appl	C 471	11.4	40.7	36	3	US-09-013-895A-9	Sequence 9, Appl
C 399	11.6	41.4	30	3	US-09-433-621-1	Sequence 1, Appl	C 472	11.4	40.7	36	3	US-09-565-918-10	Sequence 10, Appl
C 400	11.6	41.4	35	1	US-08-361-337-75	Sequence 75, Appl	C 473	11.4	40.7	36	4	US-09-448-868-9	Sequence 9, Appl
C 401	11.6	41.4	35	4	US-09-568-051-1	Sequence 1, Appl	C 474	11.4	40.7	36	4	US-09-371-772B-14190	Sequence 14190, A
C 402	11.6	41.4	36	1	US-08-373-124A-113	Sequence 113, App	C 475	11.4	40.7	38	3	US-09-266-596-41	Sequence 41, Appl
C 403	11.6	41.4	36	1	US-08-334-847-257	Sequence 257, App	C 476	11.4	40.7	38	4	US-09-944-411-41	Sequence 41, Appl
C 404	11.6	41.4	36	1	US-08-334-847-681	Sequence 681, App	C 477	11.4	40.7	39	3	US-08-675-568-120	Sequence 4, Appl
C 405	11.6	41.4	36	1	US-08-334-847-715	Sequence 715, App	C 478	11.4	40.7	39	4	US-09-223-139-4	Sequence 5, Appl
C 406	11.6	41.4	36	1	US-08-363-240A-871	Sequence 871, App	C 479	11.4	40.7	41	4	US-09-666-890-5	Sequence 32, Appl
C 407	11.6	41.4	36	1	US-08-363-240A-872	Sequence 872, App	C 480	11.4	40.7	42	4	US-09-674-677-32	Sequence 3, Appl
C 408	11.6	41.4	36	1	US-08-311-486C-332	Sequence 332, App	C 481	11.4	40.7	45	2	US-08-467-816-3	Sequence 47, Appl
C 409	11.6	41.4	36	1	US-08-435-628-113	Sequence 113, App	C 482	11.4	40.7	45	3	US-08-983-035A-47	Sequence 1251, Ap
C 410	11.6	41.4	36	2	US-08-585-684B-1111	Sequence 1111, Ap	C 483	11.4	40.7	47	4	US-09-641-638-1251	Sequence 164, App
C 411	11.6	41.4	36	2	US-08-585-684B-1112	Sequence 1112, Ap	C 484	11.4	40.7	47	4	US-09-422-978-164	Sequence 2714, Ap
C 412	11.6	41.4	36	2	US-08-585-684B-2187	Sequence 2187, Ap	C 485	11.4	40.7	47	4	US-09-422-978-2714	Sequence 1731, Ap
C 413	11.6	41.4	36	3	US-08-833-167-75	Sequence 75, Appl	C 486	11.4	40.7	47	4	US-09-422-978-3731	Sequence 1251, Ap
C 414	11.6	41.4	36	3	US-09-038-073-1111	Sequence 1111, Ap	C 487	11.4	40.7	47	4	US-10-170-097-1251	Sequence 26, Appl
C 415	11.6	41.4	36	3	US-09-038-073-1112	Sequence 1112, Ap	C 488	11.4	40.7	48	3	US-08-817-787-26	Sequence 26, Appl
C 416	11.6	41.4	36	3	US-09-038-073-2187	Sequence 2187, Ap	C 489	11.4	40.7	48	4	US-08-583-808-26	Sequence 121, App
C 417	11.6	41.4	36	3	US-09-344-837A-75	Sequence 75, Appl	C 490	11.4	40.7	49	1	US-08-384-708A-121	Sequence 121, App
C 418	11.6	41.4	38	1	US-08-373-124A-539	Sequence 539, App	C 491	11.4	40.7	49	3	US-08-667-421-121	Sequence 121, App
C 419	11.6	41.4	38	1	US-08-373-124A-1578	Sequence 1578, App	C 492	11.4	40.7	49	4	US-08-442-423-121	Sequence 19, App
C 420	11.6	41.4	38	1	US-08-373-124A-2446	Sequence 2446, Ap	C 493	11.4	40.7	50	3	US-09-298-886-19	Sequence 25, Appl
C 421	11.6	41.4	38	1	US-08-373-124A-2580	Sequence 2580, Ap	C 494	11.4	40.7	50	3	US-09-298-886-25	Sequence 28, Appl
C 422	11.6	41.4	38	1	US-08-435-628-539	Sequence 539, App	C 495	11.4	40.7	50	3	US-09-298-886-28	Sequence 10, Appl
C 423	11.6	41.4	38	1	US-08-435-628-1578	Sequence 1578, Ap	C 496	11.4	40.7	50	4	US-09-399-672-19	Sequence 19, Appl
C 424	11.6	41.4	38	1	US-08-435-628-2446	Sequence 2446, Ap	C 497	11.4	40.7	50	4	US-09-399-672-25	Sequence 25, Appl
C 425	11.6	41.4	38	1	US-08-435-628-2580	Sequence 2580, Ap	C 498	11.4	40.7	50	4	US-09-999-672-28	Sequence 28, Appl
C 426	11.6	41.4	40	4	US-09-247-890-13	Sequence 13, Appl	C 499	11.4	40.7	50	4	US-09-888-413-10	Sequence 10, Appl
C 427	11.6	41.4	40	4	US-09-724-969-13	Sequence 13, Appl	C 500	11.4	40.7	50	4	US-08-758-306-1237	Sequence 1237, Ap
C 428	11.6	41.4	40	4	US-09-724-852-13	Sequence 13, Appl	C 501	11.2	40.0	17	1	US-09-339-993-32	Sequence 32, Appl
C 429	11.6	41.4	41	4	US-09-434-354-16	Sequence 16, Appl	C 502	11.2	40.0	18	3	US-09-723-534-25	Sequence 25, Appl
C 430	11.6	41.4	41	4	US-09-568-051-2	Sequence 2, Appl	C 503	11.2	40.0	18	3	US-09-820-479-6	Sequence 6, Appl
C 431	11.6	41.4	41	4	US-09-709-785-16	Sequence 16, Appl	C 504	11.2	40.0	19	4	US-08-166-186-81	Sequence 81, Appl
C 432	11.6	41.4	42	3	US-08-679-645-23	Sequence 23, Appl	C 505	11.2	40.0	20	3	US-09-313-932-81	Sequence 81, Appl
C 433	11.6	41.4	47	4	US-09-671-317-584	Sequence 584, App	C 506	11.2	40.0	20	3	US-09-659-791A-78	Sequence 78, Appl
C 434	11.6	41.4	47	4	US-09-671-317-749	Sequence 749, App	C 507	11.2	40.0	20	3	US-08-110-161A-1	Sequence 1, Appl
C 435	11.6	41.4	47	4	US-09-422-978-2883	Sequence 2883, Ap	C 508	11.2	40.0	21	4	US-08-110-161A-5	Sequence 5, Appl
C 436	11.6	41.4	47	4	US-09-422-978-3782	Sequence 3782, Ap	C 509	11.2	40.0	21	4	PCT-US94-09350-1	Sequence 1, Appl
C 437	11.6	41.4	50	1	US-08-243-870-10	Sequence 10, Appl	C 510	11.2	40.0	21	5	PCT-US94-09350-5	Sequence 5, Appl
C 438	11.6	41.4	50	1	US-08-409-439A-10	Sequence 10, Appl	C 511	11.2	40.0	21	5	US-08-887-497A-50	Sequence 50, Appl
C 439	11.6	41.4	50	4	US-09-470-661A-36	Sequence 36, Appl	C 512	11.2	40.0	23	4	US-08-328-174A-58	Sequence 58, Appl
C 440	11.6	41.4	50	4	US-09-621-976-18753	Sequence 18753, A	C 513	11.2	40.0	24	4	US-08-887-497A-49	Sequence 49, Appl
C 441	11.4	40.7	20	4	US-09-198-452A-6346	Sequence 6346, Ap	C 514	11.2	40.0	24	4	US-08-327-832-13	Sequence 13, Appl
C 442	11.4	40.7	22	1	US-08-070-328A-9	Sequence 9, Appl	C 515	11.2	40.0	25	2	US-08-454-549-7	Sequence 7, Appl
C 443	11.4	40.7	22	1	US-08-070-328A-15	Sequence 15, Appl	C 516	11.2	40.0	25	2	US-08-828-584-13	Sequence 13, Appl
C 444	11.4	40.7	22	1	US-08-455-116-9	Sequence 9, Appl	C 517	11.2	40.0	25	2	US-08-454-552-7	Sequence 7, Appl
C 445	11.4	40.7	22	1	US-08-455-116-15	Sequence 15, Appl	C 518	11.2	40.0	25	3	US-08-447-702-3	Sequence 3, Appl
C 446	11.4	40.7	22	3	US-08-594-452-70	Sequence 70, Appl	C 519	11.2	40.0	25	4	US-08-887-497A-48	Sequence 48, Appl
C 447	11.4	40.7	22	3	US-09-258-408-70	Sequence 70, Appl	C 520	11.2	40.0	26	1	US-08-612-973-104	Sequence 104, App
C 448	11.4	40.7	23	3	US-07-972-791-9	Sequence 9, Appl	C 521	11.2	40.0	26	3	US-08-927-597-104	Sequence 10, Appl
C 449	11.4	40.7	23	5	PCT-US92-02977-7	Sequence 7, Appl	C 522	11.2	40.0	26	3	US-08-250-958-10	Sequence 10, Appl
C 450	11.4	40.7	23	5	PCT-US95-03032-8	Sequence 8, Appl	C 523	11.2	40.0	29	1	US-08-349-696-13	Sequence 13, Appl
C 451	11.4	40.7	23	6	5310649-2	Patent No. 5310649	C 524	11.2	40.0	29	1	US-08-233-009-13	Sequence 13, Appl
C 452	11.4	40.7	24	3	US-09-049-698-25	Sequence 25, Appl	C 525	11.2	40.0	29	1	US-08-232-015-54	Sequence 54, Appl
C 453	11.4	40.7	25	3	US-08-465-590-77	Sequence 77, Appl	C 526	11.2	40.0	29	2	US-08-217-210B-9	Sequence 9, Appl
C 454	11.4	40.7	25	3	US-09-721-417C-77	Sequence 77, Appl	C 527	11.2	40.0	29	2	US-08-244-121-13	Sequence 13, Appl
C 455	11.4	40.7	25	4	US-09-723-909-77	Sequence 77, Appl	C 528	11.2	40.0	29	2	US-09-080-704A-13	Sequence 13, Appl
C 456	11.4	40.7	25	5	PCT-US93-08743-19	Sequence 19, Appl	C 529	11.2	40.0	30	1	US-08-480-784-46	Sequence 46, Appl
C 457	11.4	40.7	26	4	US-09-437-568A-17	Sequence 17, Appl	C 530	11.2	40.0	30	1	US-08-480-784-46	Sequence 46, Appl
C 458	11.4	40.7	27	2	US-08-706-322-4	Sequence 4, Appl	C 531	11.2	40.0	30	1	US-08-483-553-46	Sequence 46, Appl
C 459	11.4	40.7	28	2	US-08-859-998-1123	Sequence 1123, Ap	C 532	11.2	40.0	30	1	US-08-487-002-46	Sequence 46, Appl
C 460	11.4	40.7	28	3	US-09-225-928-1123	Sequence 1123, Ap	C 533	11.2	40.0	30	1	US-08-488-011B-46	Sequence 46, Appl
C 461	11.4	40.7	28	4	US-09-225-201B-1123	Sequence 1123, Ap	C 534	11.2	40.0	30	1	US-08-488-011B-46	Sequence 46, Appl
C 462	11.4	40.7	28	4	US-09-857-716-23	Sequence 23, Appl	C 535	11.2	40.0	30	1	US-08-115-753-20	Sequence 20, Appl
C 463	11.4	40.7	29	3	US-09-189-653-7	Sequence 7, Appl	C 536	11.2	40.0	30	3	US-08-850-727-46	Sequence 46, Appl
C 464	11.4	40.7	29	4	US-09-485-539-94	Sequence 94, Appl	C 537	11.2	40.0	30	4	US-08-887-497A-85	Sequence 85, Appl
C 465	11.4	40.7	29	4	US-09-574-779B-112	Sequence 112, App	C 538	11.2	40.0	30	4		

539	11.2	40.0	30	4	US-08-887-497A-86	Sequence 86, Appl	612	11	39.3	20	4	US-09-501-612A-29	Sequence 29, Appl
540	11.2	40.0	30	5	PCT-US95-10202-46	Sequence 46, Appl	613	11	39.3	20	4	US-09-835-370-15	Sequence 15, Appl
541	11.2	40.0	30	5	PCT-US95-10203-46	Sequence 46, Appl	614	11	39.3	21	3	US-08-594-452-69	Sequence 69, Appl
542	11.2	40.0	30	5	PCT-US95-10220-46	Sequence 46, Appl	615	11	39.3	21	3	US-09-258-408-69	Sequence 69, Appl
543	11.2	40.0	33	3	US-09-476-299-6	Sequence 6, Appl	616	11	39.3	21	3	US-09-262-773-80	Sequence 80, Appl
544	11.2	40.0	33	3	US-09-609-154-6	Sequence 6, Appl	617	11	39.3	21	4	US-09-657-472-1455	Sequence 1455, Ap
545	11.2	40.0	34	1	US-08-741-881-75	Sequence 75, Appl	c 618	11	39.3	21	4	US-09-657-472-1622	Sequence 1622, Ap
546	11.2	40.0	34	1	US-08-739-158-75	Sequence 75, Appl	c 619	11	39.3	21	4	US-09-696-791-4476	Sequence 4476, Ap
547	11.2	40.0	34	2	US-08-739-158-75	Sequence 75, Appl	620	11	39.3	22	3	US-09-262-773-82	Sequence 82, Appl
548	11.2	40.0	34	3	US-08-404-796-75	Sequence 75, Appl	621	11	39.3	22	4	US-09-972-115A-37	Sequence 37, Appl
549	11.2	40.0	34	3	US-08-931-869-75	Sequence 75, Appl	622	11	39.3	23	3	US-08-666-221B-15	Sequence 15, Appl
550	11.2	40.0	34	3	US-09-011-745-13	Sequence 13, Appl	623	11	39.3	24	3	US-08-343-398-3	Sequence 3, Appl
551	11.2	40.0	34	3	US-09-350-399-75	Sequence 75, Appl	624	11	39.3	24	3	US-09-135-021-43	Sequence 43, Appl
552	11.2	40.0	34	3	US-09-236-140A-75	Sequence 75, Appl	625	11	39.3	24	3	US-09-135-020-45	Sequence 45, Appl
553	11.2	40.0	35	3	US-09-164-023-20	Sequence 20, Appl	626	11	39.3	24	3	US-09-135-010A-45	Sequence 45, Appl
554	11.2	40.0	36	3	US-09-204-208A-5	Sequence 5, Appl	627	11	39.3	24	3	US-09-444-871-45	Sequence 45, Appl
555	11.2	40.0	36	4	US-09-269-861A-5	Sequence 5, Appl	628	11	39.3	24	4	US-09-597-735-45	Sequence 45, Appl
556	11.2	40.0	36	4	US-10-072-436-5	Sequence 5, Appl	629	11	39.3	24	4	US-09-444-295-45	Sequence 45, Appl
557	11.2	40.0	37	2	US-08-291-074-4	Sequence 4, Appl	630	11	39.3	24	4	US-09-597-732-45	Sequence 45, Appl
558	11.2	40.0	37	4	US-09-470-661A-31	Sequence 31, Appl	631	11	39.3	24	4	US-09-597-731-45	Sequence 45, Appl
559	11.2	40.0	38	3	US-08-931-608A-10	Sequence 10, Appl	632	11	39.3	25	4	US-09-367-007C-29	Sequence 29, Appl
560	11.2	40.0	38	4	US-08-983-397-10	Sequence 10, Appl	633	11	39.3	25	4	US-08-887-497A-75	Sequence 75, Appl
561	11.2	40.0	38	4	US-09-851-847-10	Sequence 10, Appl	634	11	39.3	25	4	US-09-888-413-93	Sequence 93, Appl
562	11.2	40.0	39	3	US-09-213-053-28	Sequence 28, Appl	635	11	39.3	26	3	US-09-382-256-24	Sequence 24, Appl
563	11.2	40.0	39	3	US-09-476-239-12	Sequence 12, Appl	636	11	39.3	26	3	US-09-395-115-24	Sequence 24, Appl
564	11.2	40.0	39	3	US-09-609-154-12	Sequence 12, Appl	637	11	39.3	26	3	US-08-436-265-24	Sequence 24, Appl
565	11.2	40.0	39	3	US-09-415-784-71	Sequence 71, Appl	638	11	39.3	26	3	US-09-679-187-24	Sequence 24, Appl
566	11.2	40.0	39	4	US-09-415-785A-71	Sequence 71, Appl	639	11	39.3	26	4	US-09-267-963D-24	Sequence 24, Appl
567	11.2	40.0	39	4	US-08-944-465-71	Sequence 71, Appl	640	11	39.3	26	4	US-09-792-616-14	Sequence 14, Appl
568	11.2	40.0	39	4	US-09-415-868-71	Sequence 71, Appl	641	11	39.3	27	1	US-08-306-870-1	Sequence 1, Appl
569	11.2	40.0	39	4	US-09-415-900-71	Sequence 71, Appl	642	11	39.3	27	1	US-08-305-769A-1	Sequence 1, Appl
570	11.2	40.0	39	4	US-09-254-547A-2	Sequence 2, Appl	643	11	39.3	27	1	US-08-495-743-38	Sequence 38, Appl
571	11.2	40.0	39	4	US-09-507-362-71	Sequence 71, Appl	644	11	39.3	27	1	US-08-495-739-38	Sequence 38, Appl
572	11.2	40.0	40	3	US-09-254-352B-2	Sequence 2, Appl	645	11	39.3	27	1	US-08-495-741-38	Sequence 38, Appl
573	11.2	40.0	40	4	US-09-538-709-1225	Sequence 1225, Ap	646	11	39.3	27	1	US-08-555-678-62	Sequence 62, Appl
574	11.2	40.0	45	3	US-09-091-814-105	Sequence 105, Ap	647	11	39.3	27	2	US-08-643-282-1	Sequence 1, Appl
575	11.2	40.0	46	2	US-08-406-855A-18	Sequence 18, Appl	648	11	39.3	27	3	US-08-642-023-38	Sequence 38, Appl
576	11.2	40.0	46	3	US-09-206-899-18	Sequence 18, Appl	649	11	39.3	27	4	US-09-305-681A-9	Sequence 9, Appl
577	11.2	40.0	46	4	US-09-688-415-23	Sequence 23, Appl	650	11	39.3	27	4	US-08-062-021A-16	Sequence 16, Appl
578	11.2	40.0	47	3	US-09-263-904-3	Sequence 3, Appl	651	11	39.3	28	1	US-08-554-659-6	Sequence 6, Appl
579	11.2	40.0	47	4	US-09-641-638-1272	Sequence 1272, Ap	652	11	39.3	30	1	US-08-160-670A-40	Sequence 40, Appl
580	11.2	40.0	47	4	US-09-422-978-3203	Sequence 3203, Ap	653	11	39.3	30	1	US-08-488-702-14	Sequence 14, Appl
581	11.2	40.0	47	4	US-09-422-978-3641	Sequence 3641, Ap	654	11	39.3	30	2	US-08-859-998-446	Sequence 446, App
582	11.2	40.0	47	4	US-10-170-097-1272	Sequence 1272, Ap	655	11	39.3	30	3	US-08-463-903-72	Sequence 72, Appl
583	11.2	40.0	48	1	US-08-116-389-16	Sequence 16, Appl	656	11	39.3	30	3	US-08-421-207-3	Sequence 3, Appl
584	11.2	40.0	48	1	US-08-708-431-16	Sequence 16, Appl	657	11	39.3	30	3	US-07-935-695-72	Sequence 72, Appl
585	11.2	40.0	48	2	US-08-880-830-16	Sequence 16, Appl	658	11	39.3	30	3	US-09-235-928-446	Sequence 446, App
586	11.2	40.0	48	3	US-08-864-473-58	Sequence 58, Appl	659	11	39.3	30	4	US-08-225-201B-446	Sequence 446, App
587	11.2	40.0	48	3	US-09-440-523-58	Sequence 58, Appl	660	11	39.3	31	1	US-08-086-428B-116	Sequence 116, App
588	11.2	40.0	48	4	US-09-918-156-58	Sequence 58, Appl	661	11	39.3	31	2	US-08-468-570-116	Sequence 116, App
589	11.2	40.0	48	5	PCT-US94-13895-16	Sequence 16, Appl	662	11	39.3	31	2	US-08-290-665A-220	Sequence 220, App
590	11.2	40.0	50	3	US-09-208-966-14	Sequence 14, Appl	663	11	39.3	31	4	US-08-466-601A-116	Sequence 116, App
591	11.2	40.0	50	4	US-09-775-052A-14	Sequence 14, Appl	664	11	39.3	31	4	US-09-854-549A-3	Sequence 3, Appl
592	11	39.3	19	4	US-09-422-978-7202	Sequence 7202, Ap	665	11	39.3	31	5	PCT-US95-10398-220	Sequence 220, App
593	11	39.3	20	1	US-09-015-876-18	Sequence 18, Appl	666	11	39.3	32	2	US-08-747-536-9	Sequence 9, Appl
594	11	39.3	20	1	US-08-462-305-14	Sequence 14, Appl	667	11	39.3	32	2	US-08-815-718-4	Sequence 4, Appl
595	11	39.3	20	2	US-08-613-417A-14	Sequence 14, Appl	668	11	39.3	32	4	US-08-462-509B-11	Sequence 11, Appl
596	11	39.3	20	3	US-08-594-452-14	Sequence 14, Appl	669	11	39.3	32	5	PCT-US95-05616-11	Sequence 11, Appl
597	11	39.3	20	3	US-08-578-686C-13	Sequence 13, Appl	670	11	39.3	33	2	US-08-394-177-9	Sequence 9, Appl
598	11	39.3	20	3	US-08-281-203-16	Sequence 16, Appl	671	11	39.3	33	4	US-08-333-636-9	Sequence 9, Appl
599	11	39.3	20	3	US-09-094-405-16	Sequence 16, Appl	672	11	39.3	34	1	US-08-464-340A-7	Sequence 7, Appl
600	11	39.3	20	3	US-09-258-408-14	Sequence 14, Appl	673	11	39.3	34	3	US-09-334-181-1	Sequence 1, Appl
601	11	39.3	20	3	US-09-418-641-22	Sequence 22, Appl	674	11	39.3	35	2	US-08-442-497C-7	Sequence 7, Appl
602	11	39.3	20	3	US-09-196-132-14	Sequence 14, Appl	675	11	39.3	35	3	US-09-333-033-7	Sequence 7, Appl
603	11	39.3	20	3	US-09-287-796-157	Sequence 157, App	676	11	39.3	35	4	US-10-004-832-7	Sequence 7, Appl
604	11	39.3	20	3	US-09-144-112-13	Sequence 13, Appl	677	11	39.3	36	4	US-09-556-877-211	Sequence 211, App
605	11	39.3	20	3	US-09-130-616-157	Sequence 157, App	678	11	39.3	36	4	US-09-620-412C-211	Sequence 211, App
606	11	39.3	20	3	US-09-657-481A-79	Sequence 79, Appl	679	11	39.3	36	4	US-09-598-419-211	Sequence 211, App
607	11	39.3	20	3	US-09-471-016-5	Sequence 5, Appl	680	11	39.3	38	1	US-08-373-124A-401	Sequence 401, App
608	11	39.3	20	3	US-08-895-981-14	Sequence 14, Appl	681	11	39.3	38	1	US-08-435-628-401	Sequence 401, App
609	11	39.3	20	3	US-08-337-120A-16	Sequence 16, Appl	682	11	39.3	38	2	US-08-537-811-13	Sequence 13, Appl
610	11	39.3	20	3	US-09-495-797-10	Sequence 10, Appl	683	11	39.3	38	4	US-09-371-772B-7506	Sequence 7506, Ap
611	11	39.3	20	4	US-09-643-233-13	Sequence 13, Appl	684	11	39.3	38	4	US-09-371-772B-8259	Sequence 8259, Ap

C 831	10.8	38.6	30	4	US-09-954-594A-18	Sequence 18, Appl	C 904	10.8	38.6	45	2	US-08-975-902-33	Sequence 33, Appl
C 832	10.8	38.6	30	4	US-09-574-779B-114	Sequence 114, Appl	C 905	10.8	38.6	45	3	US-09-251-565-33	Sequence 33, Appl
C 833	10.8	38.6	30	4	US-09-599-002-1	Sequence 1, Appl	906	10.8	38.6	45	3	US-09-224-426-7	Sequence 7, Appl
C 834	10.8	38.6	30	4	US-09-599-002-2	Sequence 2, Appl	907	10.8	38.6	45	3	US-09-478-601-7	Sequence 7, Appl
C 835	10.8	38.6	30	5	PCT-US92-02050-31	Sequence 31, Appl	908	10.8	38.6	45	3	US-03-478-602-7	Sequence 7, Appl
C 836	10.8	38.6	31	2	US-08-718-658-5	Sequence 5, Appl	909	10.8	38.6	45	4	US-03-885-478-7	Sequence 7, Appl
C 837	10.8	38.6	31	3	US-09-195-666A-39	Sequence 39, Appl	910	10.8	38.6	46	2	US-08-882-704A-8	Sequence 8, Appl
C 838	10.8	38.6	31	3	US-09-195-666A-42	Sequence 42, Appl	911	10.8	38.6	46	4	US-09-151-957-8	Sequence 8, Appl
C 839	10.8	38.6	31	3	US-08-840-466A-13	Sequence 13, Appl	912	10.8	38.6	46	4	US-10-195-158-8	Sequence 8, Appl
C 840	10.8	38.6	31	3	US-09-227-684-5	Sequence 5, Appl	913	10.8	38.6	47	1	US-07-933-469A-9	Sequence 9, Appl
C 841	10.8	38.6	31	3	US-09-635-705-39	Sequence 39, Appl	914	10.8	38.6	47	4	US-09-641-638-903	Sequence 903, Appl
C 842	10.8	38.6	31	3	US-09-635-705-42	Sequence 42, Appl	915	10.8	38.6	47	4	US-03-641-638-1110	Sequence 1110, Appl
C 843	10.8	38.6	31	4	US-09-696-188B-13	Sequence 13, Appl	C 916	10.8	38.6	47	4	US-09-422-978-1903	Sequence 1903, Appl
C 844	10.8	38.6	31	4	US-09-634-858A-39	Sequence 39, Appl	917	10.8	38.6	47	4	US-09-422-978-2425	Sequence 2425, Appl
C 845	10.8	38.6	31	4	US-09-634-858A-42	Sequence 42, Appl	C 918	10.8	38.6	47	4	US-09-422-978-3534	Sequence 3534, Appl
C 846	10.8	38.6	31	4	US-08-869-927C-39	Sequence 39, Appl	C 919	10.8	38.6	47	4	US-09-422-978-3816	Sequence 3816, Appl
C 847	10.8	38.6	31	4	US-08-869-927C-42	Sequence 42, Appl	920	10.8	38.6	47	4	US-10-170-097-903	Sequence 903, Appl
C 848	10.8	38.6	31	4	US-08-693-234-24	Sequence 24, Appl	921	10.8	38.6	47	4	US-10-170-097-1110	Sequence 1110, Appl
C 849	10.8	38.6	31	4	US-09-877-476-54	Sequence 54, Appl	922	10.8	38.6	48	1	US-08-285-936-36	Sequence 36, Appl
C 850	10.8	38.6	31	4	US-09-785-881-3	Sequence 3, Appl	923	10.8	38.6	48	1	US-08-487-860-36	Sequence 36, Appl
C 851	10.8	38.6	31	4	US-09-785-881-4	Sequence 4, Appl	C 924	10.8	38.6	48	4	US-09-500-123-3	Sequence 3, Appl
C 852	10.8	38.6	32	1	US-08-644-664B-39	Sequence 39, Appl	C 925	10.8	38.6	50	1	US-08-171-389-343	Sequence 343, Appl
C 853	10.8	38.6	32	2	US-08-761-277A-39	Sequence 39, Appl	C 926	10.8	38.6	50	1	US-08-173-936-343	Sequence 343, Appl
C 854	10.8	38.6	32	3	US-09-191-608-25	Sequence 25, Appl	C 927	10.8	38.6	50	2	US-08-475-228A-343	Sequence 343, Appl
C 855	10.8	38.6	33	1	US-08-218-933-4	Sequence 4, Appl	C 928	10.8	38.6	50	3	US-08-482-080A-343	Sequence 343, Appl
C 856	10.8	38.6	33	3	US-08-722-719-43	Sequence 43, Appl	929	10.8	38.6	50	3	US-09-298-886-13	Sequence 13, Appl
C 857	10.8	38.6	33	4	US-09-334-951-43	Sequence 43, Appl	C 930	10.8	38.6	50	3	US-09-354-947-343	Sequence 343, Appl
C 858	10.8	38.6	33	4	US-09-334-923A-43	Sequence 43, Appl	931	10.8	38.6	50	4	US-09-999-672-13	Sequence 13, Appl
C 859	10.8	38.6	33	4	US-09-689-693-34	Sequence 34, Appl	C 932	10.8	38.6	50	5	PCT-US93-12388-343	Sequence 343, Appl
C 860	10.8	38.6	33	4	US-09-334-954A-43	Sequence 43, Appl	C 933	10.6	37.9	17	4	US-09-866-108A-1625	Sequence 1625, Appl
C 861	10.8	38.6	33	5	PCT-US95-03918-4	Sequence 4, Appl	C 934	10.6	37.9	17	4	US-09-866-108A-1626	Sequence 1626, Appl
C 862	10.8	38.6	35	4	US-09-709-103-14	Sequence 14, Appl	C 935	10.6	37.9	18	4	US-09-375-248-23	Sequence 23, Appl
C 863	10.8	38.6	35	4	US-09-709-103-15	Sequence 15, Appl	936	10.6	37.9	19	1	US-08-562-539-31	Sequence 31, Appl
C 864	10.8	38.6	35	4	US-09-439-410A-14	Sequence 14, Appl	937	10.6	37.9	19	1	US-08-621-502A-10	Sequence 10, Appl
C 865	10.8	38.6	35	4	US-09-439-410A-15	Sequence 15, Appl	938	10.6	37.9	19	3	US-08-797-722-4	Sequence 4, Appl
C 866	10.8	38.6	36	3	US-09-455-960-25	Sequence 25, Appl	939	10.6	37.9	19	3	US-09-641-599-5	Sequence 5, Appl
C 867	10.8	38.6	36	4	US-10-051-325-25	Sequence 25, Appl	940	10.6	37.9	19	4	US-09-584-216-11	Sequence 11, Appl
C 868	10.8	38.6	36	6	5258287-12	Patent No. 5258287	941	10.6	37.9	20	1	US-08-208-795-3	Sequence 3, Appl
C 869	10.8	38.6	37	1	US-08-653-740-30	Sequence 30, Appl	C 942	10.6	37.9	20	2	US-08-463-418-9	Sequence 9, Appl
C 870	10.8	38.6	37	2	US-09-073-594-30	Sequence 30, Appl	C 943	10.6	37.9	20	2	US-08-368-704C-94	Sequence 94, Appl
C 871	10.8	38.6	37	2	US-09-019-201A-10	Sequence 10, Appl	C 944	10.6	37.9	20	3	US-09-596-938-8	Sequence 8, Appl
C 872	10.8	38.6	37	3	US-09-275-925-30	Sequence 30, Appl	C 945	10.6	37.9	20	4	US-09-657-452A-58	Sequence 58, Appl
C 873	10.8	38.6	37	4	US-09-842-164A-19	Sequence 19, Appl	C 946	10.6	37.9	20	4	US-09-360-416-121	Sequence 121, Appl
C 874	10.8	38.6	37	4	US-09-455-950-10	Sequence 10, Appl	947	10.6	37.9	20	4	US-08-887-497A-5	Sequence 5, Appl
C 875	10.8	38.6	38	4	US-09-877-476-56	Sequence 56, Appl	948	10.6	37.9	20	4	US-08-887-497A-74	Sequence 74, Appl
C 876	10.8	38.6	39	2	US-08-190-199A-27	Sequence 27, Appl	949	10.6	37.9	20	4	US-09-471-913-15	Sequence 15, Appl
C 877	10.8	38.6	40	1	US-07-959-941-6	Sequence 6, Appl	950	10.6	37.9	20	4	US-08-471-974-5	Sequence 5, Appl
C 878	10.8	38.6	40	1	US-08-259-924-6	Sequence 6, Appl	C 951	10.6	37.9	20	4	US-08-188-452A-2463	Sequence 2463, Appl
C 879	10.8	38.6	40	1	US-08-276-852-36	Sequence 36, Appl	952	10.6	37.9	20	4	US-09-198-452A-2733	Sequence 2733, Appl
C 880	10.8	38.6	40	1	US-08-133-011-108	Sequence 108, Appl	953	10.6	37.9	20	4	US-09-269-939A-28	Sequence 28, Appl
C 881	10.8	38.6	40	1	US-08-301-722A-6	Sequence 6, Appl	954	10.6	37.9	20	4	US-09-758-881-131	Sequence 131, Appl
C 882	10.8	38.6	40	1	US-08-322-730A-108	Sequence 108, Appl	C 955	10.6	37.9	21	3	US-08-835-728D-73	Sequence 73, Appl
C 883	10.8	38.6	40	1	US-08-387-874-80	Sequence 80, Appl	956	10.6	37.9	21	3	US-08-835-728D-177	Sequence 177, Appl
C 884	10.8	38.6	40	1	US-08-899-575-36	Sequence 36, Appl	C 957	10.6	37.9	21	3	US-09-490-558-177	Sequence 73, Appl
C 885	10.8	38.6	40	2	US-08-899-575-36	Sequence 36, Appl	958	10.6	37.9	21	3	US-09-490-558-177	Sequence 177, Appl
C 886	10.8	38.6	40	2	US-08-899-575-36	Sequence 108, Appl	959	10.6	37.9	21	3	US-08-887-497A-76	Sequence 76, Appl
C 887	10.8	38.6	40	2	US-08-899-575-36	Sequence 37	C 960	10.6	37.9	21	4	US-09-422-978-6753	Sequence 6753, Appl
C 888	10.8	38.6	40	3	US-08-820-970-5	Sequence 5, Appl	961	10.6	37.9	21	4	US-09-657-472-239	Sequence 239, Appl
C 889	10.8	38.6	40	3	US-08-646-538-20	Sequence 20, Appl	962	10.6	37.9	21	4	US-09-657-472-1555	Sequence 1555, Appl
C 890	10.8	38.6	40	3	US-08-646-538-23	Sequence 23, Appl	963	10.6	37.9	24	2	US-08-487-727A-11	Sequence 11, Appl
C 891	10.8	38.6	40	3	US-08-767-128-44	Sequence 44, Appl	C 964	10.6	37.9	24	2	US-08-487-727A-12	Sequence 12, Appl
C 892	10.8	38.6	40	3	US-09-075-272-10	Sequence 10, Appl	965	10.6	37.9	24	3	US-08-772-440-37	Sequence 37, Appl
C 893	10.8	38.6	40	3	US-09-907-739-108	Sequence 108, Appl	C 966	10.6	37.9	25	4	US-09-388-743-23	Sequence 23, Appl
C 894	10.8	38.6	40	3	US-09-503-222-20	Sequence 20, Appl	967	10.6	37.9	25	4	US-08-887-497A-8	Sequence 8, Appl
C 895	10.8	38.6	40	3	US-09-503-222-23	Sequence 23, Appl	968	10.6	37.9	25	4	US-08-887-497A-77	Sequence 77, Appl
C 896	10.8	38.6	40	3	US-08-972-584-20	Sequence 20, Appl	969	10.6	37.9	25	4	US-08-471-974-8	Sequence 8, Appl
C 897	10.8	38.6	40	4	US-09-729-597-108	Sequence 108, Appl	C 970	10.6	37.9	25	4	US-09-866-108A-4554	Sequence 4554, Appl
C 898	10.8	38.6	40	4	US-09-812-042A-1	Sequence 1, Appl	C 971	10.6	37.9	25	4	US-09-866-108A-4563	Sequence 4563, Appl
C 899	10.8	38.6	40	5	PCT-US93-08364-80	Sequence 80, Appl	C 972	10.6	37.9	25	4	US-10-044-543-23	Sequence 23, Appl
C 900	10.8	38.6	40	5	PCT-US95-00067-22	Sequence 22, Appl	C 973	10.6	37.9	26	1	US-08-531-556-91	Sequence 91, Appl
C 901	10.8	38.6	40	5	PCT-US95-08743-36	Sequence 36, Appl	C 974	10.6	37.9	26	1	US-08-472-416-91	Sequence 91, Appl
C 902	10.8	38.6	41	2	US-08-761-277A-69	Sequence 69, Appl	975	10.6	37.9	26	2	US-08-859-998-1106	Sequence 1106, Appl
C 903	10.8	38.6	44	3	US-08-997-758-3	Sequence 3, Appl	976	10.6	37.9	26	3	US-08-891-789B-12	Sequence 12, Appl

Sequence 1106, Ap
Sequence 41, Appl
Sequence 78, Appl
Sequence 1106, Ap
Sequence 6, Appl
Sequence 140, Appl
Sequence 79, Appl
Sequence 10, Appl
Sequence 6, Appl
Sequence 756, Appl
Sequence 756, Appl
Sequence 756, Appl
Sequence 73, Appl
Sequence 165, Appl
Sequence 12, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 85, Appl

3 US-09-225-928-1106
4 US-08-887-497A-41
4 US-08-887-497A-78
4 US-09-225-201B-1106
1 US-08-274-661B-6
3 US-09-253-396A-140
4 US-08-887-497A-79
4 US-09-043-944-10
5 PCT-US93-03987-6
2 US-08-859-998-756
3 US-09-225-928-756
4 US-08-887-497A-7
4 US-09-225-201B-756
4 US-08-471-974-7
4 US-08-887-497A-73
4 US-09-304-232-165
1 US-08-150-331-12
1 US-07-940-861-24
1 US-08-459-512-24
1 US-08-616-133-24
1 US-08-802-985-24
1 US-08-459-657-24
2 US-08-460-132-24
3 US-08-783-853A-85

ALIGNMENTS

RESULT 1
US-09-422-978-1680
; Sequence 1680, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 1680
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-5604-376 : polymorphic base A or G

US-09-422-978-1680
Query Match 60.7%; Score 17; DB 4; Length 47;
Best Local Similarity 74.1%; Pred. No. 43;
Matches 20; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCGTCATGCTGT 28
Db 8 GTTATGCTATAGTACATGCTGT 34

RESULT 2
US-09-153-242-37/c
; Sequence 37, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundberg, Joakim

APPLICANT: Uhlen, Mathias
TITLE OF INVENTION: MODULAR PROBES II
FILE REFERENCE: 1181-242
CURRENT APPLICATION NUMBER: US/09/153,242
CURRENT FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: PCT/GB97/02629
PRIOR FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide H7
US-09-153-242-37

Query Match 53.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGTGGGATAGTCG 18
Db 15 TCGTGGGATAGTCG 1

RESULT 3
US-09-657-472-2496/c
; Sequence 2496, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2496
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-657-472-2496

Query Match 52.1%; Score 14.6; DB 4; Length 21;
Best Local Similarity 81.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCGTCAT 22
Db 21 GTTCGTGGAAMTGTCCGTCAT 1

RESULT 4
US-08-821-827C-25/c
; Sequence 25, Application US/08821827C
; Patent No. 6297425
; GENERAL INFORMATION:
; APPLICANT: Scelange, Christopher J.
; APPLICANT: Bidney, Dennis L.
; TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM

; TITLE OF INVENTION: ASPERGILLUS PHOENICES
; FILE REFERENCE: 0561A
; CURRENT APPLICATION NUMBER: US/08/821.827C
; CURRENT FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-08-821-827C-25

Query Match 52.1%; Score 14.6; DB 3; Length 38;
Best Local Similarity 81.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCGTCAT 22
Db 22 GATAGTGGGATGTGCGTCAT 2

RESULT 5
US-09-290-202B-25/c

; Sequence 25, Application US/09290202B
; Patent No. 6303846
; GENERAL INFORMATION:

; APPLICANT: Scelonge, Christopher J.
; APPLICANT: Bidney, Dennis L.

; TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM
; FILE REFERENCE: 0561D

; CURRENT APPLICATION NUMBER: US/09/290.202B
; CURRENT FILING DATE: 1999-04-12

; PRIOR APPLICATION NUMBER: 08/821,827
; PRIOR FILING DATE: 1997-03-21

; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25
; LENGTH: 38

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: primer

US-09-290-202B-25

Query Match 52.1%; Score 14.6; DB 3; Length 38;
Best Local Similarity 81.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCGTCAT 22
Db 22 GATAGTGGGATGTGCGTCAT 2

RESULT 6

US-09-469-211A-14/c

; Sequence 14, Application US/09469211A
; Patent No. 6660524

; GENERAL INFORMATION:
; APPLICANT: J. Turck

; APPLICANT: J. Archer

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES
; FILE REFERENCE: 9341-021

; CURRENT APPLICATION NUMBER: US/09/469.211A
; CURRENT FILING DATE: 1999-12-22

; PRIOR APPLICATION NUMBER: UK 9828660.2
; PRIOR FILING DATE: 1998-12-24

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14
; LENGTH: 50

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: CamVop2
US-09-469-211A-14

Query Match 52.1%; Score 14.6; DB 4; Length 50;
Best Local Similarity 81.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCGTCAT 22
Db 37 GATAGTGGGATGTGCGTCAT 17

RESULT 7

US-08-833-167-78/c

; Sequence 78, Application US/08833167
; Patent No. 6100070

; GENERAL INFORMATION:
; APPLICANT: ZURELUH, LINDA L.

; APPLICANT: MCWHERTER, CHARLES A

; APPLICANT: MCKEARN, JOHN P

; APPLICANT: KLEIN, BARBARA K

; APPLICANT: FENG, YIQING

; APPLICANT: BRAFORD-GOLDBERG, SARAH R

; APPLICANT: LEE, STEPHEN C

; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,

; STREET: P.O. BOX 5110
; CITY: CHICAGO

; STATE: ILLINOIS
; COUNTRY: USA

; ZIP: 60680

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833.167

; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935

; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A

; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402

; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 78:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA (synthetic)"
US-08-833-167-78

Query Match 51.4%; Score 14.4; DB 3; Length 32;
Best Local Similarity 75.0%; Pred. No. 6.9e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Wed Nov 24 08:46:11 2004

QY 2 GTTCGTGGATAGTCGTCATGGT 25
Db 29 GGTGGTGGCAAGTCAGCCATGGT 6

RESULT 8
US-09-344-837A-78/c
; Sequence 78, Application US/09344837A
; Patent No. 6358505
; GENERAL INFORMATION:
; APPLICANT: ZURFLOH, LINDA L.
; APPLICANT: MCWHETER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIONG
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. CHRISTOPHER BAUER
; ADDRESSEE: MONSANTO/G. D. SEARLE & CO.,
; ADDRESSEE: PATENT DEPARTMENT CENTRAL
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,837A
; FILING DATE: 25-JUN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. CHRISTOPHER BAUER
; REFERENCE/DOCKET NUMBER: 2907/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 636-737-6257
; TELEFAX: 636-737-5452
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA (synthetic)"
US-09-344-837A-78

Query Match 51.4%; Score 14.4; DB 3; Length 32;
Best Local Similarity 75.0%; Pred. No. 6.9e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCGTGGATAGTCGTCATGGT 25
Db 29 GGTGGTGGCAAGTCAGCCATGGT 6

RESULT 9
US-08-985-337A-6/c
; Sequence 6, Application US/08985337A
; Patent No. 5932590
; GENERAL INFORMATION:

; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: deSolms, S. Jane
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,337A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,578
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 19834Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3903
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-985-337A-6

Query Match 51.4%; Score 14.4; DB 2; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCGTCATGGTG 26
||| ||||| ||||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 10
US-08-985-124A-6/c
; Sequence 6, Application US/08985124A
; Patent No. 5972966
; GENERAL INFORMATION:
; APPLICANT: deSolms, S. Jane
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,124A

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-985-320A-6
;
Query Match          51.4%; Score 14.4; DB 2; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 ATAGTCGGTCATGGT 26
      ||| |||||
DB      28 ATATCCGTCATGGT 13

RESULT 12
US-08-984-732A-6/c
; Sequence 6, Application US/08984732A
; Patent No. 6015817
; GENERAL INFORMATION:
; APPLICANT: Halczenko, Wasyl
; APPLICANT: Stump, Craig A.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,732A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,126
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 19849Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3903
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-984-732A-6
;
Query Match          51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 ATAGTCGGTCATGGT 26
      ||| |||||
DB      28 ATATCCGTCATGGT 13

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us-10-087-631b-9.max.rn1

Wed Nov 24 08:46:11 2004

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RESULT 13
US-09-195-578-18/c
; Sequence 18, Application US/09195578
; Patent No. 6054466
; GENERAL INFORMATION:
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: deSolms, Jane S. J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 20121Y
; CURRENT APPLICATION NUMBER: US/09/195,578
; CURRENT FILING DATE: 1998-11-18
; EARLIER APPLICATION NUMBER: 60/067,552
; EARLIER FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-195-578-18
Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 14
US-09-170-951-18/c
; Sequence 18, Application US/09170951
; Patent No. 6103723
; GENERAL INFORMATION:
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 19867Y
; CURRENT APPLICATION NUMBER: US/09/170,951
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 60/064,342
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-170-951-18
Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 15
US-09-164-482-18/c
; Sequence 18, Application US/09164482A
; Patent No. 6127390
; GENERAL INFORMATION:
; APPLICANT: deSolms, S. Jane
; APPLICANT: Merck & Co., Inc.
; APPLICANT: deSolms, S. Jane
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 20025Y
; CURRENT APPLICATION NUMBER: US/09/164,482A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/060,871
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized nucleotide sequence
US-09-164-482-18
Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 16
US-09-332-769-13/c
; Sequence 13, Application US/09332769
; Patent No. 6172076
; GENERAL INFORMATION:
; APPLICANT: Embrey, Mark W.
; APPLICANT: Ferlow, Debra S.
; APPLICANT: Wai, John S.
; APPLICANT: Hoffman, Jacob M.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 19982Y
; CURRENT APPLICATION NUMBER: US/09/332,769
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: US 60/089,311
; EARLIER FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-332-769-13
Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 17
US-09-456-153-13/c
; Sequence 13, Application US/09456153
; Patent No. 6284755
; GENERAL INFORMATION:
; APPLICANT: deSolms, S. Jane
; APPLICANT: Merck & Co., Inc.
; APPLICANT: deSolms, S. Jane
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 20025Y
; CURRENT APPLICATION NUMBER: US/09/456,153
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/060,871
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-456-153-13
Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13
```


; APPLICANT: Graham, Samuel L.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: Stokker, Gerald E.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 20312Y
; CURRENT APPLICATION NUMBER: US/09/456,153
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: US 60/111,416
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 60/129,282
; EARLIER FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-456-153-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 18

US-09-167-180-18/c
; Sequence 18, Application US/09167180

; Patent No. 6297239
; GENERAL INFORMATION:
; APPLICANT: deSolms, S. Jane
; APPLICANT: Hutchinson, John H.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 19928Y
; CURRENT APPLICATION NUMBER: US/09/167,180
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: 60/062,660
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-167-180-18

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 19

US-09-455-627-13/c
; Sequence 13, Application US/09455627

; Patent No. 6316436
; GENERAL INFORMATION:

; APPLICANT: deSolms, S. Jane
; APPLICANT: Shaw, Anthony W.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 203125
; CURRENT APPLICATION NUMBER: US/09/455,627
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: US 60/111,621
; EARLIER FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-455-627-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 20

US-09-426-533-13/c
; Sequence 13, Application US/09426533

; Patent No. 6329376
; GENERAL INFORMATION:
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors Of Prenyl-Protein Transferase
; FILE REFERENCE: 20289
; CURRENT APPLICATION NUMBER: US/09/426,533
; CURRENT FILING DATE: 1999-10-26
; EARLIER APPLICATION NUMBER: 60/101,177
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-426-533-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 21

US-09-609-205-14/c
; Sequence 14, Application US/09609205

; Patent No. 6333335
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinmore, Christopher J.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Williams, Theresa M.
; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20488
; CURRENT APPLICATION NUMBER: US/09/609,205
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/145,331

```

; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Nucleotide Sequence
US-09-757-218-14

Query Match          51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
Db 28 ATATCCCGTCATGGTG 13

RESULT 22
US-09-516-945-13/c
; Sequence 13, Application US/09516945
; Patent No. 6353343
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Lumma, William C. Jr.
; APPLICANT: Smith, Anthony M.
; APPLICANT: Sisko, John T.
; APPLICANT: Tucker, Thomas J.
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Dinsmore, Christopher J.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20335V
; CURRENT APPLICATION NUMBER: US/09/516,945
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 60/122,970
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 60/127,259
; EARLIER FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-945-13

Query Match          51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
Db 28 ATATCCCGTCATGGTG 13

RESULT 23
US-09-757-218-14/c
; Sequence 14, Application US/09757218
; Patent No. 6350755
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20613
; CURRENT APPLICATION NUMBER: US/09/757,218
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,703
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-945-13

Query Match          51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
Db 28 ATATCCCGTCATGGTG 13

RESULT 24
US-09-516-757-13/c
; Sequence 13, Application US/09516757
; Patent No. 6355643
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Lumma, William C. Jr.
; APPLICANT: Sisko, John T.
; APPLICANT: Smith, Anthony M.
; APPLICANT: Tucker, Thomas J.
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Dinsmore, Christopher J.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20399Y
; CURRENT APPLICATION NUMBER: US/09/516,757
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 60/122,771
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 60/127,257
; EARLIER FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-757-13

Query Match          51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
Db 28 ATATCCCGTCATGGTG 13

RESULT 25
US-09-516-750-13/c
; Sequence 13, Application US/09516750
; Patent No. 6358956
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Hartman, George D.
; APPLICANT: Lumma, William C. Jr.
; APPLICANT: Sisko, John T.
; APPLICANT: Smith, Anthony M.
; APPLICANT: Stokker, Gerald E.
; APPLICANT: Tucker, Thomas J.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20393Y
; CURRENT APPLICATION NUMBER: US/09/516,750
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 60/122,768
; EARLIER FILING DATE: 1998-03-03
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-757-13

Query Match          51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
Db 28 ATATCCCGTCATGGTG 13

```

; EARLIER APPLICATION NUMBER: 60/127,253
; EARLIER FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-750-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 26
US-09-342-577-14/c
; Sequence 14, Application US/09342577
; Patent No. 6358985
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Anthony, Neville J.
; APPLICANT: Bell, Ian M.
; APPLICANT: Beshore, Douglas C.
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: desolms, S. Jane
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Stokker, Gerald E.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 20275Y
; CURRENT APPLICATION NUMBER: US/09/342,577
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/091,513
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-342-577-14

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 27
US-09-516-756-13/c
; Sequence 13, Application US/09516756
; Patent No. 6376496
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Hartman, George D.
; APPLICANT: Lumma, William C. Jr.
; APPLICANT: Sisko, John T.
; APPLICANT: Smith, Anthony M.
; APPLICANT: Tucker, Thomas J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20288Y
; CURRENT APPLICATION NUMBER: US/09/516,756
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 60/122,968
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 60/127,132
; EARLIER FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-756-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 28
US-09-828-061A-14/c
; Sequence 14, Application US/09828061A
; Patent No. 6380228
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Craig A. Stump
; APPLICANT: Theresa M. Williams
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20635Y
; CURRENT APPLICATION NUMBER: US/09/828,061A
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,231
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sense Nucleotide Sequence
US-09-828-061A-14

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13

RESULT 29
US-09-463-917-13/c
; Sequence 13, Application US/09463917
; Patent No. 6387903
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Hutchinson, John H.
; APPLICANT: Williams, Theresa M.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20040Y
; CURRENT APPLICATION NUMBER: US/09/463,917
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/057,080

Wed Nov 24 08:46:11 2004

; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized nucleotide sequence
US-09-463-917-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 30
US-09-347-673-14/c
; Sequence 14, Application US/09347673
; Patent No. 6410534
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinmore, Christopher J.
; APPLICANT: Bell, Ian M.
; APPLICANT: Beshore, Douglas C.
; APPLICANT: Williams, Theresa M.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20236Y
; CURRENT APPLICATION NUMBER: US/09/347,673
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/091,596
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-347-673-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 31
US-09-757-213-14/c
; Sequence 14, Application US/09757213
; Patent No. 6413964
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane desolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20605Y
; CURRENT APPLICATION NUMBER: US/09/757,213
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,708
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14

; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Nucleotide Sequence
US-09-757-213-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 32
US-09-656-653-13/c
; Sequence 13, Application US/09656653
; Patent No. 6441017
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Bell, Ian M.
; APPLICANT: Beshore, Douglas C.
; APPLICANT: Gallicchio, Steven N.
; APPLICANT: Zartman, C. Blair
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20292Y
; CURRENT APPLICATION NUMBER: US/09/656,653
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,017
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-656-653-13

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 33
US-09-757-251-14/c
; Sequence 14, Application US/09757251
; Patent No. 6525074
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane desolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20604Y
; CURRENT APPLICATION NUMBER: US/09/757,251
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,784
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Artificial Nucleotide Sequence
US-09-757-251-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 34

US-09-828-259A-14/c
; Sequence 14, Application US/09828259A
; Patent No. 6534506
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Diem N. Nguyen
; APPLICANT: Craig A. Stump
; APPLICANT: Theresa M. Williams
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20637Y
; CURRENT APPLICATION NUMBER: US/09/828,259A
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,951
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Nucleotide Sequence
US-09-828-259A-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 35

US-09-719-878-14/c
; Sequence 14, Application US/09719878
; Patent No. 6562823
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Nguyen, Diem N.
; APPLICANT: Stokker, Gerald E.
; APPLICANT: Williams, Theresa M.
; APPLICANT: Zartman, C. Blair
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20205Y
; CURRENT APPLICATION NUMBER: US/09/719,878
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/091,629
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence

US-09-719-878-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 36

US-09-757-217A-14/c
; Sequence 14, Application US/09757217A
; Patent No. 6566385
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Gerald E. Stokker
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20603Y
; CURRENT APPLICATION NUMBER: US/09/757,217A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/175,801
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Nucleotide Sequence
US-09-757-217A-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26
||| |||||
Db 28 ATATTCGTCATGGTG 13

RESULT 37

US-09-828-325A-14/c
; Sequence 14, Application US/09828325A
; Patent No. 6610722
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Craig A. Stump
; APPLICANT: Theresa M. Williams
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20636Y
; CURRENT APPLICATION NUMBER: US/09/828,325A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/196,244
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sense Nucleotide Sequence
US-09-828-325A-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

us-10-087-631b-9.max.rni

Wed Nov 24 08:46:11 2004

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Db 28 ATATCCGTCATGGTG 13

RESULT 38
US-09-756-248-13/c
; Sequence 13, Application US/09756248
; Patent No. 6632818
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinmore, Christopher J.
; TITLE OF INVENTION: Inhibitors Of Prenyl-Protein Transferase
; FILE REFERENCE: 20341
; CURRENT APPLICATION NUMBER: US/09/756,248
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/175,706
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-756-248-13

Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26
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Db 28 ATATCCGTCATGGTG 13

RESULT 39
US-08-333-565-58
; Sequence 58, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
; US-08-661-479-58

Query Match 50.7%; Score 14.2; DB 2; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 TGGGATAGTCCGTCATGGT 25
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STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
US-08-333-565-58

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Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 TGGGATAGTCCGTCATGGT 25
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Db 2 TGAGGTAGTCTGTCATGGT 20

RESULT 40
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; Sequence 58, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
; US-08-661-479-58

Query Match 50.7%; Score 14.2; DB 2; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 TGGGATAGTCCGTCATGGT 25
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Db 2 TGAGGTAGTCTGTCATGGT 20

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 131.296 Seconds
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Title: US-10-087-631B-9

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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8	21	75.0	21	18	US-10-667-271-1466
9	21	75.0	21	18	US-10-667-271-1467
c 10	21	75.0	21	18	US-10-667-271-1474
c 11	20	71.4	21	18	US-10-444-853A-216
c 12	20	71.4	21	18	US-10-667-271-1473

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c 17	19	67.9	21	18	US-10-444-853A-169	Sequence 169, App
c 18	19	67.9	21	18	US-10-444-853A-170	Sequence 170, App
c 19	19	67.9	21	18	US-10-444-853A-215	Sequence 215, App
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c 74	14.4	51.4	38	9	US-09-757-251-14	Sequence 14, Appl
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c 76	14.4	51.4	38	9	US-09-770-983-13	Sequence 13, Appl
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c 81	14.4	51.4	38	10	US-09-756-248-13	Sequence 13, Appl
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C 91	14	50.0	21	18	US-10-667-271-1605	Sequence 1605, Ap	164	13	46.4	36	9	US-10-102-704-13	Sequence 13, Appl
C 92	14	50.0	21	18	US-10-215-112-721	Sequence 721, Appl	165	13	46.4	36	13	US-10-102-704-15	Sequence 15, Appl
C 93	13.8	49.3	25	15	US-10-098-263B-95814	Sequence 95814, A	166	13	46.4	36	13	US-10-057-951-13	Sequence 13, Appl
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C 95	13.8	49.3	30	16	US-10-436-782-30	Sequence 30, Appl	168	13	46.4	47	15	US-10-128-590-8	Sequence 8, Appl
C 96	13.6	48.6	20	9	US-09-790-417-182	Sequence 182, Appl	169	13	46.4	47	15	US-10-128-590-8	Sequence 8, Appl
C 97	13.6	48.6	20	10	US-09-780-863-44	Sequence 44, Appl	170	13	46.4	47	15	US-10-128-590-8	Sequence 8, Appl
C 98	13.6	48.6	21	18	US-10-786-720-2932	Sequence 2932, Ap	171	12.8	45.7	24	9	US-09-733-692A-44	Sequence 44, Appl
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C 125	13.4	47.9	31	9	US-09-801-274-358	Sequence 358, Appl	198	12.8	45.7	38	9	US-09-828-325A-23	Sequence 23, Appl
C 126	13.4	47.9	39	15	US-10-005-956-1495	Sequence 1495, Ap	199	12.8	45.7	38	11	US-09-756-248-19	Sequence 19, Appl
C 127	13.4	47.9	39	15	US-10-005-956-1505	Sequence 1505, Ap	200	12.8	45.7	38	11	US-09-828-317A-20	Sequence 20, Appl
C 128	13.4	47.9	48	15	US-09-766-167-20	Sequence 20, Appl	201	12.8	45.7	38	11	US-09-828-317A-23	Sequence 23, Appl
C 129	13.4	47.9	48	15	US-10-208-557-20	Sequence 20, Appl	202	12.8	45.7	38	15	US-10-244-215-85	Sequence 85, Appl
C 130	13.4	47.9	48	17	US-10-774-938-20	Sequence 20, Appl	203	12.8	45.7	43	15	US-10-410-894-17	Sequence 17, Appl
C 131	13.4	47.9	50	16	US-10-062-188-78	Sequence 78, Appl	204	12.8	45.7	43	15	US-10-338-129-18	Sequence 18, Appl
C 132	13.2	47.1	20	15	US-10-126-355-40	Sequence 40, Appl	205	12.8	45.7	45	15	US-10-238-667-18	Sequence 18, Appl
C 133	13.2	47.1	24	15	US-10-126-355-4	Sequence 4, Appl	206	12.8	45.7	50	16	US-10-062-188-15	Sequence 15, Appl
C 134	13.2	47.1	25	14	US-10-215-112-5488	Sequence 5488, Ap	207	12.6	45.0	20	17	US-10-619-739-34	Sequence 34, Appl
C 135	13.2	47.1	25	15	US-10-098-263B-52644	Sequence 52644, A	208	12.6	45.0	21	18	US-10-786-720-2978	Sequence 2978, Ap
C 136	13.2	47.1	25	15	US-10-098-263B-79603	Sequence 79603, A	209	12.6	45.0	21	18	US-10-786-720-3182	Sequence 3182, Ap
C 137	13.2	47.1	25	15	US-10-098-263B-116085	Sequence 116085,	210	12.6	45.0	21	18	US-10-786-720-3287	Sequence 3287, Ap
C 138	13.2	47.1	25	15	US-10-098-263B-116086	Sequence 116086,	211	12.6	45.0	25	15	US-10-098-263B-6804	Sequence 6804, Ap
C 139	13.2	47.1	29	15	US-10-336-638-11	Sequence 11, Appl	212	12.6	45.0	25	15	US-10-098-263B-42667	Sequence 42667, A
C 140	13.2	47.1	39	17	US-10-018-245A-16	Sequence 16, Appl	213	12.6	45.0	25	15	US-10-098-263B-42668	Sequence 42668, A
C 141	13.2	47.1	43	13	US-10-004-201-30	Sequence 30, Appl	214	12.6	45.0	25	15	US-10-098-263B-126105	Sequence 126105,
C 142	13.2	47.1	45	14	US-10-111-069-37	Sequence 37, Appl	215	12.6	45.0	25	15	US-10-098-263B-126106	Sequence 126106,
C 143	13.2	47.1	50	16	US-10-220-373-27	Sequence 27, Appl	216	12.6	45.0	25	15	US-10-098-263B-126106	Sequence 126106,
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C 145	13	46.4	24	16	US-10-429-555-12	Sequence 12, Appl	218	12.6	45.0	25	17	US-10-775-169-707	Sequence 707, Appl
C 146	13	46.4	25	14	US-10-060-756A-2155	Sequence 2155, Ap	219	12.6	45.0	25	17	US-10-775-169-707	Sequence 707, Appl
C 147	13	46.4	25	14	US-10-060-756A-2156	Sequence 2156, Ap	220	12.6	45.0	30	14	US-10-133-934-11	Sequence 11, Appl
C 148	13	46.4	25	14	US-10-060-756A-2157	Sequence 2157, Ap	221	12.6	45.0	30	14	US-10-072-438-33	Sequence 33, Appl
C 149	13	46.4	25	14	US-10-060-756A-2158	Sequence 2158, Ap	222	12.6	45.0	30	14	US-10-105-697-11	Sequence 11, Appl
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C 151	13	46.4	25	14	US-10-060-756A-2160	Sequence 2160, Ap	224	12.6	45.0	30	14	US-10-137-765-25	Sequence 25, Appl
C 152	13	46.4	25	14	US-10-215-112-1607	Sequence 1607, Ap	225	12.6	45.0	30	14	US-10-146-337-25	Sequence 25, Appl
C 153	13	46.4	25	14	US-10-215-112-1607	Sequence 1607, Ap	226	12.6	45.0	30	14	US-10-154-671-11	Sequence 11, Appl
C 154	13	46.4	25	15	US-10-098-263B-22004	Sequence 22004, A	227	12.6	45.0	30	14	US-10-142-077-11	Sequence 11, Appl
C 155	13	46.4	25	15	US-10-098-263B-41172	Sequence 41172, A	228	12.6	45.0	30	14	US-10-236-508-19	Sequence 19, Appl
C 156	13	46.4	25	15	US-10-098-263B-102984	Sequence 102984,	229	12.6	45.0	30	15	US-10-304-059-44	Sequence 44, Appl
C 157	13	46.4	25	15	US-10-098-263B-122283	Sequence 122283,	230	12.6	45.0	31	15	US-10-304-059-44	Sequence 44, Appl
C 158	13	46.4	25	15	US-10-098-263B-122284	Sequence 122284,	231	12.6	45.0	39	9	US-09-797-941A-29	Sequence 29, Appl

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c 378	12	42.9	25	15	US-10-098-263B-76822	Sequence 76822, A	c 451	12	42.9	49	10	US-09-906-700-380	Sequence 380, App
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382	12	42.9	25	15	US-10-098-263B-108432	Sequence 108432, A	c 455	12	42.9	49	10	US-09-902-903-380	Sequence 380, App
383	12	42.9	25	15	US-10-098-263B-127892	Sequence 127892, A	c 456	12	42.9	49	10	US-09-903-749A-238	Sequence 238, App
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c 552	12	42.9	49	11	US-09-908-576-238	Sequence 238, App	625	11.8	42.1	25	15	US-10-098-263B-100975	Sequence 100975, A
c 553	12	42.9	49	11	US-09-908-576-380	Sequence 238, App	c 626	11.8	42.1	25	15	US-10-098-263B-104730	Sequence 104730, A
c 554	12	42.9	49	15	US-10-299-976-238	Sequence 238, App	627	11.8	42.1	25	15	US-10-098-263B-105117	Sequence 105117, A
c 555	12	42.9	49	15	US-10-299-976-380	Sequence 238, App	628	11.8	42.1	25	15	US-10-098-263B-105743	Sequence 105743, A
c 556	12	42.9	49	15	US-10-299-937-238	Sequence 238, App	629	11.8	42.1	25	15	US-10-098-263B-115673	Sequence 115673, A
c 557	12	42.9	49	15	US-10-299-937-380	Sequence 238, App	c 630	11.8	42.1	25	15	US-10-098-263B-120194	Sequence 120194, A
c 558	12	42.9	49	15	US-10-298-993-238	Sequence 238, App	c 631	11.8	42.1	25	15	US-10-098-263B-123734	Sequence 123734, A
c 559	12	42.9	49	15	US-10-298-993-380	Sequence 238, App	632	11.8	42.1	25	15	US-10-098-263B-125384	Sequence 125384, A
c 560	12	42.9	49	15	US-10-448-923-238	Sequence 238, App	c 633	11.8	42.1	25	16	US-10-288-552-7	Sequence 7, Appli
c 561	12	42.9	49	15	US-10-448-923-380	Sequence 238, App	634	11.8	42.1	25	17	US-10-723-361-13626	Sequence 13626, A
c 562	12	42.9	49	16	US-10-449-656-238	Sequence 238, App	635	11.8	42.1	25	17	US-10-723-361-13627	Sequence 13627, A
c 563	12	42.9	49	16	US-10-449-656-380	Sequence 238, App	636	11.8	42.1	25	17	US-10-723-361-13628	Sequence 13628, A
c 564	12	42.9	49	16	US-10-448-713-238	Sequence 238, App	637	11.8	42.1	26	10	US-09-921-159-12	Sequence 12, Appl
c 565	12	42.9	49	16	US-10-448-713-380	Sequence 238, App	638	11.8	42.1	26	16	US-10-072-012-943	Sequence 943, App
c 566	12	42.9	49	16	US-10-425-447-238	Sequence 238, App	c 639	11.8	42.1	28	11	US-09-874-991C-84	Sequence 84, Appl
c 567	12	42.9	49	16	US-10-425-447-380	Sequence 238, App	640	11.8	42.1	28	15	US-10-157-899A-23	Sequence 23, Appl
c 568	12	42.9	49	17	US-10-215-371-238	Sequence 238, App	641	11.8	42.1	28	15	US-10-157-899A-24	Sequence 24, Appl
c 569	12	42.9	49	17	US-10-215-371-380	Sequence 238, App	642	11.8	42.1	28	15	US-10-157-305A-200	Sequence 200, App
c 570	12	42.9	49	17	US-10-771-187-238	Sequence 238, App	643	11.8	42.1	28	15	US-10-157-391-200	Sequence 200, App
c 571	12	42.9	49	17	US-10-771-187-380	Sequence 238, App	644	11.8	42.1	28	15	US-10-157-096-200	Sequence 200, App
c 572	12	42.9	50	16	US-10-131-827-250	Sequence 230, App	645	11.8	42.1	28	15	US-10-157-302-200	Sequence 200, App
c 573	12	42.9	50	16	US-10-131-827-1030	Sequence 230, App	646	11.8	42.1	28	15	US-10-157-215A-200	Sequence 200, App
c 574	12	42.9	50	16	US-10-131-827-2977	Sequence 2377, Ap	647	11.8	42.1	28	15	US-10-157-299-200	Sequence 200, App
c 575	12	42.9	50	16	US-10-131-827-3057	Sequence 3057, Ap	648	11.8	42.1	28	15	US-10-154-951B-200	Sequence 200, App
c 576	12	42.9	50	16	US-10-131-827-4763	Sequence 4763, Ap	649	11.8	42.1	28	15	US-10-156-831-200	Sequence 200, App
c 577	12	42.9	50	16	US-10-131-827-6474	Sequence 6474, Ap	650	11.8	42.1	28	15	US-10-157-147-200	Sequence 200, App
c 578	12	42.9	50	16	US-10-131-827-6864	Sequence 6864, Ap	651	11.8	42.1	28	15	US-10-157-166-200	Sequence 200, App
c 579	12	42.9	50	16	US-10-062-188-30	Sequence 30, Appl	652	11.8	42.1	28	15	US-10-156-902-200	Sequence 200, App
c 580	11.8	42.1	17	10	US-09-740-332-1153	Sequence 1153, Ap	653	11.8	42.1	28	15	US-10-157-318-200	Sequence 200, App
c 581	11.8	42.1	17	10	US-09-740-332-3402	Sequence 3402, Ap	654	11.8	42.1	28	15	US-10-157-318-200	Sequence 200, App
c 582	11.8	42.1	17	10	US-09-817-879-1153	Sequence 1153, Ap	655	11.8	42.1	28	15	US-10-156-792A-200	Sequence 200, App
c 583	11.8	42.1	17	10	US-09-817-879-3402	Sequence 3402, Ap	656	11.8	42.1	28	15	US-10-157-213-200	Sequence 200, App
c 584	11.8	42.1	17	17	US-10-669-841-3746	Sequence 3746, Ap	657	11.8	42.1	28	15	US-10-157-073-200	Sequence 200, App
c 585	11.8	42.1	17	17	US-10-669-841-5995	Sequence 5995, Ap	658	11.8	42.1	28	15	US-10-157-073-200	Sequence 200, App
c 586	11.8	42.1	18	15	US-10-388-263-251	Sequence 251, App	659	11.8	42.1	28	15	US-10-157-320A-200	Sequence 200, App
c 587	11.8	42.1	20	9	US-09-735-368-6	Sequence 6, Appli	660	11.8	42.1	28	15	US-10-157-418A-200	Sequence 200, App
c 588	11.8	42.1	20	10	US-09-860-761-10	Sequence 10, Appl	661	11.8	42.1	28	15	US-10-157-171-200	Sequence 200, App
c 589	11.8	42.1	21	10	US-09-374-046A-199	Sequence 199, App	662	11.8	42.1	28	15	US-10-157-491-200	Sequence 200, App
c 590	11.8	42.1	21	15	US-10-229-346-22	Sequence 22, Appl	663	11.8	42.1	28	15	US-10-157-317-200	Sequence 200, App
c 591	11.8	42.1	21	16	US-10-616-263-199	Sequence 199, App	664	11.8	42.1	28	15	US-10-157-317-200	Sequence 200, App
c 592	11.8	42.1	21	18	US-10-487-846-22	Sequence 22, Appl	665	11.8	42.1	28	16	US-10-157-339-200	Sequence 200, App
c 593	11.8	42.1	22	10	US-09-898-200-22	Sequence 22, Appl	c 666	11.8	42.1	29	15	US-10-267-074-2	Sequence 2, Appli
c 594	11.8	42.1	25	8	US-08-647-444-7	Sequence 7, Appli	667	11.8	42.1	30	15	US-10-157-305A-202	Sequence 202, App
c 595	11.8	42.1	25	9	US-09-866-108-13626	Sequence 13626, A	668	11.8	42.1	30	15	US-10-157-391-202	Sequence 202, App
c 596	11.8	42.1	25	9	US-09-866-108-13627	Sequence 13627, A	669	11.8	42.1	30	15	US-10-272-865-26	Sequence 26, Appl

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670	11.8	42.1	30	15	US-10-157-096-202	Sequence 202, App	c 743	11.8	42.1	45	17	US-10-776-311-88	Sequence 88, Appl
671	11.8	42.1	30	15	US-10-157-302-202	Sequence 202, App	c 744	11.8	42.1	47	16	US-10-149-143-786	Sequence 786, App
672	11.8	42.1	30	15	US-10-157-215A-202	Sequence 202, App	c 745	11.8	42.1	47	16	US-10-294-934-804	Sequence 804, App
673	11.8	42.1	30	15	US-10-157-399-202	Sequence 202, App	c 746	11.8	42.1	50	9	US-09-909-496-6	Sequence 6, Appl
674	11.8	42.1	30	15	US-10-154-951B-202	Sequence 202, App	c 747	11.8	42.1	50	9	US-09-909-496-8	Sequence 8, Appl
675	11.8	42.1	30	15	US-10-156-831-202	Sequence 202, App	c 748	11.8	42.1	50	9	US-09-909-496-10	Sequence 10, Appl
676	11.8	42.1	30	15	US-10-157-147-202	Sequence 202, App	c 749	11.8	42.1	50	10	US-09-885-731B-8	Sequence 8, Appl
677	11.8	42.1	30	15	US-10-157-166-202	Sequence 202, App	c 750	11.8	42.1	50	10	US-09-885-731B-9	Sequence 9, Appl
678	11.8	42.1	30	15	US-10-156-902-202	Sequence 202, App	c 751	11.8	42.1	50	10	US-09-885-731B-12	Sequence 12, Appl
679	11.8	42.1	30	15	US-10-157-318-202	Sequence 202, App	c 752	11.8	42.1	50	13	US-10-103-002-7	Sequence 7, Appl
680	11.8	42.1	30	15	US-10-156-178-202	Sequence 202, App	c 753	11.8	42.1	50	13	US-10-103-002-8	Sequence 8, Appl
681	11.8	42.1	30	15	US-10-156-792A-202	Sequence 202, App	c 754	11.8	42.1	50	14	US-10-103-002-11	Sequence 11, Appl
682	11.8	42.1	30	15	US-10-157-213-202	Sequence 202, App	c 755	11.8	42.1	50	14	US-10-269-229-6	Sequence 6, Appl
683	11.8	42.1	30	15	US-10-156-811-202	Sequence 202, App	c 756	11.8	42.1	50	14	US-10-269-229-8	Sequence 8, Appl
684	11.8	42.1	30	15	US-10-157-073-202	Sequence 202, App	c 757	11.8	42.1	50	15	US-10-189-211-6	Sequence 6, Appl
685	11.8	42.1	30	15	US-10-157-106A-202	Sequence 202, App	c 758	11.8	42.1	50	15	US-10-189-211-8	Sequence 8, Appl
686	11.8	42.1	30	15	US-10-157-320A-202	Sequence 202, App	c 759	11.8	42.1	50	15	US-10-438-151-6	Sequence 10, Appl
687	11.8	42.1	30	15	US-10-157-418A-202	Sequence 202, App	c 760	11.8	42.1	50	15	US-10-438-151-8	Sequence 10, Appl
688	11.8	42.1	30	15	US-10-422-671-26	Sequence 26, Appl	c 761	11.8	42.1	50	15	US-10-438-151-10	Sequence 10, Appl
689	11.8	42.1	30	15	US-10-157-171-202	Sequence 202, App	c 762	11.8	42.1	50	16	US-10-177-029-24	Sequence 24, Appl
690	11.8	42.1	30	15	US-10-157-491-202	Sequence 202, App	c 763	11.6	41.4	18	16	US-10-177-029-26	Sequence 26, Appl
691	11.8	42.1	30	15	US-10-157-317-202	Sequence 202, App	c 764	11.6	41.4	18	16	US-10-177-029-26	Sequence 26, Appl
692	11.8	42.1	30	16	US-10-157-339-202	Sequence 202, App	c 765	11.6	41.4	19	9	US-09-725-752A-11	Sequence 11, Appl
c 693	11.8	42.1	31	9	US-09-801-274-1702	Sequence 1702, Ap	c 766	11.6	41.4	20	16	US-10-289-762-1394	Sequence 1394, Ap
694	11.8	42.1	34	16	US-10-433-238-47	Sequence 47, Appl	c 767	11.6	41.4	20	16	US-10-037-417-151	Sequence 151, App
695	11.8	42.1	36	15	US-10-267-074-6	Sequence 6, Appl	c 768	11.6	41.4	21	15	US-10-380-931-14	Sequence 14, Appl
c 696	11.8	42.1	36	15	US-10-274-638-12	Sequence 12, Appl	c 769	11.6	41.4	21	18	US-10-786-720-2803	Sequence 2803, Ap
c 697	11.8	42.1	36	15	US-10-418-182-70	Sequence 70, Appl	c 770	11.6	41.4	21	18	US-10-786-720-2804	Sequence 2804, Ap
698	11.8	42.1	36	15	US-10-418-182-346	Sequence 346, App	c 771	11.6	41.4	21	18	US-10-786-720-2805	Sequence 2805, Ap
699	11.8	42.1	37	9	US-09-939-581A-16	Sequence 16, Appl	c 772	11.6	41.4	21	18	US-10-786-720-2935	Sequence 2935, Ap
c 700	11.8	42.1	37	9	US-09-789-054A-61	Sequence 61, Appl	c 773	11.6	41.4	21	18	US-10-786-720-2965	Sequence 2965, Ap
c 701	11.8	42.1	37	17	US-10-628-969-61	Sequence 108, App	c 774	11.6	41.4	21	18	US-10-786-720-2966	Sequence 2966, Ap
c 702	11.8	42.1	37	17	US-10-628-969-61	Sequence 61, Appl	c 775	11.6	41.4	21	18	US-10-786-720-2967	Sequence 2967, Ap
c 703	11.8	42.1	38	9	US-09-770-967-16	Sequence 16, Appl	c 776	11.6	41.4	21	18	US-10-786-720-3013	Sequence 3013, Ap
c 704	11.8	42.1	38	9	US-09-858-369-16	Sequence 16, Appl	c 777	11.6	41.4	21	18	US-10-786-720-3014	Sequence 3014, Ap
c 705	11.8	42.1	38	9	US-09-819-522-16	Sequence 16, Appl	c 778	11.6	41.4	21	18	US-10-786-720-3015	Sequence 3015, Ap
c 706	11.8	42.1	38	9	US-09-828-061A-17	Sequence 17, Appl	c 779	11.6	41.4	21	18	US-10-786-720-3184	Sequence 3184, Ap
c 707	11.8	42.1	38	9	US-09-757-251-17	Sequence 17, Appl	c 780	11.6	41.4	21	18	US-10-786-720-3256	Sequence 3256, Ap
c 708	11.8	42.1	38	9	US-09-784-897A-16	Sequence 16, Appl	c 781	11.6	41.4	21	18	US-10-786-720-3257	Sequence 3257, Ap
c 709	11.8	42.1	38	9	US-09-770-983-16	Sequence 16, Appl	c 782	11.6	41.4	21	18	US-10-786-720-3258	Sequence 3258, Ap
c 710	11.8	42.1	38	9	US-09-828-325A-17	Sequence 17, Appl	c 783	11.6	41.4	22	15	US-10-325-403-27	Sequence 27, Appl
c 711	11.8	42.1	38	9	US-09-757-217A-17	Sequence 17, Appl	c 784	11.6	41.4	22	15	US-10-025-806-196	Sequence 196, App
c 712	11.8	42.1	38	9	US-09-828-359A-17	Sequence 17, Appl	c 785	11.6	41.4	22	16	US-10-325-403-27	Sequence 27, Appl
c 713	11.8	42.1	38	9	US-09-784-818-16	Sequence 16, Appl	c 786	11.6	41.4	23	9	US-09-725-897-10	Sequence 10, Appl
c 714	11.8	42.1	38	10	US-09-756-248-16	Sequence 16, Appl	c 787	11.6	41.4	23	10	US-09-291-417-48	Sequence 48, Appl
c 715	11.8	42.1	38	11	US-09-828-317A-17	Sequence 17, Appl	c 788	11.6	41.4	23	15	US-10-244-367-10	Sequence 10, Appl
c 716	11.8	42.1	39	16	US-10-244-215-82	Sequence 82, Appl	c 789	11.6	41.4	23	15	US-10-143-897-18	Sequence 18, Appl
c 717	11.8	42.1	40	16	US-10-435-935-9	Sequence 9, Appl	c 790	11.6	41.4	23	16	US-10-311-129-13	Sequence 13, Appl
c 718	11.8	42.1	40	16	US-10-411-066-76	Sequence 76, Appl	c 791	11.6	41.4	23	18	US-10-725-329-48	Sequence 48, Appl
c 719	11.8	42.1	40	16	US-10-748-055A-28	Sequence 28, Appl	c 792	11.6	41.4	25	9	US-09-866-108-4555	Sequence 4555, Ap
c 720	11.8	42.1	41	9	US-09-770-967-11	Sequence 4, Appl	c 793	11.6	41.4	25	9	US-09-866-108-4556	Sequence 4556, Ap
c 721	11.8	42.1	41	9	US-09-858-369-11	Sequence 11, Appl	c 794	11.6	41.4	25	9	US-09-866-108-4557	Sequence 4557, Ap
c 722	11.8	42.1	41	9	US-09-819-522-11	Sequence 11, Appl	c 795	11.6	41.4	25	9	US-09-866-108-4558	Sequence 4558, Ap
c 723	11.8	42.1	41	9	US-09-819-522-11	Sequence 11, Appl	c 796	11.6	41.4	25	9	US-09-866-108-4559	Sequence 4559, Ap
c 724	11.8	42.1	41	9	US-09-828-061A-12	Sequence 12, Appl	c 797	11.6	41.4	25	9	US-09-866-108-4560	Sequence 4560, Ap
c 725	11.8	42.1	41	9	US-09-757-251-12	Sequence 12, Appl	c 798	11.6	41.4	25	9	US-09-866-108-4561	Sequence 4561, Ap
c 726	11.8	42.1	41	9	US-09-784-897A-11	Sequence 11, Appl	c 799	11.6	41.4	25	9	US-09-866-108-4562	Sequence 4562, Ap
c 727	11.8	42.1	41	9	US-09-770-983-11	Sequence 11, Appl	c 800	11.6	41.4	25	14	US-10-215-112-1310	Sequence 1310, Ap
c 728	11.8	42.1	41	9	US-09-828-325A-12	Sequence 12, Appl	c 801	11.6	41.4	25	14	US-10-215-112-2622	Sequence 2622, Ap
c 729	11.8	42.1	41	9	US-09-757-217A-12	Sequence 12, Appl	c 802	11.6	41.4	25	14	US-10-215-112-5614	Sequence 5614, Ap
c 730	11.8	42.1	41	9	US-09-828-259A-12	Sequence 12, Appl	c 803	11.6	41.4	25	14	US-10-215-112-7011	Sequence 7011, Ap
c 731	11.8	42.1	41	9	US-09-925-664-66	Sequence 66, Appl	c 804	11.6	41.4	25	14	US-10-215-112-7449	Sequence 7449, Ap
c 732	11.8	42.1	41	9	US-09-784-818-11	Sequence 11, Appl	c 805	11.6	41.4	25	14	US-10-215-112-7980	Sequence 7980, Ap
c 733	11.8	42.1	41	10	US-09-756-248-11	Sequence 11, Appl	c 806	11.6	41.4	25	14	US-10-215-112-8107	Sequence 8107, Ap
c 734	11.8	42.1	41	11	US-09-925-192-66	Sequence 66, Appl	c 807	11.6	41.4	25	14	US-10-215-112-13543	Sequence 13543, A
c 735	11.8	42.1	41	11	US-09-828-317A-12	Sequence 12, Appl	c 808	11.6	41.4	25	14	US-10-215-112-13910	Sequence 13910, A
c 736	11.8	42.1	41	15	US-10-244-215-77	Sequence 77, Appl	c 809	11.6	41.4	25	14	US-10-215-112-14219	Sequence 14219, A
c 737	11.8	42.1	41	16	US-10-035-833A-1445	Sequence 1446, Ap	c 810	11.6	41.4	25	15	US-10-098-263B-1232	Sequence 1232, Ap
c 738	11.8	42.1	41	16	US-10-035-833A-3943	Sequence 3943, Ap	c 811	11.6	41.4	25	15	US-10-098-263B-1520	Sequence 1520, Ap
c 739	11.8	42.1	42	15	US-10-381-779-155	Sequence 155, App	c 812	11.6	41.4	25	15	US-10-098-263B-3854	Sequence 3854, Ap
c 740	11.8	42.1	44	13	US-10-001-051B-8	Sequence 8, Appl	c 813	11.6	41.4	25	15	US-10-098-263B-4660	Sequence 4660, Ap
c 741	11.8	42.1	45	15	US-10-060-793-21	Sequence 21, Appl	c 814	11.6	41.4	25	15	US-10-098-263B-5777	Sequence 5777, Ap
c 742	11.8	42.1	45	17	US-10-606-133-21	Sequence 21, Appl	c 815	11.6	41.4	25	15	US-10-098-263B-12561	Sequence 12561, A

816	11.6	41.4	25	15	US-10-098-263B-18596	Sequence 18696, A	C 889	11.6	41.4	50	16	US-10-131-827-7324	Sequence 7324, Ap
817	11.6	41.4	25	15	US-10-098-263B-52643	Sequence 52643, A	C 890	11.6	41.4	50	16	US-10-131-827-7680	Sequence 7680, Ap
818	11.6	41.4	25	15	US-10-098-263B-67571	Sequence 67571, A	C 891	11.6	41.4	50	17	US-10-643-752A-10	Sequence 10, Appl
819	11.6	41.4	25	15	US-10-098-263B-68189	Sequence 68189, A	C 892	11.4	40.7	19	18	US-10-683-990-5	Sequence 5, Appli
820	11.6	41.4	25	15	US-10-098-263B-75550	Sequence 75550, A	C 893	11.4	40.7	19	18	US-10-683-990-102	Sequence 102, App
821	11.6	41.4	25	15	US-10-098-263B-79604	Sequence 79604, A	C 894	11.4	40.7	20	14	US-10-001-076-82	Sequence 82, Appl
822	11.6	41.4	25	15	US-10-098-263B-80035	Sequence 80035, A	C 895	11.4	40.7	20	16	US-10-289-762-6346	Sequence 6346, Ap
823	11.6	41.4	25	15	US-10-098-263B-81637	Sequence 81637, A	C 896	11.4	40.7	20	16	US-10-642-802-82	Sequence 82, Appl
824	11.6	41.4	25	15	US-10-098-263B-83379	Sequence 83379, A	C 897	11.4	40.7	20	17	US-10-365-352-52	Sequence 52, Appl
825	11.6	41.4	25	15	US-10-098-263B-90706	Sequence 90706, A	C 898	11.4	40.7	21	18	US-10-786-720-9592	Sequence 9592, Ap
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873	11.6	41.4	48	10	US-09-745-237A-4311	Sequence 4311, Ap	C 946	11.4	40.7	26	15	US-10-319-236A-19	Sequence 19, Appl
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876	11.6	41.4	48	15	US-10-027-632-176491	Sequence 176491, A	C 949	11.4	40.7	27	15	US-10-157-899A-40	Sequence 40, Appl
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ALIGNMENTS

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; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 208
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-208

Query Match      75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-444-853A-209
; Sequence 209, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fossnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-209

Query Match      75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 210, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fossnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
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; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
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; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-210

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Best Local Similarity 71.4%; Pred. No. 8.5;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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US-10-444-853A-209

Query Match      75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-10-444-853A-210
; Sequence 210, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fossnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-210

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Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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APPLICANT: Morrissey, David
 TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
 FILE REFERENCE: 400/129 (MBHB02-763B)
 CURRENT APPLICATION NUMBER: US/10/667,271
 CURRENT FILING DATE: 2003-09-16
 PRIOR APPLICATION NUMBER: US 10/444,853
 PRIOR FILING DATE: 2003-05-23
 PRIOR APPLICATION NUMBER: PCT / US03/05043
 PRIOR FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: PCT / US02/09187
 PRIOR FILING DATE: 2002-03-26
 PRIOR APPLICATION NUMBER: USSN 60/401,104
 PRIOR FILING DATE: 2002-08-05
 PRIOR APPLICATION NUMBER: USSN 60/358,580
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: USSN 60/363,124
 PRIOR FILING DATE: 2002-03-11
 PRIOR APPLICATION NUMBER: USSN 60/386,782
 PRIOR FILING DATE: 2002-06-06
 PRIOR APPLICATION NUMBER: USSN 60/406,784
 PRIOR FILING DATE: 2002-08-29
 PRIOR APPLICATION NUMBER: USSN 60/408,378
 PRIOR FILING DATE: 2002-09-05
 PRIOR APPLICATION NUMBER: USSN 60/409,293
 PRIOR FILING DATE: 2002-09-09
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1705
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1465
 LENGTH: 21
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 US-10-667-271-1465
 Query Match 75.0%; Score 21; DB 18; Length 21;
 Best Local Similarity 66.7%; Pred. No. 8.5;
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 GGGATAGTCCGTCATGGTGT 21
 RESULT 8
 US-10-667-271-1466
 Sequence 1466, Application US/10667271
 Publication No. US20040209831A1
 GENERAL INFORMATION:
 APPLICANT: Sirna Therapeutics
 APPLICANT: McSwiggen, James
 APPLICANT: Macejak, Dennis
 APPLICANT: Beigelman, Leonid
 APPLICANT: Morrissey, David
 TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
 FILE REFERENCE: 400/129 (MBHB02-763B)
 CURRENT APPLICATION NUMBER: US/10/667,271
 CURRENT FILING DATE: 2003-09-16
 PRIOR APPLICATION NUMBER: US 10/444,853
 PRIOR FILING DATE: 2003-05-23
 PRIOR APPLICATION NUMBER: PCT / US03/05043
 PRIOR FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: PCT / US02/09187
 PRIOR FILING DATE: 2002-03-26
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 PRIOR FILING DATE: 2002-08-29
 PRIOR APPLICATION NUMBER: USSN 60/408,378
 PRIOR FILING DATE: 2002-09-05
 PRIOR APPLICATION NUMBER: USSN 60/409,293
 PRIOR FILING DATE: 2002-09-09
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 626
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 217
 LENGTH: 21
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
 US-10-444-853A-217
 Query Match 75.0%; Score 21; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GGGATAGTCCGTCATGGTGT 28
 DB 21 GGGATAGTCCGTCATGGTGT 1
 RESULT 7
 US-10-667-271-1465
 Sequence 1465, Application US/10667271
 Publication No. US20040209831A1
 GENERAL INFORMATION:
 APPLICANT: Sirna Therapeutics
 APPLICANT: McSwiggen, James
 APPLICANT: Macejak, Dennis
 APPLICANT: Beigelman, Leonid

;; PRIOR APPLICATION NUMBER: USSN 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: USSN 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: USSN 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: USSN 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1466
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1466

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCGTCATGCTGT 27
:||||:||||:||||:||||:
Db 1 UGGGAUAGUCCGCAUGGUGU 21

RESULT 9
US-10-667-271-1467
;; Sequence 1467, Application US/10667271
;; Publication No. US20040209831A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics
;; APPLICANT: McSwiggen, James
;; APPLICANT: Macejak, Dennis
;; APPLICANT: Beigelman, Leonid
;; APPLICANT: Morrissey, David
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
;; FILE REFERENCE: 400/129 (WBH02-763B)
;; CURRENT APPLICATION NUMBER: US/10/667,271
;; CURRENT FILING DATE: 2003-09-16
;; PRIOR APPLICATION NUMBER: US 10/444,853
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: PCT / US03/05043
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT / US02/09187
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: USSN 60/401,104
;; PRIOR FILING DATE: 2002-08-05
;; PRIOR APPLICATION NUMBER: USSN 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: USSN 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: USSN 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: USSN 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: USSN 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: USSN 60/409,293
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1467
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1467

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 71.4%; Pred. No. 8.5;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTGGATAGTCGTCATGCTG 26
:||||:||||:||||:||||:
Db 1 GUGGAUAGUCCGCAUGGUG 21

RESULT 10
US-10-667-271-1474/C
;; Sequence 1474, Application US/10667271
;; Publication No. US20040209831A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics
;; APPLICANT: McSwiggen, James
;; APPLICANT: Macejak, Dennis
;; APPLICANT: Beigelman, Leonid
;; APPLICANT: Morrissey, David
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
;; FILE REFERENCE: 400/129 (WBH02-763B)
;; CURRENT APPLICATION NUMBER: US/10/667,271
;; CURRENT FILING DATE: 2003-09-16
;; PRIOR APPLICATION NUMBER: US 10/444,853
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: PCT / US03/05043
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT / US02/09187
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: USSN 60/401,104
;; PRIOR FILING DATE: 2002-08-05
;; PRIOR APPLICATION NUMBER: USSN 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: USSN 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: USSN 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: USSN 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: USSN 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: USSN 60/409,293
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1474
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1474

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGGATAGTCGTCATGCTGTT 28
:||||:||||:||||:||||:
Db 21 GGGATAGTCGTCATGCTGTT 1

RESULT 11
US-10-444-853A-216/c
;; Sequence 216, Application US/10444853A
;; Publication No. US20040192626A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics, Inc.
;; APPLICANT: Haerberli, Peter
;; APPLICANT: McSwiggen, James

Wed Nov 24 08:46:11 2004

us-10-087-631b-9.max.rnpb

```

; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/114 (MEHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 216
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; US-10-444-853A-216

Query Match 71.4%; Score 20; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATAGTCGTCATGCTGTT 28
DB 21 GGATAGTCGTCATGCTGTT 2

RESULT 12
US-10-667-271-1473/c
; Sequence 1473, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20

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; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1473
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; US-10-667-271-1473

Query Match 71.4%; Score 20; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATAGTCGTCATGCTGTT 28
DB 21 GGATAGTCGTCATGCTGTT 2

RESULT 13
US-10-444-853A-161
; Sequence 161, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haeblerli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/114 (MEHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378

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```
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
; NAME/KEY: misc feature
; LOCATION: (1)-(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-161

Query Match      67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 73.7%; Pred. No. 69;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGGATAGTCGTCATGGTG 26
Db 3 GCGAUGUCCGUGAUGGUG 21
||||:||||:||||:|

RESULT 14
US-10-444-853A-162
; Sequence 162, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MEH803-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
; NAME/KEY: misc feature
; LOCATION: (1)-(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-162

Query Match      67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 68.4%; Pred. No. 69;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGATAGTCGTCATGGTGT 27
Db 3 GGAUAGUCCGUGAUGGUGU 21
||||:||||:||||:|

RESULT 15
US-10-444-853A-163
; Sequence 163, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MEH803-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
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us-10-087-631b-9.max.rnpb

FEATURE: 67.9%; Score 19; DB 18; Length 21;
NAME/KEY: misc_feature
LOCATION: (1)..(2)
OTHER INFORMATION: n stands for thymidine
US-10-444-853A-163

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 63.2%; Pred. No. 69;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCGTCATGGTGT 28
Db 3 GAUAGUCCGUAUGGUU 21

RESULT 16
US-10-444-853A-168/c
Sequence 168, Application US/10444853A
Publication No. US20040192626A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Haerberli, Peter
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Macejak, Dennis
APPLICANT: Zinnen, Shawn
APPLICANT: Pavco, Pamela
APPLICANT: Morrissey, David
APPLICANT: Fossnaugh, Kathy
APPLICANT: Mokier, Victor
APPLICANT: Jamison, Sharon
APPLICANT: Valsh, Nereandra
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
FILE REFERENCE: 400/114 (MBHB03-465)
CURRENT APPLICATION NUMBER: US/10/444,853A
CURRENT FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 10/417,012
PRIOR FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US03/05028
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 168
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA antise
NAME/KEY: misc feature
LOCATION: (1)..(2)
OTHER INFORMATION: n stands for thymidine
US-10-444-853A-168

Query Match 67.9%; Score 19; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GGGATAGTCCGTCATGGTG 26
Db 21 GGGATAGTCCGTCATGGTG 3

RESULT 17
US-10-444-853A-169/c
Sequence 169, Application US/10444853A
Publication No. US20040192626A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Haerberli, Peter
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Macejak, Dennis
APPLICANT: Zinnen, Shawn
APPLICANT: Pavco, Pamela
APPLICANT: Morrissey, David
APPLICANT: Fossnaugh, Kathy
APPLICANT: Mokier, Victor
APPLICANT: Jamison, Sharon
APPLICANT: Valsh, Nereandra
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
FILE REFERENCE: 400/114 (MBHB03-465)
CURRENT APPLICATION NUMBER: US/10/444,853A
CURRENT FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 10/417,012
PRIOR FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT/US03/05028
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 169
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA antise
NAME/KEY: misc feature
LOCATION: (1)..(2)
OTHER INFORMATION: n stands for thymidine
US-10-444-853A-169

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GGGATAGTCCGTCATGGTGT 27
Db 21 GGGATAGTCCGTCATGGTGT 3

```
RESULT 18
US-10-444-853A-170/c
; Sequence 170, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-170

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GATAGTCGTCATGCTGTT 28
Db 21 GATAGTCGTCATGCTGTT 3

RESULT 19
US-10-444-853A-215/c
; Sequence 215, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-170

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GATAGTCGTCATGCTGTT 28
Db 21 GATAGTCGTCATGCTGTT 3

RESULT 19
US-10-444-853A-215/c
; Sequence 215, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
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; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-444-853A-215

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GATAGTCGTCATGCTGTT 28
Db 21 GATAGTCGTCATGCTGTT 3

RESULT 20
US-10-444-853A-477
; Sequence 477, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
```

1
Db
1
GUUCGUGGAUGUCCGUC 19
RESULT 21
US-10-444-853A-478/c
; Sequence 478, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haeberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBH03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 477
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: siNA inverted control/siNA
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(4)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(16)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
US-10-444-853A-477
Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 68.4%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 GTTCGTGGGATAGTCGTC 20

1
Db
1
GUUCGUGGAUGUCCGUC 19
RESULT 21
US-10-444-853A-478/c
; Sequence 478, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haeberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBH03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 478
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: siNA inverted control/siNA
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(13)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (19)..(19)
 ; OTHER INFORMATION: 2'-O-methyl
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (20)..(20)
 ; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
 US-10-444-853A-478

Query Match 67.9%; Score 19; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCGTC 20
 Db 19 GTTCGTGGGATAGTCGTC 1

RESULT 22

US-10-667-271-1439
 ; Sequence 1439, Application US/10667271
 ; Publication No. US20040209831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sirna Therapeutics
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Macejak, Dennis
 ; APPLICANT: Beigelman, Leonid
 ; APPLICANT: Morrissey, David
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
 ; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
 ; FILE REFERENCE: 400/129 (MBHB02-763B)
 ; CURRENT APPLICATION NUMBER: US/10/667,271
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: US 10/444,853
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: PCT / US03/05043
 ; PRIOR FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: PCT / US02/09187
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: USSN 60/401,104
 ; PRIOR FILING DATE: 2002-08-05
 ; PRIOR APPLICATION NUMBER: USSN 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: USSN 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: USSN 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: USSN 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: USSN 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: USSN 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1439
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(2)
 ; OTHER INFORMATION: n stands for thymidine
 US-10-667-271-1439

Query Match 67.9%; Score 19; DB 18; Length 21;
 Best Local Similarity 73.7%; Pred. No. 69;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 GGGATAGTCGTCATGGTG 26
 Db 3 GGGAUAGUCCGUCAUGGUG 21

RESULT 23

US-10-667-271-1440
 ; Sequence 1440, Application US/10667271
 ; Publication No. US20040209831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sirna Therapeutics
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Macejak, Dennis
 ; APPLICANT: Beigelman, Leonid
 ; APPLICANT: Morrissey, David
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
 ; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
 ; FILE REFERENCE: 400/129 (MBHB02-763B)
 ; CURRENT APPLICATION NUMBER: US/10/667,271
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: US 10/444,853
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: PCT / US03/05043
 ; PRIOR FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: PCT / US02/09187
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: USSN 60/401,104
 ; PRIOR FILING DATE: 2002-08-05
 ; PRIOR APPLICATION NUMBER: USSN 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: USSN 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: USSN 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: USSN 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: USSN 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: USSN 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1440
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(2)
 ; OTHER INFORMATION: n stands for thymidine
 US-10-667-271-1440

Query Match 67.9%; Score 19; DB 18; Length 21;
 Best Local Similarity 68.4%; Pred. No. 69;
 Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGATAGTCGTCATGGTGT 27
 Db 3 GGAUAGUCCGUCAUGGUG 21

RESULT 24

US-10-667-271-1441
 ; Sequence 1441, Application US/10667271
 ; Publication No. US20040209831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sirna Therapeutics
 ; APPLICANT: McSwiggen, James

Wed Nov 24 08:46:11 2004

us-10-087-631b-9.max.rnpb

```
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, David
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1441
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1441

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 63.2%; Pred. No. 69;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCGTCATGTTGTT 28
|||:||||:||||:||||:
3 GAUAGUCGUGCAUGGUGU 21

Db

RESULT 25
US-10-667-271-1446/c
; Sequence 1446, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1441
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1441

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 63.2%; Pred. No. 69;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCGTCATGTTGTT 28
|||:||||:||||:||||:
3 GAUAGUCGUGCAUGGUGU 21

Db

RESULT 26
US-10-667-271-1447/c
; Sequence 1447, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1446
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1446

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1447

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: siNA antisense region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(2)

; OTHER INFORMATION: n stands for thymidine

US-10-667-271-1447

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGATAGTCCGTCATGGTGT 27

Db 21 GGATAGTCCGTCATGGTGT 3
|||||

RESULT 27

US-10-667-271-1448/c

; Sequence 1448, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBHB02-763B)

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US/10/667,271

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: USSN 60/409,293

; PRIOR FILING DATE: 2002-09-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1448

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(2)

; OTHER INFORMATION: n stands for thymidine

US-10-667-271-1448

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GATAGTCCGTCATGGTGT 28

Db 21 GATAGTCCGTCATGGTGT 3
|||||

RESULT 28

US-10-667-271-1472/c

; Sequence 1472, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBHB02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: USSN 60/409,293

; PRIOR FILING DATE: 2002-09-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1472

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-667-271-1472

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GATAGTCCGTCATGGTGT 28

Db 21 GATAGTCCGTCATGGTGT 3
|||||

RESULT 29

US-10-667-271-1528

; Sequence 1528, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBHB02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: USSN 60/409,293

; PRIOR FILING DATE: 2002-09-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1448

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(2)

; OTHER INFORMATION: n stands for thymidine

US-10-667-271-1448

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; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1528
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
; US-10-667-271-1528
; Query Match 67.9%; Score 19; DB 18; Length 21;
; Best Local Similarity 68.4%; Pred. No. 69;
; Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
; Qy 7 TGGGATAGTCCGTCATGGT 25
; Db 1 UGGGAUAGUCCGUAUGGU 19
; :|||:||||:||||:
; RESULT 30
; US-10-667-271-1529
; Sequence 1529, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1529
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
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Wed Nov 24 08:46:11 2004

LOCATION: (11)..(13)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (14)..(14)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)..(16)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (17)..(17)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
US-10-667-271-1530

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 73.7%; Pred. No. 69;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGTGGGATAGTCCTCATG 23
Db 1 CGUGGAUAGUCGCUCAUG 19

RESULT 32
US-10-667-271-1531
Sequence 1531, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667.271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378

PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1531
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(2)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc feature
LOCATION: (3)..(3)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)..(8)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(9)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (10)..(11)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)..(14)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (16)..(17)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
US-10-667-271-1531

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 68.4%; Pred. No. 69;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCGTGGGATAGTCCGT 19
 Db 1 CGUUCUGGGAGUAGUCCGU 19

RESULT 35
 US-10-667-271-1540/c
 ; Sequence 1540, Application US/10667271
 ; Publication No. US20040209831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sirna Therapeutics
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Macejak, Dennis
 ; APPLICANT: Beigelman, Leonid
 ; APPLICANT: Morrisey, David
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
 ; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siRNA)
 ; FILE REFERENCE: 400/129 (MBHB02-763B)
 ; CURRENT APPLICATION NUMBER: US/10/667,271
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: US 10/444,853
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: PCT / US03/05043
 ; PRIOR FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: PCT / US02/09187
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: USSN 60/401,104
 ; PRIOR FILING DATE: 2002-08-05
 ; PRIOR APPLICATION NUMBER: USSN 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: USSN 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: USSN 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: USSN 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: USSN 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: USSN 60/409,293
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1705
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1540
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: 2'-O-methyl
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2)..(3)
 ; OTHER INFORMATION: 2'-deoxy-2'-fluoro
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4)..(4)
 ; OTHER INFORMATION: 2'-O-methyl
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5)..(5)
 ; OTHER INFORMATION: 2'-deoxy-2'-fluoro
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (6)..(7)
 ; OTHER INFORMATION: 2'-O-methyl
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (8)..(8)
 ; OTHER INFORMATION: 2'-deoxy-2'-fluoro

US-10-667-271-1533

Query Match 67.9%; Score 19; DB 18; Length 21;
 Best Local Similarity 68.4%; Pred. No. 69;
 Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: USSN 60/409,293
 PRIOR FILING DATE: 2002-09-09
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1705
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1533
 LENGTH: 21
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(1)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(1)
 OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (2)..(2)
 OTHER INFORMATION: 2'-deoxy
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (3)..(5)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (6)..(6)
 OTHER INFORMATION: 2'-deoxy
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (7)..(7)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8)..(11)
 OTHER INFORMATION: 2'-deoxy
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (12)..(12)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (13)..(14)
 OTHER INFORMATION: 2'-deoxy
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (15)..(17)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (18)..(18)
 OTHER INFORMATION: 2'-deoxy
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (19)..(19)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (20)..(21)
 OTHER INFORMATION: n stands for thymidine
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (21)..(21)
 OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety

FEATURE: NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (12)..(13)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (14)..(14)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (15)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE: NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
US-10-667-271-1540

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGGGATAGTCGTCATGGT 25
|||||
DB 19 TGGGATAGTCGTCATGGT 1

RESULT 36
US-10-667-271-1541/c
Sequence 1541, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293

PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1541
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
FEATURE: NAME/KEY: misc_feature
LOCATION: (1)..(2)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (3)..(3)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (5)..(6)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (7)..(7)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (8)..(10)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (11)..(12)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (13)..(13)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (14)..(17)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (18)..(18)
OTHER INFORMATION: 2'-O-methyl
FEATURE: NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE: NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE: NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
US-10-667-271-1541

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTGGGATAGTCGTCATGG 24
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DB 19 GTGGGATAGTCGTCATGG 1

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RESULT 37
US-10-667-271-1542/c
; Sequence 1542, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1542
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (13)..(16)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
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; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; US-10-667-271-1542

Query Match      67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CQTGGGATAGTCCGTCATG 23
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Db 19 CQTGGGATAGTCCGTCATG 1

RESULT 38
US-10-667-271-1543/c
; Sequence 1543, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1543
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(4)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(8)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
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; LOCATION: (16)..(16)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
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; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1543

Query Match          67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      19 TCGTGGGATAGTCCGTCAT 1

RESULT 39
US-10-667-271-1544/c
; Sequence 1544, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
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; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1544
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(6)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(13)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (16)..(18)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
US-10-667-271-1544
Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCGCTC 20
Db 19 GTTCGTGGGATAGTCGCTC 1

RESULT 40
US-10-667-271-1545/c
; Sequence 1545, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggan, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1545
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; FEATURE:
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; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(5)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)..(7)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(12)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; US-10-667-271-1545
Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCGTGGGATAGTCGCT 19
Db 19 CGTTCGTGGGATAGTCGCT 1

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Job time : 140.396 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1342.43 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-9

Perfect score: 28
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

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6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	13.2	47.1	31	1	AI472592
5	13.2	47.1	34	8	AZ803210
6	13.2	47.1	46	8	AZ770060
7	13.2	47.1	49	6	CB189272
8	13.2	47.1	49	6	AA220557
9	13.2	47.1	49	6	AA220557
10	13.2	47.1	49	6	AA220557
11	13.2	47.1	49	6	AA220557
12	13.2	47.1	49	6	AA220557
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16	12.8	45.7	47	8	BH791451
17	12.8	45.7	48	9	CL234325
18	12.8	45.7	49	1	AA657267
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20	12.8	45.7	49	8	BZ769405
21	12.6	45.0	42	9	TA242A07Q
22	12.6	45.0	46	9	CC886211
23	12.4	44.3	24	8	AZ436588
24	12.4	44.3	38	8	BH865601

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C 26	12.4	44.3	43	7	W87658
C 27	12.4	44.3	44	8	AZ991513
C 28	12.4	44.3	46	8	AZ313975
C 29	12.4	44.3	46	9	CL213822
C 30	12.4	44.3	50	8	BH791926
C 31	12.2	43.6	32	8	AZ341655
C 32	12.2	43.6	38	8	AZ852234
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C 34	12.2	43.6	46	1	CC795653
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C 36	12.2	43.6	50	1	AU104471
C 37	12	42.9	27	8	BZ356733
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C 47	12	42.9	48	9	CC893922
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C 54	11.8	42.1	46	8	AZ470558
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C 56	11.8	42.1	48	9	BX27151
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C 58	11.8	42.1	50	1	AI323788
C 59	11.8	42.1	50	1	AU107633
C 60	11.6	41.4	27	8	AZ626879
C 61	11.6	41.4	28	9	TA227E04Q
C 62	11.6	41.4	29	8	AZ598779
C 63	11.6	41.4	31	8	AZ939202
C 64	11.6	41.4	34	7	CK151349
C 65	11.6	41.4	34	7	CK151355
C 66	11.6	41.4	38	2	BH793039
C 67	11.6	41.4	40	1	AA779179
C 68	11.6	41.4	40	1	AA878858
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C 70	11.6	41.4	42	7	H40647
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C 72	11.6	41.4	45	1	AA809610
C 73	11.6	41.4	47	9	BX120110
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C 77	11.6	41.4	49	1	AI689495
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C 79	11.4	40.7	26	8	AZ480391
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C 84	11.4	40.7	37	9	AG203813
C 85	11.4	40.7	41	8	BZ585244
C 86	11.4	40.7	41	8	BZ765629
C 87	11.4	40.7	41	9	CR397089
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C 97	11.4	40.7	50	9	BX288701

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W87658	zh67e12.e1
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CL213822	M046P03.G
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BZ661004	SALK_0244
AU104471	AU104471
BZ356733	SALK_1296
CL212897	G025E06.G
N44191	YV51g11.r1
AZ433353	1M0219J12
AZ480548	1M0302H12
CR398171	Arabidops
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CNS07H4K	AL610598 Anopheles
BX287762	Arabidops
CC325105	XL053.Bay
CC893922	RRM075.Ba
AA390198	mr41c06.r
AU105558	AU105558
CR038415	Reverse.s
AZ584946	1M0389N22
AA934426	0049e01.s
AF039768	AF039768
AZ470558	1M0284M12
AL754983	Arabidops
BX27151	Danio rer
R71730	YJ85b09.s1
AI323788	mm44h08.x
AU107633	AU107633
AZ626879	1M0467D22
TA227E04Q	T. brucei
AZ598779	1M0413G16
AZ939202	2M0198N02
CK151349	GS1-024.S
CK151355	GS1-039.S
BH793039	601585455
AA779179	2J43C07.s
AA878858	of84e04.s
AU257420	AU257420
H40647	Yn79c12.r1
CA965921	CCL03a11
AA809610	nzt17e04.s
BX120110	Danio rer
N68498	za30a10.s1
AZ576103	AST-T2980
AA903916	oe73a09.s
AI689495	tx94h11.x
CR014420	Forward.s
AZ480391	1M0301G21
CB305194	3'EST-NF1
AZ767725	1M0567108
BZ291428	SALK_1207
AG203307	Pan trogl
AG203813	Pan trogl
BZ585244	3590_1.30
BZ765629	SALK_1319
CR397089	Arabidops
AZ615918	1M0445C02
AL944631	Arabidops
AZ433667	1M0219F12
AZ476466	1M0295A22
BX197524	Danio rer
AZ801292	2M0059M10
BX531931	Arabidops
CG869718	XR0278.Sa
AI168783	ox71d05.s
BX288701	Arabidops

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C 98	11.2	40.0	17	1	AJ660551	AJ660551	171	11	39.3	50	1	AU104804	AU104804
C 99	11.2	40.0	28	4	BQ927514	HNC43-1-G	C 172	11	39.3	50	1	AU105325	AU105325
C 100	11.2	40.0	30	7	CK151329	GS1-128 S	C 173	11	39.3	50	1	AU105853	AU105853
C 101	11.2	40.0	32	2	BE385694	601275691	C 174	11	39.3	50	8	AZ810461	2M0076C06
C 102	11.2	40.0	32	8	BZ381016	BZ381016	C 175	11	39.3	50	8	BH813383	SALK 0640
C 103	11.2	40.0	32	8	BZ381017	BZ381017	C 176	10.8	38.6	22	2	AA3938474	0056H02.8
C 104	11.2	40.0	32	8	BZ381019	SALK 1161	C 177	10.8	38.6	24	8	AZ395654	1M0159G20
C 105	11.2	40.0	32	8	BZ763300	SALK 1161	C 178	10.8	38.6	25	8	AZ313750	1M0030P10
C 106	11.2	40.0	34	1	AL142864	AL142864	C 179	10.8	38.6	27	9	TA308805P	T. brucei
C 107	11.2	40.0	35	1	AL047410	DKFZP586D	C 180	10.8	38.6	30	8	AZ666470	1M0548F07
C 108	11.2	40.0	36	9	CG7290D1Q	CG7290D1Q	C 181	10.8	38.6	31	1	AI583675	1M0533J12
C 109	11.2	40.0	37	9	CG77689	CG77689	C 182	10.8	38.6	31	1	AI583675	1M0533J12
C 110	11.2	40.0	39	1	AV970688	AV970688	C 183	10.8	38.6	31	9	AJ593868	Arabidops
C 111	11.2	40.0	39	8	AZ611736	AZ611736	C 184	10.8	38.6	32	9	BX658549	Arabidops
C 112	11.2	40.0	40	1	AI377260	te59h12.x	C 185	10.8	38.6	32	9	BX658549	Arabidops
C 113	11.2	40.0	40	4	AI377506	602314157	C 186	10.8	38.6	33	2	AW720425	LjNEST229
C 114	11.2	40.0	41	7	H30861	H30861	C 187	10.8	38.6	34	1	AI1233900	qz478908.x
C 115	11.2	40.0	41	8	CC249540	XF270 Bay	C 188	10.8	38.6	34	1	W69493	qd47908.s1
C 116	11.2	40.0	42	8	AZ597310	AZ597310	C 189	10.8	38.6	35	9	AL949183	Arabidops
C 117	11.2	40.0	42	8	AZ820762	2M0093K09	C 190	10.8	38.6	37	1	AI000163	0s44d06.s
C 118	11.2	40.0	43	8	AZ784615	AZ784615	C 191	10.8	38.6	37	1	AI559425	3q3e11.x
C 119	11.2	40.0	46	1	AA923151	on18f11.s	C 192	10.8	38.6	37	1	AA531222	nj5c12.s
C 120	11.2	40.0	46	9	BX290645	BX290645	C 193	10.8	38.6	38	9	AJ587486	Arabidops
C 121	11.2	40.0	47	8	AZ586480	1M0392K22	C 194	10.8	38.6	38	9	AJ591113	Arabidops
C 122	11.2	40.0	47	9	DMES45250	DMES45250	C 195	10.8	38.6	39	9	BX662675	Arabidops
C 123	11.2	40.0	49	8	CC199620	CC199620	C 196	10.8	38.6	39	9	BX894643	Arabidops
C 124	11.2	40.0	50	1	AI043318	AI043318	C 197	10.8	38.6	40	1	AI074647	ox81g12.s
C 125	11.2	40.0	50	9	CC565133	CC565133	C 198	10.8	38.6	41	8	BH758401	SALK 0186
C 126	11.2	40.0	50	9	CC565133	CC565133	C 199	10.8	38.6	42	8	BH758401	SALK 0186
C 127	11.2	40.0	50	9	CC565133	CC565133	C 200	10.8	38.6	42	8	BH758401	SALK 0186
C 128	11.2	40.0	50	9	CC565133	CC565133	C 201	10.8	38.6	42	8	BH758401	SALK 0186
C 129	11.2	40.0	50	9	CC565133	CC565133	C 202	10.8	38.6	42	8	BH758401	SALK 0186
C 130	11.2	40.0	50	9	CC565133	CC565133	C 203	10.8	38.6	42	8	BH758401	SALK 0186
C 131	11.2	40.0	50	9	CC565133	CC565133	C 204	10.8	38.6	42	8	BH758401	SALK 0186
C 132	11.2	40.0	50	9	CC565133	CC565133	C 205	10.8	38.6	42	8	BH758401	SALK 0186
C 133	11.2	40.0	50	9	CC565133	CC565133	C 206	10.8	38.6	42	8	BH758401	SALK 0186
C 134	11.2	40.0	50	9	CC565133	CC565133	C 207	10.8	38.6	42	8	BH758401	SALK 0186
C 135	11.2	40.0	50	9	CC565133	CC565133	C 208	10.8	38.6	42	8	BH758401	SALK 0186
C 136	11.2	40.0	50	9	CC565133	CC565133	C 209	10.8	38.6	42	8	BH758401	SALK 0186
C 137	11.2	40.0	50	9	CC565133	CC565133	C 210	10.8	38.6	42	8	BH758401	SALK 0186
C 138	11.2	40.0	50	9	CC565133	CC565133	C 211	10.8	38.6	42	8	BH758401	SALK 0186
C 139	11.2	40.0	50	9	CC565133	CC565133	C 212	10.8	38.6	42	8	BH758401	SALK 0186
C 140	11.2	40.0	50	9	CC565133	CC565133	C 213	10.8	38.6	42	8	BH758401	SALK 0186
C 141	11.2	40.0	50	9	CC565133	CC565133	C 214	10.8	38.6	42	8	BH758401	SALK 0186
C 142	11.2	40.0	50	9	CC565133	CC565133	C 215	10.8	38.6	42	8	BH758401	SALK 0186
C 143	11.2	40.0	50	9	CC565133	CC565133	C 216	10.8	38.6	42	8	BH758401	SALK 0186
C 144	11.2	40.0	50	9	CC565133	CC565133	C 217	10.8	38.6	42	8	BH758401	SALK 0186
C 145	11.2	40.0	50	9	CC565133	CC565133	C 218	10.8	38.6	42	8	BH758401	SALK 0186
C 146	11.2	40.0	50	9	CC565133	CC565133	C 219	10.8	38.6	42	8	BH758401	SALK 0186
C 147	11.2	40.0	50	9	CC565133	CC565133	C 220	10.8	38.6	42	8	BH758401	SALK 0186
C 148	11.2	40.0	50	9	CC565133	CC565133	C 221	10.8	38.6	42	8	BH758401	SALK 0186
C 149	11.2	40.0	50	9	CC565133	CC565133	C 222	10.8	38.6	42	8	BH758401	SALK 0186
C 150	11.2	40.0	50	9	CC565133	CC565133	C 223	10.8	38.6	42	8	BH758401	SALK 0186
C 151	11.2	40.0	50	9	CC565133	CC565133	C 224	10.8	38.6	42	8	BH758401	SALK 0186
C 152	11.2	40.0	50	9	CC565133	CC565133	C 225	10.8	38.6	42	8	BH758401	SALK 0186
C 153	11.2	40.0	50	9	CC565133	CC565133	C 226	10.8	38.6	42	8	BH758401	SALK 0186
C 154	11.2	40.0	50	9	CC565133	CC565133	C 227	10.8	38.6	42	8	BH758401	SALK 0186
C 155	11.2	40.0	50	9	CC565133	CC565133	C 228	10.8	38.6	42	8	BH758401	SALK 0186
C 156	11.2	40.0	50	9	CC565133	CC565133	C 229	10.8	38.6	42	8	BH758401	SALK 0186
C 157	11.2	40.0	50	9	CC565133	CC565133	C 230	10.8	38.6	42	8	BH758401	SALK 0186
C 158	11.2	40.0	50	9	CC565133	CC565133	C 231	10.8	38.6	42	8	BH758401	SALK 0186
C 159	11.2	40.0	50	9	CC565133	CC565133	C 232	10.8	38.6	42	8	BH758401	SALK 0186
C 160	11.2	40.0	50	9	CC565133	CC565133	C 233	10.8	38.6	42	8	BH758401	SALK 0186
C 161	11.2	40.0	50	9	CC565133	CC565133	C 234	10.8	38.6	42	8	BH758401	SALK 0186
C 162	11.2	40.0	50	9	CC565133	CC565133	C 235	10.8	38.6	42	8	BH758401	SALK 0186
C 163	11.2	40.0	50	9	CC565133	CC565133	C 236	10.8	38.6	42	8	BH758401	SALK 0186
C 164	11.2	40.0	50	9	CC565133	CC565133	C 237	10.8	38.6	42	8	BH758401	SALK 0186
C 165	11.2	40.0	50	9	CC565133	CC565133	C 238	10.8	38.6	42	8	BH758401	SALK 0186
C 166	11.2	40.0	50	9	CC565133	CC565133	C 239	10.8	38.6	42	8	BH758401	SALK 0186
C 167	11.2	40.0	50	9	CC565133	CC565133	C 240	10.8	38.6	42	8	BH758401	SALK 0186
C 168	11.2	40.0	50	9	CC565133	CC565133	C 241	10.8	38.6	42	8	BH758401	SALK 0186
C 169	11.2	40.0	50	9	CC565133	CC565133	C 242	10.8	38.6	42	8	BH758401	SALK 0186
C 170	11.2	40.0	50	9	CC565133	CC565133	C 243	10.8	38.6	42	8	BH758401	SALK 0186

C 244	10.6	37.9	43	9	BX892893	Arabidops	BX892893	Arabidops	317	10.4	37.1	42	9	BX532481	Arabidops
C 245	10.6	37.9	44	9	BX532319	Arabidops	BX532319	Arabidops	C 318	10.4	37.1	42	9	DNE545209	Drosophil
C 246	10.6	37.9	44	9	TA129804P	T. brucei	AL463981	T. brucei	C 319	10.4	37.1	43	8	BX655276	1M011C24
C 247	10.6	37.9	45	1	AV961530	Arabidops	AV961530	Arabidops	C 320	10.4	37.1	43	9	BX661340	Arabidops
C 248	10.6	37.9	45	8	AZ385914	Arabidops	AZ385914	1M014E09	C 321	10.4	37.1	44	5	BX625656	BX625656
C 249	10.6	37.9	45	9	BX229715	Danio rer	BX229715	Danio rer	C 322	10.4	37.1	44	8	AZ340483	1M0072N19
C 250	10.6	37.9	45	9	AG202104	Pan trogl	AG202104	Pan trogl	C 323	10.4	37.1	44	8	AZ347569	1M0083P11
C 251	10.6	37.9	46	1	AI196568	ui70e05.x	AI196568	ui70e05.x	C 324	10.4	37.1	44	8	AZ628166	1M0480C12
C 252	10.6	37.9	46	1	AA389458	mp25e02.r	AA389458	mp25e02.r	C 325	10.4	37.1	44	8	CC199999	XH435 Bay
C 253	10.6	37.9	46	8	AZ429933	1M0214H10	AZ429933	1M0214H10	C 326	10.4	37.1	44	8	BX654077	Arabidops
C 254	10.6	37.9	46	9	AL760236	Arabidops	AL760236	Arabidops	C 327	10.4	37.1	45	1	AJ239826	AJ239826
C 255	10.6	37.9	46	9	CG805368	Arabidops	CG805368	1118059F0	C 328	10.4	37.1	45	8	AZ764357	1M0560G35
C 256	10.6	37.9	47	8	BH790193	SALK_0565	BH790193	SALK_0565	C 329	10.4	37.1	45	8	BH907586	SALK_0431
C 257	10.6	37.9	47	8	BZ663870	SALK_0274	BZ663870	SALK_0274	C 330	10.4	37.1	45	8	BZ596472	SALK_0936
C 258	10.6	37.9	47	9	AJ588138	Arabidops	AJ588138	Arabidops	C 331	10.4	37.1	45	9	CG728115	1119098S0
C 259	10.6	37.9	47	9	DR46K238	Danio rer	AL974349	Danio rer	C 332	10.4	37.1	46	1	AA932841	oe57a07.s
C 260	10.6	37.9	47	9	CL302815	P013A12 G	CL302815	P013A12 G	C 333	10.4	37.1	46	1	AA931225	oe40e03.s
C 261	10.6	37.9	47	9	CL528024	EY07441-5	CL528024	EY07441-5	C 334	10.4	37.1	46	7	CO790652	NT010B_A0
C 262	10.6	37.9	48	1	AS501194	vh75d02.r	AS501194	vh75d02.r	C 335	10.4	37.1	46	9	BX003177	Arabidops
C 263	10.6	37.9	48	9	TA2780D9P	Arabidops	AL485506	T. brucei	C 336	10.4	37.1	46	9	CR397736	Arabidops
C 264	10.6	37.9	49	1	AI16542	sal0e02.y	AI16542	sal0e02.y	C 337	10.4	37.1	47	4	BG777442	BG777442
C 265	10.6	37.9	49	1	AI883392	fc63c06.y	AI883392	fc63c06.y	C 338	10.4	37.1	47	6	CF293703	30DGS--02
C 266	10.6	37.9	49	2	BE914650	BH903786	BE914650	601655158	C 339	10.4	37.1	47	8	BH903786	BH903786
C 267	10.6	37.9	49	8	AZ395400	1M0159N24	AZ395400	1M0159N24	C 340	10.4	37.1	47	9	BX130256	Danio rer
C 268	10.6	37.9	49	8	BH901878	SALK_0844	BH901878	SALK_0844	C 341	10.4	37.1	48	1	AV959231	AV959231
C 269	10.6	37.9	49	9	BX891921	Arabidops	BX891921	Arabidops	C 342	10.4	37.1	48	8	AZ412179	1M0185H06
C 270	10.6	37.9	50	1	AU102314	AU102314	AU102314	AU102314	C 343	10.4	37.1	48	8	AZ576812	01d05 Sho
C 271	10.6	37.9	50	1	AU102316	AU102316	AU102316	AU102316	C 344	10.4	37.1	48	8	BH792289	BH792289
C 272	10.6	37.9	50	1	AU102317	AU102317	AU102317	AU102317	C 345	10.4	37.1	48	8	CC459378	SALK_1279
C 273	10.6	37.9	50	1	AU102632	AU102632	AU102632	AU102632	C 346	10.4	37.1	48	9	AG197101	Pan trogl
C 274	10.6	37.9	50	7	CN850182	000917AAF	CN850182	000917AAF	C 347	10.4	37.1	49	1	AA934271	AA934271
C 275	10.6	37.9	50	7	CN850182	000917AAF	CN850182	000917AAF	C 348	10.4	37.1	49	1	AL047237	SKOVL3CAN
C 276	10.6	37.9	50	8	AZ654289	1M0528E22	AZ654289	1M0528E22	C 349	10.4	37.1	49	5	BQ548140	rd20h05.y
C 277	10.6	37.9	50	8	AZ931879	474.dh291	AZ931879	474.dh291	C 350	10.4	37.1	49	9	BX289417	Arabidops
C 278	10.6	37.9	50	9	CC456725	SALK_1001	CC456725	SALK_1001	C 351	10.4	37.1	49	9	BX531841	Arabidops
C 279	10.6	37.9	50	9	CL679776	PR0127a	CL679776	PR0127a	C 352	10.4	37.1	50	1	AU012341	AU012341
C 280	10.4	37.1	22	8	AZ854926	2M0158F14	AZ854926	2M0158F14	C 353	10.4	37.1	50	1	AU012398	AU012398
C 281	10.4	37.1	27	8	AZ450102	1M0248L08	AZ450102	1M0248L08	C 354	10.4	37.1	50	1	AU104771	AU104771
C 282	10.4	37.1	28	9	AG193662	Pan trogl	AG193662	Pan trogl	C 355	10.4	37.1	50	1	AU107570	AU107570
C 283	10.4	37.1	29	8	BH865195	SALK_0975	BH865195	SALK_0975	C 356	10.4	37.1	50	1	AU255974	AU255974
C 284	10.4	37.1	30	8	AZ489295	1M0321L05	AZ489295	1M0321L05	C 357	10.4	37.1	50	2	BF861971	963030H05
C 285	10.4	37.1	31	9	AL756692	Arabidops	AL756692	Arabidops	C 358	10.4	37.1	50	8	AZ592438	1M0403D22
C 286	10.4	37.1	32	8	AZ513719	1M0359L13	AZ513719	1M0359L13	C 359	10.4	37.1	50	9	AJ622111	Drosophil
C 287	10.4	37.1	33	8	AZ455934	1M0258G01	AZ455934	1M0258G01	C 360	10.4	37.1	50	9	AJ622124	Drosophil
C 288	10.4	37.1	33	8	AZ662153	1M0541003	AZ662153	1M0541003	C 361	10.4	37.1	50	9	AL947641	Arabidops
C 289	10.4	37.1	33	8	BZ357116	SALK_1302	BZ357116	SALK_1302	C 362	10.4	37.1	50	9	BX984033	Reverse s
C 290	10.4	37.1	34	1	AI366127	ao94f04.x	AI366127	ao94f04.x	C 363	10.4	37.1	50	9	CF404841	Arabidops
C 291	10.4	37.1	34	8	AZ624946	1M0463121	AZ624946	1M0463121	C 364	10.2	36.4	22	8	AZ647408	Arabidops
C 292	10.4	37.1	34	8	AZ624946	1M0463121	AZ624946	1M0463121	C 365	10.2	36.4	23	8	AZ780690	2M0018E06
C 293	10.4	37.1	35	8	BH902525	SALK_0919	BH902525	SALK_0919	C 366	10.2	36.4	23	9	TA372F07P	TA372F07P
C 294	10.4	37.1	35	9	AG193215	Pan trogl	AG193215	Pan trogl	C 367	10.2	36.4	24	8	AZ807089	2M0069003
C 295	10.4	37.1	35	9	AG193215	Pan trogl	AG193215	Pan trogl	C 368	10.2	36.4	24	8	AZ831914	2M0111L20
C 296	10.4	37.1	36	9	AG202742	Pan trogl	AG202742	Pan trogl	C 369	10.2	36.4	24	9	AG193817	Pan trogl
C 297	10.4	37.1	37	1	AA056316	zf62g08.r	AA056316	zf62g08.r	C 370	10.2	36.4	25	1	AI660931	wf2aall.x
C 298	10.4	37.1	37	7	T70764	Ydi4e02.r1	T70764	Ydi4e02.r1	C 371	10.2	36.4	25	8	AZ817189	2M0086E24
C 299	10.4	37.1	37	8	BH811969	SALK_0609	BH811969	SALK_0609	C 372	10.2	36.4	25	8	BH910108	SALK_0577
C 300	10.4	37.1	37	9	BX285355	Arabidops	BX285355	Arabidops	C 373	10.2	36.4	26	8	AZ387156	1M0146E19
C 301	10.4	37.1	37	9	DME546370	Arabidops	AJ546370	Arabidops	C 374	10.2	36.4	26	8	AZ760876	1M0534J20
C 302	10.4	37.1	37	9	TA322H02Q	Arabidops	AL491432	T. brucei	C 375	10.2	36.4	26	8	BH910109	SALK_0577
C 303	10.4	37.1	37	9	TA58H04Q	T. brucei	AL455755	T. brucei	C 376	10.2	36.4	26	8	BH910398	SALK_0594
C 304	10.4	37.1	38	9	AG202374	Drosophil	AJ622374	Drosophil	C 377	10.2	36.4	28	8	AZ628209	1M0480L12
C 305	10.4	37.1	39	1	AV851787	AV851787	AV851787	AV851787	C 378	10.2	36.4	29	8	AZ635260	1M0491E06
C 306	10.4	37.1	39	5	BX554651	BX554651	BX554651	BX554651	C 379	10.2	36.4	29	8	AZ8339196	2M0135P09
C 307	10.4	37.1	39	8	AZ435630	1M0222G14	AZ435630	1M0222G14	C 380	10.2	36.4	30	9	CG717040	1119046G1
C 308	10.4	37.1	39	8	BH906658	SALK_0351	BH906658	SALK_0351	C 381	10.2	36.4	31	1	AI004493	0F57C08.8
C 309	10.4	37.1	39	9	TA65G07P	T. brucei	AL457393	T. brucei	C 382	10.2	36.4	31	8	AQ254745	EP(3)3682
C 310	10.4	37.1	39	9	AG203895	Pan trogl	AG203895	Pan trogl	C 383	10.2	36.4	32	6	CD531013	09A03 Ara
C 311	10.4	37.1	40	1	AA911268	oe75b07.s	AA911268	oe75b07.s	C 384	10.2	36.4	32	6	CF329231	NACL--04
C 312	10.4	37.1	40	1	AZ226145	nc09f09.r	AZ226145	nc09f09.r	C 385	10.2	36.4	32	8	BH909978	SALK_0568
C 313	10.4	37.1	40	8	AZ784839	2M0028C09	AZ784839	2M0028C09	C 386	10.2	36.4	32	9	AL949878	Arabidops
C 314	10.4	37.1	41	8	CC182922	XG195 Bay	CC182922	XG195 Bay	C 387	10.2	36.4	33	1	AJ649239	AJ649239
C 315	10.4	37.1	42	8	CC050109	01S0530-0	CC050109	01S0530-0	C 388	10.2	36.4	33	5	BQ595597	E014690-0
C 316	10.4	37.1	42	9	AL947400	Arabidops	AL947400	Arabidops	C 389	10.2	36.4	34	1	AI798272	tr32e04.x

390	10.2	36.4	34	8	AZ845465	2M0145H18	463	10	35.7	19	8	AZ491592	AZ491592	IM0325F16
391	10.2	36.4	35	8	AZ477231	IM0296A11	464	10	35.7	21	6	AZ645644	AZ645644	IM0511N11
392	10.2	36.4	35	8	AZ504481	IM0344M18	C 465	10	35.7	19	6	CF281815	CF281815	14ETL--09
393	10.2	36.4	36	9	CT796901	SALK 1442	C 466	10	35.7	22	8	AZ761328	AZ761328	IM0555A11
394	10.2	36.4	37	1	AA972483	Qe42d12.s	C 467	10	35.7	25	8	AZ345848	AZ345848	IM0080C16
395	10.2	36.4	37	1	AI185944	AJ29b02.s	C 468	10	35.7	25	8	AZ792292	AZ792292	2M0043H11
396	10.2	36.4	37	1	AV833316	AV833316	C 469	10	35.7	26	8	BH610036	BH610036	KG00300.5
397	10.2	36.4	37	1	AV833316	AV833316	C 470	10	35.7	26	8	TA95C11P	TA95C11P	T. brucei
398	10.2	36.4	38	8	AZ480603	IM0302F18	C 471	10	35.7	27	1	AZ603545	AZ603545	IM0422O19
399	10.2	36.4	38	8	AZ806456	AZ806456	C 472	10	35.7	28	1	AI538375	AI538375	tp64h01.x
400	10.2	36.4	40	1	AA328240	on87c07.s	C 473	10	35.7	28	8	AZ781477	AZ781477	2M0019H24
401	10.2	36.4	40	1	AA133553	zo14b11.r	C 474	10	35.7	28	8	BH861588	BH861588	SALK 0875
402	10.2	36.4	40	7	R34628	Y957c12.r1	C 475	10	35.7	29	9	TA91B11P	TA91B11P	T. brucei
403	10.2	36.4	41	9	AG203784	Pan trogl	C 476	10	35.7	31	1	AI793821	AI793821	fc54e10.x
404	10.2	36.4	41	7	T98725	Y661g03.r1	C 477	10	35.7	31	1	AI793821	AI793821	fc54e10.x
405	10.2	36.4	41	8	AZ663413	IM0543J01	C 478	10	35.7	32	6	CF291137	CF291137	14ROOT--0
406	10.2	36.4	41	9	CL639523	Q009D01 G	C 479	10	35.7	32	6	CF291137	CF291137	14ROOT--0
407	10.2	36.4	42	8	AZ427649	IM0209A15	C 480	10	35.7	32	8	AZ519233	AZ519233	IM0402F21
408	10.2	36.4	42	8	AZ993438	2M0278A04	C 481	10	35.7	32	8	AZ810628	AZ810628	2M0076H18
409	10.2	36.4	42	9	CG778648	1123029F0	C 482	10	35.7	33	8	AZ514079	AZ514079	IM0360P07
410	10.2	36.4	43	1	AI663963	ui15g07.r	C 483	10	35.7	33	8	AZ841576	AZ841576	2M0139F07
411	10.2	36.4	43	8	AZ308202	IM0010F20	C 484	10	35.7	34	1	AA929647	AA929647	VY81f07.r
412	10.2	36.4	43	8	AZ324750	IM0046016	C 485	10	35.7	34	1	AI082825	AI082825	ox78b07.x
413	10.2	36.4	43	9	AG217315	Drosophil	C 486	10	35.7	34	5	Q0586749	Q0586749	E012389.0
414	10.2	36.4	43	9	AG217315	Drosophil	C 487	10	35.7	34	7	CO784715	CO784715	BL281C.A0
415	10.2	36.4	44	1	AV952167	AV952167	C 488	10	35.7	34	8	BH854533	BH854533	KG02257-3
416	10.2	36.4	44	9	CL256321	AB0029 Sa	C 489	10	35.7	34	9	AJ598642	AJ598642	ArabiDops
417	10.2	36.4	44	9	AG188343	Pan trogl	C 490	10	35.7	34	9	AJ598642	AJ598642	ArabiDops
418	10.2	36.4	45	7	N48168	Yz02g09.s1	C 491	10	35.7	35	2	BE545364	BE545364	601078624
419	10.2	36.4	45	8	AZ513376	IM0359N23	C 492	10	35.7	35	8	AQ06431	AQ06431	ms(3)0509
420	10.2	36.4	45	9	DM545659	Drosophil	C 493	10	35.7	35	8	AZ767704	AZ767704	IM0567B11
421	10.2	36.4	45	9	TA372A04P	TA372A04P	C 494	10	35.7	35	8	BZ661989	BZ661989	SALK 0254
422	10.2	36.4	45	9	AG192232	Pan trogl	C 495	10	35.7	36	2	BE395465	BE395465	601309990
423	10.2	36.4	46	1	AA903958	AA903958	C 496	10	35.7	36	2	BZ287056	BZ287056	SALK 0204
424	10.2	36.4	46	1	AA436017	AA436017	C 497	10	35.7	36	8	CL528584	CL528584	ASV21E09.
425	10.2	36.4	46	8	AZ318180	IM0037J10	C 498	10	35.7	36	9	AZ2420346	AZ2420346	IM0198G12
426	10.2	36.4	46	8	AZ778033	2M0013D03	C 499	10	35.7	37	8	BH789296	BH789296	SALK 0016
427	10.2	36.4	46	9	AJ592635	ArabiDops	C 500	10	35.7	37	8	AL042835	AL042835	DKF2P4367
428	10.2	36.4	47	8	AZ624454	IM0463I10	C 501	10	35.7	38	1	AL042835	AL042835	DKF2P4367
429	10.2	36.4	47	8	AZ624454	IM0463I10	C 502	10	35.7	38	2	BF663249	BF663249	602144367
430	10.2	36.4	47	9	TA347C08Q	TA347C08Q	C 503	10	35.7	38	6	CF297975	CF297975	7LEAF--01
431	10.2	36.4	47	9	CL521062	DAJ2H03 F	C 504	10	35.7	38	9	AZ309141	AZ309141	IM0012P21
432	10.2	36.4	48	8	AZ818575	2M0088M10	C 505	10	35.7	38	9	TA117804P	TA117804P	AL646666 T. brucei
433	10.2	36.4	48	9	AJ587603	ArabiDops	C 506	10	35.7	39	8	AZ815545	AZ815545	2M0083B19
434	10.2	36.4	48	9	AJ594944	ArabiDops	C 507	10	35.7	39	8	BZ665538	BZ665538	EY01062-3
435	10.2	36.4	48	9	AJ594944	ArabiDops	C 508	10	35.7	39	8	CC060041	CC060041	EY00755-5
436	10.2	36.4	49	1	AA882475	AA882475	C 509	10	35.7	39	9	AL943084	AL943084	ArabiDops
437	10.2	36.4	49	1	AI326039	mr66c09.x	C 510	10	35.7	39	9	CG722883	CG722883	1119073H0
438	10.2	36.4	49	1	AI326039	mr66c09.x	C 511	10	35.7	39	9	AG198386	AG198386	Pan trogl
439	10.2	36.4	49	1	AA140338	AA140338	C 512	10	35.7	40	1	AI538827	AI538827	tp61b08.x
440	10.2	36.4	49	5	BQ101179	BQ101179	C 513	10	35.7	40	1	AA149946	AA149946	zo68f05.s
441	10.2	36.4	49	7	H14959	Ym19c11.s1	C 514	10	35.7	40	1	AV969419	AV969419	AV969419
442	10.2	36.4	49	7	W73879	W73879	C 515	10	35.7	40	1	AA402839	AA402839	zu54c01.x
443	10.2	36.4	49	8	AQ025828	1(2)K0731	C 516	10	35.7	40	8	AZ423678	AZ423678	IM0202D23
444	10.2	36.4	49	8	AQ025828	1(2)K0731	C 517	10	35.7	40	8	AZ2829670	AZ2829670	2M0107P14
445	10.2	36.4	49	9	CG133615	1119032F0	C 518	10	35.7	40	9	AL760347	AL760347	ArabiDops
446	10.2	36.4	50	1	AJ672742	AJ672742	C 519	10	35.7	40	9	BX653467	BX653467	ArabiDops
447	10.2	36.4	50	1	AJ672742	AJ672742	C 520	10	35.7	40	9	C00436	C00436	HUMGS00621
448	10.2	36.4	50	1	AJ672742	AJ672742	C 521	10	35.7	41	6	C00436	C00436	HUMGS00621
449	10.2	36.4	50	1	AJ672742	AJ672742	C 522	10	35.7	41	7	H98601	H98601	yx16b01.s1
450	10.2	36.4	50	1	AJ672742	AJ672742	C 523	10	35.7	41	8	BH790790	BH790790	SALK 0579
451	10.2	36.4	50	1	AJ672742	AJ672742	C 524	10	35.7	41	8	BX655288	BX655288	ArabiDops
452	10.2	36.4	50	1	AJ672742	AJ672742	C 525	10	35.7	41	9	TA77D030	TA77D030	T. brucei
453	10.2	36.4	50	1	AJ672742	AJ672742	C 526	10	35.7	42	6	CB172988	CB172988	OR 2o3C09
454	10.2	36.4	50	1	AJ672742	AJ672742	C 527	10	35.7	42	6	AZ324143	AZ324143	IM0045O24
455	10.2	36.4	50	1	AJ672742	AJ672742	C 528	10	35.7	42	8	AZ480327	AZ480327	IM0301F14
456	10.2	36.4	50	1	AJ672742	AJ672742	C 529	10	35.7	42	8	BZ379922	BZ379922	SALK 1142
457	10.2	36.4	50	1	AJ672742	AJ672742	C 530	10	35.7	42	9	AJ588338	AJ588338	ArabiDops
458	10.2	36.4	50	1	AJ672742	AJ672742	C 531	10	35.7	42	9	BX122348	BX122348	Danio rer
459	10.2	36.4	50	1	AJ672742	AJ672742	C 532	10	35.7	42	9	BX141156	BX141156	Danio rer
460	10.2	36.4	50	5	BX556043	BX556043	C 533	10	35.7	42	9	BX532481	BX532481	ArabiDops
461	10.2	36.4	50	8	BH412566	1007027H1	C 534	10	35.7	42	9	BX655289	BX655289	ArabiDops
462	10.2	36.4	50	9	BX949622	ArabiDops	C 535	10	35.7	43	1	AA903096	AA903096	OK46f02.s

C 536	10	35.7	43	1	AL138513	AL138513	ta74d07.x	C 609	9.8	35.0	20	8	AZ330662	AZ330662	1M0056F15
C 537	10	35.7	43	1	AL540308	AL540308	ta74e02.x	C 610	9.8	35.0	21	8	AZ397567	AZ397567	1M0162C09
C 538	10	35.7	43	1	AV958957	AV958957	AV958957	C 611	9.8	35.0	22	1	AU006620	AU006620	AU006620
C 539	10	35.7	43	1	AA541608	AA541608	1A86a06.s	C 612	9.8	35.0	22	1	AU006633	AU006633	AU006633
C 540	10	35.7	43	8	AZ806794	AZ806794	2M0069006	C 613	9.8	35.0	24	2	AW245220	AW245220	2819706.5
C 541	10	35.7	43	9	AJ596086	AJ596086	ArabiDops	C 614	9.8	35.0	24	8	AZ505513	AZ505513	1M0346B13
C 542	10	35.7	43	9	AG198159	AG198159	Pan trogl	C 615	9.8	35.0	24	8	BZ767553	BZ767553	SALK_1390
C 543	10	35.7	44	1	AA503637	AA503637	ne49d07.s	C 616	9.8	35.0	25	8	AZ794799	AZ794799	2M0048C15
C 544	10	35.7	44	9	AJ595196	AJ595196	ArabiDops	C 617	9.8	35.0	26	8	AZ466122	AZ466122	1M0276003
C 545	10	35.7	44	9	CL308428	CL308428	03F3668-0	C 618	9.8	35.0	26	8	AZ580104	AZ580104	1M0368009
C 546	10	35.7	45	2	BF538233	BF538233	602053710	C 619	9.8	35.0	27	5	BQ588135	BQ588135	E012336-0
C 547	10	35.7	45	7	CP888693	CP888693	TcTF-495	C 620	9.8	35.0	27	8	AZ840144	AZ840144	2M0136L03
C 548	10	35.7	45	7	TC9149	TC9149	YC32e08.81	C 621	9.8	35.0	28	8	BH903329	BH903329	SALK_1024
C 549	10	35.7	45	8	AQ025049	AQ025049	EP(2)1187	C 622	9.8	35.0	30	8	AZ390145	AZ390145	1M0151A24
C 550	10	35.7	45	8	AZ441332	AZ441332	1M0233D04	C 623	9.8	35.0	30	8	AL759156	AL759156	ArabiDops
C 551	10	35.7	45	8	AZ814276	AZ814276	2M0082K05	C 624	9.8	35.0	30	9	DR19J38	DR19J38	Danio rer
C 552	10	35.7	45	8	BH854778	BH854778	SALK_0886	C 625	9.8	35.0	31	1	AA935085	AA935085	ny38e09.s
C 553	10	35.7	45	8	CC039350	CC039350	3591_1_10	C 626	9.8	35.0	31	1	AL120884	AL120884	ub73e03.x
C 554	10	35.7	45	9	AL943002	AL943002	ArabiDops	C 627	9.8	35.0	31	8	AZ598183	AZ598183	1M0412A22
C 555	10	35.7	45	9	AL943467	AL943467	ArabiDops	C 628	9.8	35.0	31	8	BH906192	BH906192	SALK_1094
C 556	10	35.7	45	9	BX292945	BX292945	ArabiDops	C 629	9.8	35.0	31	8	BH906199	BH906199	SALK_1094
C 557	10	35.7	46	1	AA839967	AA839967	vw67a04.r	C 630	9.8	35.0	32	4	BG391939	BG391939	602409874
C 558	10	35.7	46	1	AA846083	AA846083	ak79h06.s	C 631	9.8	35.0	32	4	BM051667	BM051667	603638419
C 559	10	35.7	46	1	AA500769	AA500769	vg01b03.r	C 632	9.8	35.0	32	8	AZ345674	AZ345674	1M0080A03
C 560	10	35.7	46	1	CK447695	CK447695	N13D1.SP6	C 633	9.8	35.0	32	8	AZ49485	AZ49485	1M0337113
C 561	10	35.7	46	7	TI7574	TI7574	mps v5 The	C 634	9.8	35.0	32	9	CL692844	CL692844	PR1015a.F
C 562	10	35.7	46	7	TS6929	TS6929	Y483f08.r2	C 635	9.8	35.0	33	8	AZ959267	AZ959267	2M0226D21
C 563	10	35.7	46	8	AZ632597	AZ632597	1M0487N15	C 636	9.8	35.0	33	8	BH909395	BH909395	SALK_0533
C 564	10	35.7	46	8	AZ663261	AZ663261	1M0542L15	C 637	9.8	35.0	34	1	AA619106	AA619106	or68d08.s
C 565	10	35.7	46	8	BH811759	BH811759	SALK_0600	C 638	9.8	35.0	34	1	AL682978	AL682978	tw47h06.x
C 566	10	35.7	46	8	BH909849	BH909849	SALK_0562	C 639	9.8	35.0	34	8	CC458626	CC458626	SALK_1214
C 567	10	35.7	46	8	BZ761665	BZ761665	SALK_0749	C 640	9.8	35.0	34	9	CL437149	CL437149	PST4587-N
C 568	10	35.7	46	9	AJ600734	AJ600734	ArabiDops	C 641	9.8	35.0	35	1	AV967387	AV967387	AV967387
C 569	10	35.7	46	9	BX663261	BX663261	ArabiDops	C 642	9.8	35.0	35	2	BE782279	BE782279	601470033
C 570	10	35.7	47	8	AZ509442	AZ509442	1M0352G23	C 643	9.8	35.0	35	6	CF298864	CF298864	7LEAF--02
C 571	10	35.7	47	8	AZ843462	AZ843462	2M0142P18	C 644	9.8	35.0	35	8	BZ761423	BZ761423	SALK_0004
C 572	10	35.7	47	9	AL760555	AL760555	ArabiDops	C 645	9.8	35.0	36	1	AV851790	AV851790	AV851790
C 573	10	35.7	47	9	CG426758	CG426758	01S0623-0	C 646	9.8	35.0	36	6	CD533247	CD533247	30M2 Arab
C 574	10	35.7	48	8	AZ510557	AZ510557	1M0355E12	C 647	9.8	35.0	36	6	CD533247	CD533247	30M2 Arab
C 575	10	35.7	48	8	AZ601433	AZ601433	1M0419N11	C 648	9.8	35.0	36	7	D44934	D44934	HUMSUPV417
C 576	10	35.7	48	8	AZ611732	AZ611732	1M0442A17	C 649	9.8	35.0	36	8	AZ603547	AZ603547	1M0422O21
C 577	10	35.7	48	8	BZ663044	BZ663044	SALK_0265	C 650	9.8	35.0	36	9	AJ593292	AJ593292	ArabiDops
C 578	10	35.7	48	9	AL763114	AL763114	ArabiDops	C 651	9.8	35.0	37	1	AA986717	AA986717	cy55f02.s
C 579	10	35.7	48	9	BX892610	BX892610	ArabiDops	C 652	9.8	35.0	37	1	AI079739	AI079739	cy55f02.s
C 580	10	35.7	49	1	AA862822	AA862822	ch47a04.s	C 653	9.8	35.0	37	1	AA088913	AA088913	1Z69b11.s
C 581	10	35.7	49	1	AA915234	AA915234	vz08g04.r	C 654	9.8	35.0	37	6	CF337139	CF337139	JMT--07-H
C 582	10	35.7	49	1	AI014639	AI014639	0836B09.s	C 655	9.8	35.0	37	9	AZ351733	AZ351733	1M0089K21
C 583	10	35.7	49	1	AI246743	AI246743	qk40C09.x	C 656	9.8	35.0	37	9	CC884512	CC884512	SALK_1134
C 584	10	35.7	49	1	AJ649227	AJ649227	qk40C09.x	C 657	9.8	35.0	38	8	BH812118	BH812118	SALK_0612
C 585	10	35.7	49	7	D45787	D45787	HUMSUPV417	C 658	9.8	35.0	39	8	AZ825961	AZ825961	2M0101K20
C 586	10	35.7	49	7	H44851	H44851	YU03d09.r1	C 659	9.8	35.0	39	8	CC057354	CC057354	SALK_1406
C 587	10	35.7	49	8	AZ456464	AZ456464	1M0259L12	C 660	9.8	35.0	40	1	AA972469	AA972469	op42a04.s
C 588	10	35.7	49	8	BH909315	BH909315	SALK_0529	C 661	9.8	35.0	40	1	AI970772	AI970772	wr13g04.x
C 589	10	35.7	49	8	BZ764339	BZ764339	SALK_1244	C 662	9.8	35.0	40	1	AL039224	AL039224	DKF2g(mul
C 590	10	35.7	49	9	AJ589587	AJ589587	ArabiDops	C 663	9.8	35.0	40	1	AA484490	AA484490	zv29d01.s
C 591	10	35.7	49	9	BX223334	BX223334	Danio rer	C 664	9.8	35.0	40	2	BE960473	BE960473	601653217
C 592	10	35.7	50	1	AI013020	AI013020	ArabiDops	C 665	9.8	35.0	40	8	AZ760260	AZ760260	1M0553G21
C 593	10	35.7	50	1	AI013586	AI013586	ArabiDops	C 666	9.8	35.0	40	8	BH629306	BH629306	100707080
C 594	10	35.7	50	1	AI013587	AI013587	ArabiDops	C 667	9.8	35.0	40	8	BH850455	BH850455	SALK_0713
C 595	10	35.7	50	1	AI0105378	AI0105378	ArabiDops	C 668	9.8	35.0	40	9	AG217566	AG217566	DrOgoph11
C 596	10	35.7	50	1	AI0105410	AI0105410	ArabiDops	C 669	9.8	35.0	41	1	AU243521	AU243521	AU243521
C 597	10	35.7	50	1	AI0106551	AI0106551	ArabiDops	C 670	9.8	35.0	41	2	BE386704	BE386704	601274126
C 598	10	35.7	50	1	AV836775	AV836775	ArabiDops	C 671	9.8	35.0	41	6	CF304527	CF304527	ABF1--05-
C 599	10	35.7	50	4	BG538913	BG538913	602568565	C 672	9.8	35.0	41	7	H62327	H62327	Yr15f04.r1
C 600	10	35.7	50	8	AF179998	AF179998	ArabiDops	C 673	9.8	35.0	41	8	AZ449036	AZ449036	1M0247P02
C 601	10	35.7	50	8	AZ463756	AZ463756	1M0272L16	C 674	9.8	35.0	41	8	BH802322	BH802322	1008121F0
C 602	10	35.7	50	8	BH850602	BH850602	SALK_0715	C 675	9.8	35.0	41	8	CC022435	CC022435	3591_1_2
C 603	10	35.7	50	8	BH854860	BH854860	SALK_0881	C 676	9.8	35.0	42	6	CA966788	CA966788	CcLX06a23
C 604	10	35.7	50	8	CC023862	CC023862	3591_1_36	C 677	9.8	35.0	42	8	BH624960	BH624960	1007091C0
C 605	10	35.7	50	9	AL751968	AL751968	ArabiDops	C 678	9.8	35.0	42	8	BH865278	BH865278	SALK_0980
C 606	10	35.7	50	9	AL944393	AL944393	ArabiDops	C 679	9.8	35.0	42	8	BZ356384	BZ356384	SALK_1289
C 607	10	35.7	50	9	CR141606	CR141606	Forward s	C 680	9.8	35.0	42	9	AG229867	AG229867	Lotus cor
C 608	9.8	35.0	19	8	AZ351194	AZ351194	1M0089A08	C 681	9.8	35.0	43	1	AA829397	AA829397	od06d01.s

C 682	9.8	35.0	43	1	A1917027	ts51a12.x	C 755	9.8	35.0	50	1	AUI05353	AUI05353
C 683	9.8	35.0	43	4	BG756501	602715642	C 756	9.8	35.0	50	1	AUI05354	AUI05354
C 684	9.8	35.0	43	4	BJ001161	BJ001161	C 757	9.8	35.0	50	1	AUI05355	AUI05355
C 685	9.8	35.0	43	5	BX553258	BX553258	C 758	9.8	35.0	50	1	AUI05356	AUI05356
C 686	9.8	35.0	43	8	BH903418	SALK 1025	C 759	9.8	35.0	50	1	AUI05361	AUI05361
C 687	9.8	35.0	43	9	AL764203	Arabidops	C 760	9.8	35.0	50	1	AUI05362	AUI05362
C 688	9.8	35.0	43	9	BX546941	Arabidops	C 761	9.8	35.0	50	1	AUI05363	AUI05363
C 689	9.8	35.0	44	4	BI645989	BI645989	C 762	9.8	35.0	50	1	AUI05364	AUI05364
C 690	9.8	35.0	45	5	BX626763	603274968	C 763	9.8	35.0	50	1	AUI05365	AUI05365
C 691	9.8	35.0	45	5	BH810609	SALK 0509	C 764	9.8	35.0	50	1	AUI05367	AUI05367
C 692	9.8	35.0	45	8	BH846431	SALK 0079	C 765	9.8	35.0	50	1	AUI05369	AUI05369
C 693	9.8	35.0	45	8	BH848090	SALK 0674	C 766	9.8	35.0	50	1	AUI05370	AUI05370
C 694	9.8	35.0	45	9	BX153691	Danilo rer	C 767	9.8	35.0	50	1	AUI05371	AUI05371
C 695	9.8	35.0	45	9	BX658036	Arabidops	C 768	9.8	35.0	50	1	AUI05372	AUI05372
C 696	9.8	35.0	45	9	CR399267	Arabidops	C 769	9.8	35.0	50	1	AUI05373	AUI05373
C 697	9.8	35.0	45	9	TA247B07Q	Arabidops	C 770	9.8	35.0	50	1	AUI05374	AUI05374
C 698	9.8	35.0	45	9	AG191484	Pan trogl	C 771	9.8	35.0	50	1	AUI05375	AUI05375
C 699	9.8	35.0	46	1	A1356755	QV22f06.x	C 772	9.8	35.0	50	1	AUI05376	AUI05376
C 700	9.8	35.0	46	1	AV847044	AV847044	C 773	9.8	35.0	50	1	AUI05377	AUI05377
C 701	9.8	35.0	46	6	C02279	HUMGS000664	C 774	9.8	35.0	50	1	AUI05379	AUI05379
C 702	9.8	35.0	46	8	AZ807543	2M0070021	C 775	9.8	35.0	50	1	AUI05380	AUI05380
C 703	9.8	35.0	46	8	BH901203	SALK_0736	C 776	9.8	35.0	50	1	AUI05381	AUI05381
C 704	9.8	35.0	47	8	AZ581261	1M0369P06	C 777	9.8	35.0	50	1	AUI05382	AUI05382
C 705	9.8	35.0	47	8	BH801184	1008126A0	C 778	9.8	35.0	50	1	AUI05383	AUI05383
C 706	9.8	35.0	47	8	BH903423	SALK 1025	C 779	9.8	35.0	50	1	AUI05384	AUI05384
C 707	9.8	35.0	47	9	CNS07FDV	Arabidops	C 780	9.8	35.0	50	1	AUI05385	AUI05385
C 708	9.8	35.0	47	9	CG869956	XT0078 Sa	C 781	9.8	35.0	50	1	AUI05386	AUI05386
C 709	9.8	35.0	48	1	AA429295	2M07a04.r	C 782	9.8	35.0	50	1	AUI05387	AUI05387
C 710	9.8	35.0	48	2	BE896146	601438738	C 783	9.8	35.0	50	1	AUI05388	AUI05388
C 711	9.8	35.0	48	8	BH811707	SALK_0596	C 784	9.8	35.0	50	1	AUI05389	AUI05389
C 712	9.8	35.0	48	9	DMES46992	Arabidops	C 785	9.8	35.0	50	1	AUI05390	AUI05390
C 713	9.8	35.0	48	9	AG229425	Lotus cor	C 786	9.8	35.0	50	1	AUI05391	AUI05391
C 714	9.8	35.0	49	1	AA903833	ok60g11.s	C 787	9.8	35.0	50	1	AUI05392	AUI05392
C 715	9.8	35.0	49	1	A1680337	2M0214G12	C 788	9.8	35.0	50	1	AUI05393	AUI05393
C 716	9.8	35.0	49	8	AZ399748	Arabidops	C 789	9.8	35.0	50	1	AUI05394	AUI05394
C 717	9.8	35.0	49	8	AZ950523	2M0214G12	C 790	9.8	35.0	50	1	AUI05395	AUI05395
C 718	9.8	35.0	49	8	BZ594709	SALK_0851	C 791	9.8	35.0	50	1	AUI05396	AUI05396
C 719	9.8	35.0	49	9	AL758948	Arabidops	C 792	9.8	35.0	50	1	AUI05397	AUI05397
C 720	9.8	35.0	49	9	AL943577	Arabidops	C 793	9.8	35.0	50	1	AUI05398	AUI05398
C 721	9.8	35.0	49	9	EX161887	Danio rer	C 794	9.8	35.0	50	1	AUI05399	AUI05399
C 722	9.8	35.0	50	1	AUI02669	Arabidops	C 795	9.8	35.0	50	1	AUI05400	AUI05400
C 723	9.8	35.0	50	1	AUI03372	Arabidops	C 796	9.8	35.0	50	1	AUI05401	AUI05401
C 724	9.8	35.0	50	1	AUI03698	Arabidops	C 797	9.8	35.0	50	1	AUI05402	AUI05402
C 725	9.8	35.0	50	1	AUI04010	Arabidops	C 798	9.8	35.0	50	1	AUI05403	AUI05403
C 726	9.8	35.0	50	1	AUI04734	Arabidops	C 799	9.8	35.0	50	1	AUI05404	AUI05404
C 727	9.8	35.0	50	1	AUI05265	Arabidops	C 800	9.8	35.0	50	1	AUI05405	AUI05405
C 728	9.8	35.0	50	1	AUI05319	Arabidops	C 801	9.8	35.0	50	1	AUI05406	AUI05406
C 729	9.8	35.0	50	1	AUI05321	Arabidops	C 802	9.8	35.0	50	1	AUI05407	AUI05407
C 730	9.8	35.0	50	1	AUI05322	Arabidops	C 803	9.8	35.0	50	1	AUI05408	AUI05408
C 731	9.8	35.0	50	1	AUI05323	Arabidops	C 804	9.8	35.0	50	1	AUI05409	AUI05409
C 732	9.8	35.0	50	1	AUI05324	Arabidops	C 805	9.8	35.0	50	1	AUI05410	AUI05410
C 733	9.8	35.0	50	1	AUI05325	Arabidops	C 806	9.8	35.0	50	1	AUI05411	AUI05411
C 734	9.8	35.0	50	1	AUI05326	Arabidops	C 807	9.8	35.0	50	1	AUI05412	AUI05412
C 735	9.8	35.0	50	1	AUI05327	Arabidops	C 808	9.8	35.0	50	1	AUI05413	AUI05413
C 736	9.8	35.0	50	1	AUI05328	Arabidops	C 809	9.8	35.0	50	1	AUI05414	AUI05414
C 737	9.8	35.0	50	1	AUI05329	Arabidops	C 810	9.8	35.0	50	1	AUI05415	AUI05415
C 738	9.8	35.0	50	1	AUI05330	Arabidops	C 811	9.8	35.0	50	1	AUI05416	AUI05416
C 739	9.8	35.0	50	1	AUI05331	Arabidops	C 812	9.8	35.0	50	1	AUI05417	AUI05417
C 740	9.8	35.0	50	1	AUI05332	Arabidops	C 813	9.8	35.0	50	1	AUI05418	AUI05418
C 741	9.8	35.0	50	1	AUI05333	Arabidops	C 814	9.8	35.0	50	1	AUI05419	AUI05419
C 742	9.8	35.0	50	1	AUI05334	Arabidops	C 815	9.8	35.0	50	1	AUI05420	AUI05420
C 743	9.8	35.0	50	1	AUI05335	Arabidops	C 816	9.8	35.0	50	1	AUI05421	AUI05421
C 744	9.8	35.0	50	1	AUI05336	Arabidops	C 817	9.8	35.0	50	1	AUI05422	AUI05422
C 745	9.8	35.0	50	1	AUI05337	Arabidops	C 818	9.8	35.0	50	1	AUI05423	AUI05423
C 746	9.8	35.0	50	1	AUI05338	Arabidops	C 819	9.8	35.0	50	1	AUI05424	AUI05424
C 747	9.8	35.0	50	1	AUI05339	Arabidops	C 820	9.8	35.0	50	1	AUI05425	AUI05425
C 748	9.8	35.0	50	1	AUI05340	Arabidops	C 821	9.8	35.0	50	1	AUI05426	AUI05426
C 749	9.8	35.0	50	1	AUI05341	Arabidops	C 822	9.8	35.0	50	1	AUI05427	AUI05427
C 750	9.8	35.0	50	1	AUI05342	Arabidops	C 823	9.8	35.0	50	1	AUI05428	AUI05428
C 751	9.8	35.0	50	1	AUI05343	Arabidops	C 824	9.8	35.0	50	1	AUI05429	AUI05429
C 752	9.8	35.0	50	1	AUI05344	Arabidops	C 825	9.8	35.0	50	1	AUI05430	AUI05430
C 753	9.8	35.0	50	1	AUI05345	Arabidops	C 826	9.8	35.0	50	1	AUI05431	AUI05431
C 754	9.8	35.0	50	1	AUI05346	Arabidops	C 827	9.8	35.0	50	1	AUI05432	AUI05432
C 755	9.8	35.0	50	1	AUI05347	Arabidops	C 828	9.8	35.0	50	1	AUI05433	AUI05433
C 756	9.8	35.0	50	1	AUI05348	Arabidops	C 829	9.8	35.0	50	1	AUI05434	AUI05434
C 757	9.8	35.0	50	1	AUI05349	Arabidops	C 830	9.8	35.0	50	1	AUI05435	AUI05435
C 758	9.8	35.0	50	1	AUI05350	Arabidops	C 831	9.8	35.0	50	1	AUI05436	AUI05436
C 759	9.8	35.0	50	1	AUI05351	Arabidops	C 832	9.8	35.0	50	1	AUI05437	AUI05437
C 760	9.8	35.0	50	1	AUI05352	Arabidops	C 833	9.8	35.0	50	1	AUI05438	AUI05438
C 761	9.8	35.0	50	1	AUI05353	Arabidops	C 834	9.8	35.0	50	1	AUI05439	AUI05439
C 762	9.8	35.0	50	1	AUI05354	Arabidops	C 835	9.8	35.0	50	1	AUI05440	AUI05440
C 763	9.8	35.0	50	1	AUI05355	Arabidops	C 836	9.8	35.0	50	1	AUI05441	AUI05441
C 764	9.8	35.0	50	1	AUI05356	Arabidops	C 837	9.8	35.0	50	1	AUI05442	AUI05442
C 765	9.8	35.0	50	1	AUI05357	Arabidops	C 838	9.8	35.0	50	1	AUI05443	AUI05443
C 766	9.8	35.0	50	1	AUI05358	Arabidops	C 839	9.8	35.0	50	1	AUI05444	AUI05444
C 767	9.8	35.0	50	1	AUI05359	Arabidops	C 840	9.8	35.0	50	1	AUI05445	AUI05445
C 768	9.8	35.0	50	1	AUI05360	Arabidops	C 841	9.8	35.0	50	1	AUI05446	AUI05446
C 769	9.8	35.0	50	1	AUI05361	Arabidops	C 842	9.8	35.0	50	1	AUI05447	AUI05447
C 770	9.8	35.0	50	1	AUI05362	Arabidops	C 843	9.8	35.0	50	1	AUI05448	AUI05448
C 771	9.8	35.0	50	1	AUI05363	Arabidops	C 844	9.8	35.0	50	1	AUI05449	AUI05449
C 772	9.8	35.0	50	1	AUI05364	Arabidops	C 845	9.8	35.0	50	1	AUI05450	AUI05450
C 773	9.8	35.0	50	1	AUI05365	Arabidops	C 846	9.8	35.0	50	1	AUI05451	AUI05451
C 774	9.8	35.0	50	1	AUI05366	Arabidops	C 847	9.8	35.0	50	1	AUI05452	AUI05452
C 775	9.8	35.0	50	1	AUI05367	Arabidops	C 848	9.8	35.0	50	1	AUI05453	AUI05453
C 776	9.8	35.0	50	1	AUI05368	Arabidops	C 849	9.8	35.0	50	1	AUI05454	AUI05454
C 777	9.8	35.0	50	1	AUI05369	Arabidops	C 850	9.8	35.0	50	1	AUI05455	AUI05455
C 778	9.8	35.0	50	1	AUI05370	Arabidops	C 851	9.8	35.0	50	1	AUI05456	AUI05456
C 779	9.8	35.0	50	1	AUI05371	Arabidops	C 852	9.8	35.0	50	1	AUI05457	AUI05457
C 780	9.												

828	9.8	35.0	50	4	BG261065	602372686	901	9.6	34.3	38	8	AZ609074	1M0433H11
829	9.8	35.0	50	4	BI744116	ku55h03.y	C 902	9.6	34.3	38	8	BH855997	SALK_0838
830	9.8	35.0	50	6	CB277369	ku75f01.y	C 903	9.6	34.3	38	8	BZ596524	SALK_0927
831	9.8	35.0	50	7	R70221	Y180f12.r1	C 904	9.6	34.3	38	9	TA241B11Q	T. brucei
832	9.8	35.0	50	7	T82774	Ni0084	C 905	9.6	34.3	38	9	AG019398	Homo sapi
833	9.8	35.0	50	8	A0073798	EP(3)3181	C 906	9.6	34.3	39	1	AJ799081	AJ799081
834	9.8	35.0	50	8	AZ592619	IM040310	C 907	9.6	34.3	39	2	BZ598028	601645348
835	9.8	35.0	50	8	AZ621023	1M0454C04	C 908	9.6	34.3	39	8	AZ485216	1M0312F05
836	9.8	35.0	50	8	B07507	21-5'A Rand	C 909	9.6	34.3	39	8	AZ595333	1M0407F23
837	9.8	35.0	50	9	AL771848	Arabidops	C 910	9.6	34.3	39	8	AZ832494	2M0112L21
838	9.8	35.0	50	9	AL952981	Arabidops	C 911	9.6	34.3	39	8	BZ354203	SALK_1233
839	9.8	35.0	50	9	BX969349	Forward s	C 912	9.6	34.3	39	8	BZ593796	SALK_0820
840	9.8	35.0	50	9	TA230801Q	Forward s	C 913	9.6	34.3	39	8	CC054876	SALK_0801
841	9.6	34.3	17	9	AJ592362	Arabidops	C 914	9.6	34.3	39	9	CG427920	01S0783-0
842	9.6	34.3	20	8	AJ440002	1M0230E19	C 915	9.6	34.3	39	9	CL517573	SAASH03 F
843	9.6	34.3	21	8	AZ607204	1M0429H03	C 916	9.6	34.3	39	9	AG019397	Homo sapi
844	9.6	34.3	22	8	AZ476575	1M0295F02	C 917	9.6	34.3	40	1	AI049834	an37g11.x
845	9.6	34.3	23	1	AU254061	AU254061	C 918	9.6	34.3	40	1	AA160572	Zq46d11.r
846	9.6	34.3	24	8	AZ416129	IM0191D16	C 919	9.6	34.3	40	7	H87885	Yw16d04.r1
847	9.6	34.3	24	8	AZ481314	1M0303A06	C 920	9.6	34.3	40	8	AZ452300	1M0252002
848	9.6	34.3	27	8	BZ356916	SALK_1299	C 921	9.6	34.3	40	8	AZ841730	2M0139G21
849	9.6	34.3	28	1	AI006798	ua74502.r	C 922	9.6	34.3	40	8	BH848610	SALK_0685
850	9.6	34.3	28	1	AI168501	ow90g01.s	C 923	9.6	34.3	40	8	BZ288532	SALK_0219
851	9.6	34.3	28	1	AI442350	sa23d04.x	C 924	9.6	34.3	40	8	BZ764171	SALK_1240
852	9.6	34.3	28	1	AA191808	1M0191D16	C 925	9.6	34.3	40	8	CG733826	1115F5960
853	9.6	34.3	28	8	AZ591964	1M0402A01	C 926	9.6	34.3	40	9	CL212513	Gen trogl
854	9.6	34.3	29	8	AZ623171	1M0460O03	C 927	9.6	34.3	40	9	AG192165	AG192165
855	9.6	34.3	30	9	CG733855	1119159H1	C 928	9.6	34.3	41	1	AU251358	AU251358
856	9.6	34.3	30	9	AG189187	Pan trogl	C 929	9.6	34.3	41	2	BF569468	602185954
857	9.6	34.3	31	1	AA983092	am24c01.s	C 930	9.6	34.3	41	7	D74277	CELK079AXF
858	9.6	34.3	31	6	CF291819	14ROOT--0	C 931	9.6	34.3	41	7	N80572	ZD02C07.s1
859	9.6	34.3	31	9	CF359652	Arabidops	C 932	9.6	34.3	41	7	N90699	ZB43F04.s1
860	9.6	34.3	31	9	CL309426	03S2011-0	C 933	9.6	34.3	41	8	AZ304505	1M0004B10
861	9.6	34.3	32	8	AZ623046	1M0040P21	C 934	9.6	34.3	41	8	AZ330647	1M0056B15
862	9.6	34.3	32	9	DME545736	Drosophil	C 935	9.6	34.3	41	8	AZ442277	1M0234P20
863	9.6	34.3	32	9	CC866917	SALK_1492	C 936	9.6	34.3	41	8	AZ785156	2M028P13
864	9.6	34.3	33	8	BH902610	SALK_0977	C 937	9.6	34.3	41	8	AZ992210	2M0276H13
865	9.6	34.3	33	9	AA553935	T. brucei	C 938	9.6	34.3	41	9	TA94F02Q	TA94F02Q
866	9.6	34.3	34	1	AA959736	vw54d06.s	C 939	9.6	34.3	41	9	CT799936	01S0783-0
867	9.6	34.3	34	1	AA116347	mq70g12.r	C 940	9.6	34.3	42	1	AI191530	qe49a09.x
868	9.6	34.3	34	2	BE914450	601668834	C 941	9.6	34.3	42	8	BH847647	SALK_0551
869	9.6	34.3	34	8	AZ799773	2M0057124	C 942	9.6	34.3	42	9	DR1LJ38	DaniG rrr
870	9.6	34.3	34	9	AJ597693	Arabidops	C 943	9.6	34.3	43	1	AA967042	ua39e07.r
871	9.6	34.3	34	9	CR360358	Arabidops	C 944	9.6	34.3	43	1	AI098967	ub99g04.r
872	9.6	34.3	35	2	AW245489	2822716.5	C 945	9.6	34.3	43	1	AI789878	ue65f10.r
873	9.6	34.3	35	8	AZ439115	1M0229N05	C 946	9.6	34.3	43	1	AJ651163	AJ651163
874	9.6	34.3	35	8	AZ820699	2M0093L02	C 947	9.6	34.3	43	1	AA231183	mw33f06.r
875	9.6	34.3	35	8	AZ821491	2M0094H18	C 948	9.6	34.3	43	1	AV833807	AV833807
876	9.6	34.3	35	8	BH011362	BG01007-5	C 949	9.6	34.3	43	8	AZ778245	2M0013022
877	9.6	34.3	35	9	AL936282	Arabidops	C 950	9.6	34.3	43	8	BZ583006	3590_1_48
878	9.6	34.3	35	9	BX654143	Arabidops	C 951	9.6	34.3	43	9	AL756095	Arabidops
879	9.6	34.3	35	9	TA246706Q	T. brucei	C 952	9.6	34.3	44	1	AA111655	mo35h10.r
880	9.6	34.3	35	9	CL659130	PR10133b	C 953	9.6	34.3	44	4	BJ037636	BJ037636
881	9.6	34.3	36	4	BG765238	602738656	C 954	9.6	34.3	44	8	AZ836041	2M0130B12
882	9.6	34.3	36	4	B1651926	603298664	C 955	9.6	34.3	44	8	BZ353146	SALK_1198
883	9.6	34.3	36	8	AZ434008	1M0220N08	C 956	9.6	34.3	44	9	AJ600107	Arabidops
884	9.6	34.3	36	8	AZ493433	1M0328A12	C 957	9.6	34.3	44	9	TA165050Q	TA165050Q
885	9.6	34.3	36	8	AZ599432	1M0414G13	C 958	9.6	34.3	44	9	CG783767	01S0585-0
886	9.6	34.3	36	8	BZ287178	SALK_0205	C 959	9.6	34.3	44	9	CL300531	02S0047-0
887	9.6	34.3	36	9	AJ587667	Arabidops	C 960	9.6	34.3	45	1	AA276118	VC36d12.r
888	9.6	34.3	37	1	AA906103	OJ86b05.s	C 961	9.6	34.3	45	5	BQ582321	E012305-0
889	9.6	34.3	37	1	AI634572	t230a01.x	C 962	9.6	34.3	45	8	AZ311865	1M0027A05
890	9.6	34.3	37	1	AI647510	uk40e11.x	C 963	9.6	34.3	45	8	AZ772088	1M0574P09
891	9.6	34.3	37	1	AJ239943	AJ239943	C 964	9.6	34.3	45	8	AZ779998	2M0016122
892	9.6	34.3	37	1	AA519848	TgESTz569	C 965	9.6	34.3	45	8	BH171077	SALK_0037
893	9.6	34.3	37	6	CD987913	QAO6e08.y	C 966	9.6	34.3	45	8	BH813038	SALK_0636
894	9.6	34.3	37	8	AQ073641	EP(2)2504	C 967	9.6	34.3	45	8	BZ595896	SALK_0897
895	9.6	34.3	37	8	AZ817320	2M0086B23	C 968	9.6	34.3	45	8	BZ769795	SALK_1427
896	9.6	34.3	37	9	BH812715	SALK_0629	C 969	9.6	34.3	46	1	AV855174	AV855174
897	9.6	34.3	37	9	CL640636	G078C07 G	C 970	9.6	34.3	46	1	AA480238	re31d04.s
898	9.6	34.3	38	4	BM007143	603615283	C 971	9.6	34.3	46	1	AA547190	vk81d07.s
899	9.6	34.3	38	5	BQ589313	S014007-0	C 972	9.6	34.3	46	8	AZ429933	1M0214H10
900	9.6	34.3	38	8	AZ514073	1M0360D08	C 973	9.6	34.3	46	8	AZ460164	1M0265G23

9.6 34.3 46 8 AZ611861 1M0438022
9.6 34.3 46 8 AZ808310 2M0071H17
9.6 34.3 46 8 AZ810710 2M0076M21
9.6 34.3 46 8 AZ810715 LBE14P83P
9.6 34.3 47 7 H45354 YN99A08.r1
9.6 34.3 47 8 B2355838 SALK.1276
9.6 34.3 47 8 BZ665134 SALK.1107
9.6 34.3 47 8 BZ665134 SALK.1107
9.6 34.3 47 8 BZ665134 SALK.1107
9.6 34.3 47 9 AL751461 Arabidops
9.6 34.3 47 9 AL945750 Arabidops
9.6 34.3 47 9 TA122802P
9.6 34.3 48 5 BX551876 BX551876
9.6 34.3 48 7 CO781458 BL012C.A0
9.6 34.3 48 7 CO781458 BL012C.A0
9.6 34.3 48 7 CO781458 BL012C.A0
9.6 34.3 48 8 AZ344159 1M0078G03
9.6 34.3 48 8 AZ371084 1M0122C03
9.6 34.3 48 8 AZ810805 2M0076A11
9.6 34.3 48 8 AZ810805 2M0076A11
9.6 34.3 48 8 CC044288 3591.1.16
9.6 34.3 48 8 CC044288 3591.1.16
9.6 34.3 48 9 DR15D3T
9.6 34.3 48 9 DR15D3T
9.6 34.3 49 1 AA907765 om33h05.s
9.6 34.3 49 1 AI003826 CT43F04.s
9.6 34.3 49 1 AI941380 sc12ell.Y
9.6 34.3 49 1 AJ666269 AJ666269
9.6 34.3 49 1 AJ666269 AJ666269
9.6 34.3 49 2 AW041893 SWL4CAK02
9.6 34.3 49 2 AW041893 SWL4CAK02
9.6 34.3 49 5 BQ482698 ke54all.Y
9.6 34.3 49 5 BQ482698 ke54all.Y
9.6 34.3 49 6 CF311120 ABF--06-D
9.6 34.3 49 6 CF311120 ABF--06-D
9.6 34.3 49 7 D11989 HUM000S134
9.6 34.3 49 8 AZ430355 1M0214K18
9.6 34.3 49 8 AZ430355 1M0214K18

ALIGNMENTS

RESULT 1
LOCUS AA223130 43 bp mRNA linear EST 19-FEB-1997
DEFINITION cDNA clone IMAGE:650739 5' similar to TR:G984325 G984325
PHOSPHOGLUCONATE DEHYDROGENASE. ; mRNA sequence.

ACCESSION AA223130.1 GI:1843689
VERSION AA223130.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Madis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone. Similarity on wrong strand
Seq primer: -28m13 rev1 Et from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="GDB:5277328"
/db_xref="taxon:9606"
/clone="IMAGE:650739"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene NT2 neuronal precursor 937230"
/note="Organ: brain; Vector: pBluescript SK-; Site: 1:
EcORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Uninduced, exponentially growing neuroepithelial
cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGCGCAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

ORIGIN
Query Match 51.4%; Score 14.4; DB 1; Length 43;
Best Local Similarity 75.0%; Pred. No. 5.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CGTTCGTGGGATGATCGTCATCG 24
Db 15 CGTGCATCGGATTCGCGTCATCG 38

RESULT 2
LOCUS AU104451/c 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU104451 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC00222, mRNA sequence.

ACCESSION AU104451.1 GI:13553972
VERSION AU104451.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Sugama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

TITLE EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
PUBMED
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC00222"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 49.3%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GTTCGTGGGATGATCGTCATCGT 26
Db 35 GTTCGTGGGATGATCGTCATCGT 11

RESULT 3


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/clonename="UUGC2M0063C02"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clonelib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

```

Query Match 47.1%; Score 13.2; DB 8; Length 34;
Best Local Similarity 69.2%; Pred. No. 1.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 TTCTGGGATAGTCGGTCATGGTGT 28
    ||||| ||||| ||||| |||||
DB 2 TTCTGGTGTGGTGGTGGTGGTGT 27
    ||||| ||||| ||||| |||||

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RESULT 6
LOCUS AZ770060/c 46 bp DNA linear GSS 16-FEB-2001
DEFINITION M0571F19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0571F19 F, genomic survey sequence.
ACCESSION AZ770060
VERSION AZ770060.1 GI:12890851
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weies,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: F column: 19
Seq primer: CGTGTAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="C57BL/6J"

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/clonename="UUGC1M0571F19"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clonelib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

```

Query Match 47.1%; Score 13.2; DB 8; Length 46;
Best Local Similarity 69.2%; Pred. No. 2e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 TTCTGGGATAGTCGGTCATGGTGT 28
    ||||| ||||| ||||| |||||
DB 2 TTCTGGAACTGTAGTCAGGAGTT 3
    ||||| ||||| ||||| |||||

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RESULT 7

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CB189272/c 49 bp mRNA linear EST 06-FEB-2003
LOCUS ks31b10.y1 Trichuris vulpis pAMP1 v1 Trichuris vulpis cDNA 5' similar to contains element MER33 repetitive element ;, mRNA sequence.
ACCESSION CB189272
VERSION CB189272.1 GI:28252664
SOURCE EST.
ORGANISM Trichuris vulpis
REFERENCE Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichuridae; Trichuris. 1 (bases 1 to 49)
AUTHORS McGarver,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wyllie,T., Dante,W., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Willson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Adult nematodes were collected from infected dogs by Dr. Prema Arasu of North Carolina State University, Raleigh.
Seq primer: -40RP from Gibco.
Location/Qualifiers

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FEATURES

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source
1..49
/organism="Trichuris vulpis"
/mol_type="mRNA"
/db_xref="taxon:219738"
/dev_stage="adult"
/lab_host="DH10B"
(clone_lib="Trichuris vulpis pAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
made by using Dynabead oligo-dT priming (Dyna) PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Adult nematodes were collected from
infected dogs by Dr. Prema Arasu of North Carolina State
University, Raleigh, NC (Prema.Arasu@ncsu.edu) and RNA was
prepared by Merry McLaire of Divergence Inc, St. Louis, MO
[mclaire@divergence.com].")
ORIGIN
Query Match 47.1%; Score 13.2; DB 6; Length 49;
Best Local Similarity 69.2%; Pred. NO. 2e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 TTCGTGGATAGTCGCTCATGTTT 28
DB 40 TTTTGTGATAGTCCTTTATTCCGTT 15
RESULT 8
AA220557
LOCUS
DEFINITION
my09f10.r1 Barstead mouse lung MPLR2 Mus musculus cDNA clone
IMAGE:695371 5' similar to TR:G1280422 COMMISSURELESS. ;
mRNA sequence.
ACCESSION
AA220557.1 GI:1838377
VERSION
EST.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Mus.
1 (bases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterson, R.
REFERENCE
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:428931
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:695371"
/sex="mixed"
/tissue type="lung"
FEATURES
source
/dev_stage="6 weeks"
/lab_host="DH10B"
(clone_lib="Barstead mouse lung MPLR2"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACGAATCTGAATGGAGCGGCCCTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[GTAGTTCGTTACC], digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead."
ORIGIN
Query Match 46.4%; Score 13; DB 1; Length 28;
Best Local Similarity 76.2%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5 CGTGGATAGTCGCTCATGTT 25
DB 2 CGTTGGATAATCCGTGTGCT 22
RESULT 9
DME546920/c
LOCUS
DEFINITION
Drosophila melanogaster flanking sequence of RS P element insertion
P{RS3}CB-5276-3, clone library P{RS3}, genomic survey sequence.
ACCESSION
AJ546920
VERSION
AJ546920.1 GI:28555110
KEYWORDS
GSS; genome survey sequence.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1
Ryder, E.J., Ashburner, M., Bagunya, J., Blows, F., Bucheton, A.,
Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N.,
Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P.,
Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A.,
Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and
Russell, S.
REFERENCE
Mapping of RS P element insertions in Drosophila melanogaster for
the Drosbel second generation deficiency kit
Unpublished
2 (bases 1 to 34)
Ryder, E.J.
AUTHORS
Direct Submission
Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,
University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
The insertion point of the P element is before base 1 of the
sequence. Further information about this P element insertion line
can be found at http://www.flyseq.org.uk and
http://www.drosdel.org.uk.
Location/Qualifiers
1..34
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="3R"
/clone="P{RS3}CB-5276-3"
/clone_lib="P{RS3}"
/note="read=5' end"
misc_feature
1..34
/note="P element insertion in the 3' to 5' orientation"
ORIGIN
Query Match 46.4%; Score 13; DB 9; Length 34;
Best Local Similarity 76.2%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 8 CGGATAGTCGCTCATGTTT 28

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Db	34	CGCGTAGTCCGTTATGAGTT 14	
RESULT 10			
LOCUS	A1588805/c		
DEFINITION	40 bp mRNA linear EST 07-JUN-2001		
	fb99f01.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone		
	IMAGE:3720025 5' similar to SM:COX1_SALTUR P29653 CYTOCHROME C		
	OXIDASE POLYPEPTIDE 1 ; mRNA sequence.		
ACCESSION	A1588805		
VERSION	A1588805.1	GI:4597852	
KEYWORDS	EST		
SOURCE	Danio rerio (zebrafish)		
ORGANISM	Danio rerio		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.		
AUTHORS	1 (bases 1 to 40)		
	Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.		
TITLE	WashU Zebrafish EST Project 1998		
JOURNAL	Unpublished (1998)		
COMMENT	Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrafis@watson.wustl.edu cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumFrimardatenbank, Berlin, Germany (web address: www.rzpd.de)		
FEATURES	source	Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: T3 ET from Amersham High quality sequence stop: 1	
	POLYA-No.	Location/Qualifiers	
	1..40	/organism="Danio rerio"	
		/mol_type="mRNA"	
		/db_xref="taxon:7955"	
		/clone="IMAGE:3720025"	
		/sex="mixed"	
		/tissue_type="26 somite embryos, adult livers, shield stage embryos"	
		/lab_host="XLI-blue MRF"	
		/clone_lib="Zebrafish WashU MPIMG EST"	
		/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTTCAGATCCGAGCGCCGCCCTTTTCTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality	
ORIGIN		control."	
Query Match	46.4%;	Score 13;	DB 1; Length 40;
Best Local Similarity	76.2%;	Pred. No. 2.4e+05;	
Matches	16;	Conservative 0;	Mismatches 5; Indels 0; Gaps 0;
Qy	5	CGTGGGATAGTCGTCATGCT 25	
Db	38	CGTAGTATGTCACACATGCT 18	
RESULT 11			
LOCUS	AJ649066		
DEFINITION	AJ649066 CSFQRAN19 Sus scrofa cDNA clone C0003271_H04, mRNA		EST 07-JUL-2004
	Sequence.		
ACCESSION	AJ649066		
VERSION	AJ649066.1	GI:49325911	
KEYWORDS	EST		
SOURCE	Sus scrofa (pig)		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
AUTHORS	1 (bases 1 to 43)		
TITLE	Anderson, S.I., Finlayson, H.A. and Archibald, A.L.		
JOURNAL	Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle		
COMMENT	Unpublished (2004) Contact: Anderson SI Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UNITED KINGDOM Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector: pBluescriptII (KS) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.		
FEATURES	Location/Qualifiers		
	1..43	/organism="Sus scrofa"	
		/mol_type="mRNA"	
		/db_xref="taxon:9823"	
		/clone="C0003271_H04"	
		/tissue_type="ovary"	
		/clone_lib="CSEQRAN19"	
		/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"	
ORIGIN			
Query Match	46.4%;	Score 13;	DB 1; Length 43;
Best Local Similarity	76.2%;	Pred. No. 2.4e+05;	
Matches	16;	Conservative 0;	Mismatches 5; Indels 0; Gaps 0;
Qy	6	GTGGGATAGTCGTCATGCTG 26	
Db	22	GTGGTATTCTCTCTCTGCTG 42	
RESULT 12			
LOCUS	BG523557/c		
DEFINITION	33-14 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA		
	sequence.		
ACCESSION	BG523557		
VERSION	BG523557.1	GI:16946975	
KEYWORDS	EST		
SOURCE	Stevia rebaudiana		
ORGANISM	Stevia rebaudiana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroidae; Eupatoriaceae; Stevia.

1 (bases 1 to 47)

Leaf ESTs from *Stevia rebaudiana*: A resource for gene discovery in diterpene synthesis unpublished (2001)

JOURNAL

COMMENT

Contact: Jim Brandle

Genomics and Biotechnology

Agriculture and Agri-Food Canada - SCPPRC

1391 Sandford St., London, Ontario, CANADA, N5V 4T3

Tel: 519 457 1470

Fax: 519 457 3997

Email: brandleje@agr.gc.ca

Seq primer: T3 promoter primer.

FEATURES

source

1. 47 Location/Qualifiers

/organism="Stevia rebaudiana"

/mol_type="mRNA"

/strain="751/1501"

/cultivar="Landrace"

/db_xref="taxon:55670"

/tissue_type="leaf"

/dev_stages="field grown, mid-size"

/lab_host="E. coli strain XLOLR"

/clone_lib="Stevia field grown leaf cDNA"

/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an XhoI-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XLI-Blue MRF'. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XLOLR. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACCTCCTCAAGGGA 3'. This library was constructed by Alex Richman."

ORIGIN

Query Match 46.4%; Score 13; DB 4; Length 47;
Best Local Similarity 69.6%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CTTCTGGGATAGTCGTCATG 23

DB 45 CTTCTGGGAAAGTAGGTNANG 23

RESULT 13

LOCUS

A1581062 49 bp mRNA linear EST 13-DEC-1999
ti97d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2139937 3', similar to SW:NUIM HUMAN P03886 NADH-UBIQUINONE OXIDOREDUCTASE

CHAIN 1; mRNA sequence.

ACCESSION A1581062

VERSION A1581062.1 GI:4565438

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moshaluk, M.D., Ph.D., Michael R. Emmer-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/brrp/image/image.html

Trace considered overall poor quality

Insert Length: 883 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

FEATURES

source

1. 49 Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2139937"

/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"

/lab_host="DH10B"

/clone_lib="NCI CGAP Gas4"

/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.69 kb. Life Technologies catalog #:

11549-011"

ORIGIN

Query Match 46.4%; Score 13; DB 1; Length 49;
Best Local Similarity 76.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCGTCAT 22

DB 16 GTTCACGGGAGAGTGGTAAAT 36

RESULT 14

LOCUS

AZ585210 33 bp DNA linear GSS 13-DEC-2000
1M0390B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0390B16 F, genomic survey sequence.

ACCESSION AZ585210

VERSION AZ585210.1 GI:11706870

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0390 row: B column: 16

Seq primer: CQTGTGAAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 33.

FEATURES

Location/Qualifiers

1. .35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M033322"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0390B16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 45.7%; Score 12.8; DB 8; Length 35;
Best Local Similarity 87.5%; Pred.No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCGTGGGATAGTCCG 19
|||||
DB 30 TCGTGGGATAGTCCAT 15

RESULT 16
BH791451 47 bp DNA linear GSS 02-APR-2002
LOCUS
DEFINITION
SALK 059978.40.35.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_059978.40.35.x, genomic survey sequence.

ACCESSION
BH791451
VERSION
BH791451.1 GI:19885328
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)

REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.

FEATURES
source
1. .47
Location/Qualifiers
/organism="Arabidopsis thaliana"

ORIGIN
Query Match 45.7%; Score 12.8; DB 8; Length 33;
Best Local Similarity 87.5%; Pred.No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCC 17
|||||
DB 2 GTTCGTGGGATAGTCC 17

RESULT 15
AZ497161/c 35 bp DNA linear GSS 05-OCT-2000
LOCUS
DEFINITION
IM033322R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M033322 R, genomic survey sequence.

ACCESSION
AZ497161
VERSION
AZ497161.1 GI:10673865
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0333 row: G column: 22
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers

FEATURES
source
1. .47
Location/Qualifiers
/organism="Arabidopsis thaliana"

ACCESSION	BH802890
VERSION	BH802890.1 GI:20317479
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	1 (bases 1 to 49)
AUTHORS	Walbot,V.
TITLE	Maize genomic sequences found using engineered RescueMu transposon
JOURNAL	Unpublished (2001)
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1008097 row: 13 Class: transposon-tagged.
FEATURES	Location/Qualifiers
source	1..49
	/organism="Zea mays"
	/mol_type="genomic DNA"
	/cultivar="mixed background W23/A188/B73"
	/db_xref="taxon:4577"
	/tissue_types="leaf"
	/dev_stage="adult"
	/lab_host="DH10B"
	/clone_lib="1008 - RescueMu Grid I"
	/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmldb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
ORIGIN	
Query Match	45.7%; Score 12.8; DB 8; Length 49;
Best Local Similarity	70.8%; Pred. No.3e+05;
Matches	17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	2 GTTCTGGGATAGTCGTCATGGT 25
Dd	9 GTTGTGGGTCAGTTGCCAGGCT 32
RESULT 20	
BZ769405	
LOCUS	SALK_142144.44.90.x Arabidopsis thaliana TDNA insertion lines
DEFINITION	Arabidopsis thaliana genomic clone SALK_142144.44.90.x, genomic survey sequence.
ACCESSION	BZ769405
VERSION	BZ769405.1 GI:28943089
KEYWORDS	GSS.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.	
REFERENCE	1 (bases 1 to 49)
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Cadzow,C., Jacke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

```

source
1. .42
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="242a07"

ORIGIN
Query Match 45.0%; Score 12.6; DB 9; Length 42;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTTCGTGGATAGTCGTC 20
    ||| ||| ||| ||| |||
Db 42 GTTACTGTGAAGTCGTC 24

RESULT 22
CC886211 46 bp DNA linear GSS 31-JUL-2003
LOCUS SALK_148336.25.55.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_148336.25.55.x, genomic
survey sequence.
ACCESSION CC886211
VERSION CC886211.1 GI:33362567
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 46)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At4g28980.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
source
1. .46
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_148336.25.55.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 45.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 66.7%; Pred. No. 3.7e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GTTCGTGGATAGTCGTCATGCTT 28
    ||| ||| ||| ||| ||| |||
Db 6 GTTCGCTGTTCTCCATCTTGTCTT 32

RESULT 23
AZ436588 24 bp DNA linear GSS 03-OCT-2000
LOCUS iM0224H20F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0224H20 F, genomic survey sequence.
ACCESSION AZ436588
VERSION AZ436588.1 GI:10560601
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0224 row: H column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
Location/Qualifiers
source
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0224H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 44.3%; Score 12.4; DB 8; Length 24;
Best Local Similarity 72.7%; Pred. No. 4.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 CGTGGATAGTCGTCATGGTG 26
    ||| ||| ||| ||| |||
Db 3 CGTGGACGTCGCGAGGGTG 24

```

RESULT 24
BH865601/c
LOCUS
DEFINITION
SALK_099025 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_099025, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
GSS.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 38)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At3g18730 and 300 bases of the 5' end of At3g18740.
Class: TDNA tagged
Location/Qualifiers
1. 38
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_099025"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 44.3%; Score 12.4; DB 8; Length 38;
Best Local Similarity 72.7%; Pred. No. 4.5e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 TTCGTGGGATAGTCGGTCATG 24
||| ||||| ||||| |||||
DB 27 TTGGCGGGATAGTTTGGGATG 6
RESULT 25
AI793875/c
LOCUS
DEFINITION
fc55e01.x1 Zebrafish Washu MPIMG EST Danio rerio cDNA clone
IMAGE:3725304 3', similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION
SITE PROTEIN INT-6. [1]; mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 43)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone Distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
WARNING: This trace was re-sequenced and found NOT to hit the
original sample
Seq primer: T7 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 43
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3725304"
/sex="mixed"
/tissue type="26 somite embryos, adult livers, shield
stage embryos"
/lab host="XLI-blue MRF"
/clone lib="Zebrafish Washu MPIMG EST"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT3'];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."

TITLE
JOURNAL
COMMENT
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone Distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
WARNING: This trace was re-sequenced and found NOT to hit the
original sample
Seq primer: T7 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 43
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3725304"
/sex="mixed"
/tissue type="26 somite embryos, adult livers, shield
stage embryos"
/lab host="XLI-blue MRF"
/clone lib="Zebrafish Washu MPIMG EST"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT3'];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."

ORIGIN

Query Match 44.3%; Score 12.4; DB 1; Length 43;
Best Local Similarity 72.7%; Pred. No. 4.5e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 7 TGGGATAGTCGGTCATGGTGT 28
||| ||||| ||||| |||||
DB 27 TGAGAGAGTGGGAGACCGTGT 6
RESULT 26
W87658/c
LOCUS
DEFINITION
zh67e12.s1 Soares fetal liver spleen INFUS_S1 Homo sapiens cDNA
clone IMAGE:417166 3', similar to SW:TCFH_MOUSE P80313 T-COMPLEX
PROTEIN 1, ETA SUBUNIT ;, mRNA sequence.
W87658
ACCESSION

Wed Nov 24 08:46:12 2004

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)

REFERENCE
AUTHORS
 Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, P., Wurst, W., Von Melchner, H. and Ruiz, P.
 A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)

JOURNAL
MEDLINE
PUBMED
COMMENT
 On Jun 30, 2004 this sequence version replaced gi:40730723.
 Contact: GGTC
 German Genetrap Consortium (GGTC)
 Email: info@genetrap.de
 U3betago gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
 'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=M046F03'. ES cell line harboring insertion mutation of target gene is available at:
 'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
 1' Inhouse Sequence Identifier: 03523
 Class: Gene Trap. Location/Qualifiers

FEATURES
 source
 1..46
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 Sv"
 /db_xref="taxon:10090"
 /clone="M046F03"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /cell_line="ES cells 129S2 (formerly 129/SvPas)"
 /clone_lib="GGTC Gene Trap Library GV05C04"
 /note="Vector: U3betago"

ORIGIN
 Query Match 44.3%; Score 12.4; DB 9; Length 46;
 Best Local Similarity 72.7%; Pred. No. 4.6e+05;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 3 TTCGGGATAGTCGTCATGG 24
 Db 34 TTCAGGTACAGTCCATCATGG 13

RESULT 30
LOCUS
DEFINITION
 BH791926 50 bp DNA linear GSS 02-APR-2002
 SALK_062026.27.05.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_062026.27.05.x, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
AUTHORS
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)

REFERENCE
AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0030 row: K column: 06
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 46.
 Location/Qualifiers

FEATURES
 source
 1..46
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0030K06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 44.3%; Score 12.4; DB 8; Length 46;
 Best Local Similarity 92.9%; Pred. No. 4.6e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 GGGATAGTCCTGCA 21
 Db 20 GGGATAGTCCTGCA 7

RESULT 29
LOCUS
DEFINITION
 CL213822 46 bp mRNA linear GSS 30-JUN-2004
 M046F03 GGTC Gene Trap Library GV05C04 Mus musculus cDNA clone
 M046F03, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Mus musculus (house mouse)
 Mus musculus


```

FEATURES
source
Location/Qualifiers
1. .46
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1314214"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"

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ORIGIN	Query Match	Score	DB	Length
	43.6%	12.2	9	46

Best Local Similarity 82.4%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GATAGTCGCTCATGTGTG 26
|||||
12 GATAGTCGCTCAAGAG 28

Db 12 GATAGTCGCTCAAGAG 28

RESULT 35
LOCUS BZ661004/c 48 bp DNA linear GSS 31-JAN-2003
DEFINITION SALK_024466.34.10.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_024466.34.10.x, genomic
survey sequence.

ACCESSION BZ661004
VERSION BZ661004.1 GI:28174151
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 48)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At4g03270.
Class: TDNA tagged.

FEATURES
source Location/Qualifiers
1..48
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_024466.34.10.x"
/note="PCR was performed on Arabidopsis thaliana lines
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 43.6%; Score 12.2; DB 8; Length 48;
Best Local Similarity 68.0%; Pred. No. 5.7e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 TCGTGAGATGTCGCTCATGTGTG 28
|||||
39 TTGTGAGATGAGAGAGATGTTT 15

Db 39 TTGTGAGATGAGAGAGATGTTT 15

RESULT 36
LOCUS AU104471 50 bp mRNA linear EST 28-JUN-2004
DEFINITION AU104471 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT05864, mRNA sequence.
ACCESSION AU104471
VERSION AU104471.1 GI:13553992
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

TITLE
JOURNAL MEDLINE
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT05864"
/clone_11b="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 43.6%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GATAGTCGCTCATGTGTG 26
|||||
9 GTTACTACGACATGTGTG 25

Db 9 GTTACTACGACATGTGTG 25

RESULT 37
LOCUS BZ356733/c 27 bp DNA linear GSS 14-NOV-2002
DEFINITION SALK_129645.42.60.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_129645.42.60.x, genomic
survey sequence.

ACCESSION BZ356733
VERSION BZ356733.1 GI:24948373
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 27)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At4g02555.
Class: TDNA tagged.

FEATURES
Location/Qualifiers

source

1. 27
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_129645.42.60.x"
/note="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tDNA_protocols.html"

ORIGIN

Query Match 42.9%; Score 12; DB 8; Length 27;
Best Local Similarity 75.0%; Pred. No. 6.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TTGCGATGATGCGTCAT 22
Db 23 TTGCGATGATGCGTCAT 4

RESULT 38
CL212897/c 34 bp mRNA linear GSS 30-JUN-2004
LOCUS CL212897
DEFINITION G025506 GGC Gene Trap Library GV07C05 Mus musculus cDNA clone
ACCESSION G025506, mRNA sequence.
CL212897
VERSION CL212897.2 GI:49489377
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
22810117
PUBMED 12904583
COMMENT On Jun 30, 2004 this sequence version replaced gi:40729798.
Contact: GGC
German GeneTrap Consortium (GGC)
Email: info@geneTrap.de
USCBO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
/http://geneTrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=G025506' RS cell line harboring insertion mutation of
target gene is available at:
/http://geneTrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 15772
Class: Gene Trap.
Location/Qualifiers
1. 34
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 SV"
/db_xref="taxon:10090"
/clone="G025E06"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129SvEvTac] F1"
/clone_id="GGC Gene Trap Library GV07C05"
/note="Vector: USCBO"

ORIGIN

Query Match 42.9%; Score 12; DB 9; Length 34;
Best Local Similarity 75.0%; Pred. No. 6.8e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CGTGATGATGCGTCATGG 24
Db 28 CATGGATGATGCGTCATGG 9

RESULT 39
N44191 36 bp mRNA linear EST 07-FEB-1996
LOCUS N44191
DEFINITION y51g11.r1 Soares multiple sclerosis 2NBHSP Homo sapiens cDNA
clone IMAGE:277124 5' similar to gb:J04173 PHOSPHOGLYCERATE MUTASE,
BRAIN FORM (HUMAN)), mRNA sequence.
N44191
ACCESSION N44191.1 GI:1182719
VERSION N44191
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 36)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, B., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: 17
High quality sequence stop: 1.
Location/Qualifiers
1. 36
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3895500"
/db_xref="taxon:9606"
/clone="IMAGE:277124"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_id="Soares multiple sclerosis_2NBHSP"
/note="Vector: pVT3D (Pharmacia) with a modified
polylinker V type: phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo (dT)
primer (5',
TGTTCACATGAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pVT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldi. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH). "

ORIGIN

Query Match 42.9%; Score 12; DB 7; Length 36;
Best Local Similarity 71.4%; Pred. No. 6.8e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 TGGATGATGCGTCATGATGT 27
Db 7 TGGATGATGCGTCATGATGT 27

RESULT 40
AZ433353/C

LOCUS

DEFINITION AZ433353 36 bp DNA linear GSS 03-OCT-2000
1M0219U12F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0219U12 F, genomic survey sequence.

ACCESSION

AZ433353

VERSION

AZ433353.1 GI:10557366

KEYWORDS

GSS, musculus (house mouse)

SOURCE

Mus musculus

REFERENCE

AUTHORS

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0219 row: J column: 12

Seq primer: CGTTGTAACAGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 36.

FEATURES

source

1. 36

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCLM0219U12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCLM library"

/note="Vector: PWD42nt; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match

42.9%; Score 12; DB 8; Length 36;

Best Local Similarity 64.3%; Pred. No. 6.8e+05;

Matches 18; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGTTGTTGGGATGTCCTGATGCTT 28

DB 36 CCTTCATTTGATGCTCTGCTTCTGTT 9

Search completed: November 23, 2004, 22:25:15
Job time : 1367.43 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 378.157 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-17
Perfect score: 21
Sequence: 1 cgcgcattagaccgtacgcga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl: *
1: gb ba: *
2: gb hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	100.0	21	6	BD181363	BD181363 A method
C 2	100.0	21	6	BD181378	BD181378 A method
C 3	100.0	21	6	AX523943	AX523943 Sequence
C 4	100.0	21	6	AX524841	AX524841 Sequence
C 5	100.0	21	6	AX524856	AX524856 Sequence
C 6	13.6	64.8	29	BD227377	BD227377 Secreted
C 7	12.8	61.0	30	AX752106	AX752106 Sequence
C 8	12.6	60.0	20	AX295474	AX295474 Sequence
C 9	12.6	60.0	24	AX290841	AX290841 Sequence
C 10	12.6	60.0	26	BD260345	BD260345 Methods
C 11	12.6	60.0	26	AX044290	AX044290 Sequence
C 12	12.6	60.0	31	AR168721	AR168721 Sequence
C 13	12.6	60.0	33	AR047950	AR047950 Sequence
C 14	12.6	60.0	38	AR334533	AR334533 Sequence
C 15	12.6	60.0	38	AR335779	AR335779 Sequence
C 16	12.6	60.0	38	AR336409	AR336409 Sequence
C 17	12.6	60.0	38	AR455837	AR455837 Sequence
C 18	12.6	60.0	38	AX219207	AX219207 Sequence
C 19	12.6	60.0	38	AX219231	AX219231 Sequence

C 20	12.6	60.0	38	6	AX351248	AX351248 Sequence
C 21	12.6	60.0	38	6	AX424618	AX424618 Sequence
C 22	12.6	60.0	38	6	AX424731	AX424731 Sequence
C 23	12.6	60.0	38	6	AX581188	AX581188 Sequence
C 24	12.6	60.0	38	6	AX581359	AX581359 Sequence
C 25	12.6	60.0	42	6	AX581359	AX581359 Sequence
C 26	12.4	59.0	20	6	AX295733	AX295733 Sequence
C 27	12.4	59.0	24	6	AX291100	AX291100 Sequence
C 28	12.4	59.0	34	6	AX464504	AX464504 Sequence
C 29	12.4	59.0	38	6	AR046887	AR046887 Sequence
C 30	12.4	59.0	38	6	153939	153939 Sequence
C 31	12.4	59.0	38	6	AX220204	AX220204 Sequence
C 32	12.2	58.1	20	6	AR314417	AR314417 Sequence
C 33	12.2	58.1	21	6	AR364921	AR364921 Sequence
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C 35	12.2	58.1	32	6	AX755148	AX755148 Sequence
C 36	12.2	58.1	32	6	AX755156	AX755156 Sequence
C 37	12.2	58.1	37	6	AX581239	AX581239 Sequence
C 38	12.2	58.1	37	6	AX581788	AX581788 Sequence
C 39	12.2	58.1	37	6	AX581793	AX581793 Sequence
C 40	12.2	58.1	37	6	AX581826	AX581826 Sequence
C 41	12.2	58.1	40	6	CO759972	CO759972 Sequence
C 42	12.2	58.1	41	6	AR238615	AR238615 Sequence
C 43	12	57.1	25	6	AR1179	AR1179 Sequence
C 44	12	57.1	25	6	AR1919	AR1919 Sequence
C 45	12	57.1	25	6	AR085879	AR085879 Sequence
C 46	12	57.1	29	6	AR474494	AR474494 Sequence
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C 48	12	57.1	29	6	AX260008	AX260008 Sequence
C 49	12	57.1	29	6	AX262370	AX262370 Sequence
C 50	12	57.1	37	6	AX581813	AX581813 Sequence
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C 52	12	57.1	38	6	AR330395	AR330395 Sequence
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C 65	11.8	56.2	21	6	BD014023	BD014023 Plant gen
C 66	11.8	56.2	28	6	AB6797	AB6797 Sequence 5
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C 73	11.6	55.2	25	6	BD225557	BD225557 Assay for
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387	11	52.4	38	6	AX581242	AX581242 Sequence	460	10.6	50.5	18	6	AR293681	AR293681 Sequence
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395	11	52.4	40	6	AR095875	AR095875 Sequence	468	10.6	50.5	24	6	BD260387	BD260387 Method.
396	11	52.4	40	6	AR157230	AR157230 Sequence	469	10.6	50.5	24	6	AR261951	AR261951 Sequence
397	11	52.4	40	6	AR351064	AR351064 Sequence	470	10.6	50.5	24	6	AX044332	AX044332 Sequence
398	11	52.4	40	6	AX767184	AX767184 Sequence	471	10.6	50.5	24	6	AX181781	AX181781 Sequence
399	11	52.4	40	6	AR007099	AR007099 Sequence	472	10.6	50.5	24	6	AX290523	AX290523 Sequence
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404	11	52.4	42	6	BD086796	BD086796 Nucleic a	477	10.6	50.5	26	6	BD260289	BD260289 Method.
405	11	52.4	44	6	AX752645	AX752645 Sequence	478	10.6	50.5	26	6	BD260331	BD260331 Method.
406	11	52.4	44	6	AX752646	AX752646 Sequence	479	10.6	50.5	26	6	BD260385	BD260385 Method.
407	11	52.4	50	6	AX951984	AX951984 Sequence	480	10.6	50.5	26	6	BD260396	BD260396 Method.
408	11	52.4	50	6	AX952578	AX952578 Sequence	481	10.6	50.5	26	6	BD260396	BD260396 Method.
409	10.8	51.4	17	6	BD199105	BD199105 Method an	482	10.6	50.5	26	6	BD260398	BD260398 Method.
410	10.8	51.4	19	6	AR096607	AR096607 Sequence	483	10.6	50.5	26	6	BD260399	BD260399 Method.
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413	10.8	51.4	24	6	AX443621	AX443621 Sequence	486	10.6	50.5	26	6	BD260402	BD260402 Method.
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415	10.8	51.4	25	6	C0797626	C0797626 Sequence	488	10.6	50.5	26	6	BD260405	BD260405 Method.
416	10.8	51.4	25	6	AX447603	AX447603 Sequence	489	10.6	50.5	26	6	BD260405	BD260405 Method.
417	10.8	51.4	27	6	BD177071	BD177071 Standard	490	10.6	50.5	26	6	AX044213	AX044213 Sequence
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425	10.8	51.4	30	6	BD252904	BD252904 Regulatio	498	10.6	50.5	26	6	AX044342	AX044342 Sequence
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452	10.8	51.4	39	6	AR148367	AR148367 Sequence	525	10.6	50.5	36	6	BD259773	BD259773 Regulatio
453	10.8	51.4	43	6	AX484526	AX484526 Sequence	526	10.6	50.5	36	6	BD259834	BD259834 Regulatio
454	10.8	51.4	45	6	A05538	A05538 Oligonucleo	527	10.6	50.5	36	6	BD259835	BD259835 Regulatio
455	10.8	51.4	45	6	AR001631	AR001631 Sequence	528	10.6	50.5	36	6	BD259864	BD259864 Regulatio
456	10.8	51.4	45	6	109088	109088 Sequence 3	529	10.6	50.5	36	6	BD259865	BD259865 Regulatio
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551	10.6	50.5	38	6	AR334394	C 624		10.6	50.5	38	6	AX044050	AX044050 Sequence
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562	10.6	50.5	38	6	AR334598	635	10.6	50.5	38	6	AX219170	AX219170 Sequence	
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583	10.6	50.5	38	6	AR335026	656	10.6	50.5	38	6	AX219592	AX219592 Sequence	
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C 828	10.4	49.5	36	6	AX633661	Sequence	901	10.4	49.5	38	6	AR331809	AR331809	Sequence
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C 830	10.4	49.5	36	6	AX634002	Sequence	903	10.4	49.5	38	6	AR331966	AR331966	Sequence
C 831	10.4	49.5	36	6	AX634041	Sequence	904	10.4	49.5	38	6	AR332052	AR332052	Sequence
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C 837	10.4	49.5	36	6	AX740356	Sequence	910	10.4	49.5	38	6	AR332233	AR332233	Sequence
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C 839	10.4	49.5	36	6	AX955552	Sequence	912	10.4	49.5	38	6	AR332362	AR332362	Sequence
C 840	10.4	49.5	37	6	AX274702	Sequence	913	10.4	49.5	38	6	AR332404	AR332404	Sequence
C 841	10.4	49.5	37	6	AX581816	Sequence	914	10.4	49.5	38	6	AR332419	AR332419	Sequence
C 842	10.4	49.5	37	6	AX581867	Sequence	915	10.4	49.5	38	6	AR332436	AR332436	Sequence
C 843	10.4	49.5	37	6	AX582003	Sequence	916	10.4	49.5	38	6	AR332475	AR332475	Sequence
C 844	10.4	49.5	38	6	AR329799	Sequence	917	10.4	49.5	38	6	AR332479	AR332479	Sequence
C 845	10.4	49.5	38	6	AR329891	Sequence	918	10.4	49.5	38	6	AR332532	AR332532	Sequence
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C 850	10.4	49.5	38	6	AR329988	Sequence	923	10.4	49.5	38	6	AR332651	AR332651	Sequence
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C 852	10.4	49.5	38	6	AR329999	Sequence	925	10.4	49.5	38	6	AR332662	AR332662	Sequence
C 853	10.4	49.5	38	6	AR330022	Sequence	926	10.4	49.5	38	6	AR332666	AR332666	Sequence
C 854	10.4	49.5	38	6	AR330026	Sequence	927	10.4	49.5	38	6	AR332770	AR332770	Sequence
C 855	10.4	49.5	38	6	AR330039	Sequence	928	10.4	49.5	38	6	AR332780	AR332780	Sequence
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C 864	10.4	49.5	38	6	AR330217	Sequence	937	10.4	49.5	38	6	AR332961	AR332961	Sequence
C 865	10.4	49.5	38	6	AR330250	Sequence	938	10.4	49.5	38	6	AR332963	AR332963	Sequence
C 866	10.4	49.5	38	6	AR330294	Sequence	939	10.4	49.5	38	6	AR332966	AR332966	Sequence
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C 870	10.4	49.5	38	6	AR330571	Sequence	943	10.4	49.5	38	6	AR333035	AR333035	Sequence
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C 874	10.4	49.5	38	6	AR330764	Sequence	947	10.4	49.5	38	6	AR333083	AR333083	Sequence
C 875	10.4	49.5	38	6	AR330766	Sequence	948	10.4	49.5	38	6	AR333089	AR333089	Sequence
C 876	10.4	49.5	38	6	AR330771	Sequence	949	10.4	49.5	38	6	AR333116	AR333116	Sequence
C 877	10.4	49.5	38	6	AR330807	Sequence	950	10.4	49.5	38	6	AR333187	AR333187	Sequence
C 878	10.4	49.5	38	6	AR331065	Sequence	951	10.4	49.5	38	6	AR333229	AR333229	Sequence
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C 881	10.4	49.5	38	6	AR331247	Sequence	954	10.4	49.5	38	6	AR333367	AR333367	Sequence
C 882	10.4	49.5	38	6	AR331256	Sequence	955	10.4	49.5	38	6	AR333380	AR333380	Sequence
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C 884	10.4	49.5	38	6	AR331292	Sequence	957	10.4	49.5	38	6	AR333500	AR333500	Sequence
C 885	10.4	49.5	38	6	AR331308	Sequence	958	10.4	49.5	38	6	AR333503	AR333503	Sequence
C 886	10.4	49.5	38	6	AR331337	Sequence	959	10.4	49.5	38	6	AR333533	AR333533	Sequence
C 887	10.4	49.5	38	6	AR331419	Sequence	960	10.4	49.5	38	6	AR333567	AR333567	Sequence
C 888	10.4	49.5	38	6	AR331454	Sequence	961	10.4	49.5	38	6	AR333568	AR333568	Sequence
C 889	10.4	49.5	38	6	AR331461	Sequence	962	10.4	49.5	38	6	AR333570	AR333570	Sequence
C 890	10.4	49.5	38	6	AR331464	Sequence	963	10.4	49.5	38	6	AR333603	AR333603	Sequence
C 891	10.4	49.5	38	6	AR331495	Sequence	964	10.4	49.5	38	6	AR333657	AR333657	Sequence
C 892	10.4	49.5	38	6	AR331543	Sequence	965	10.4	49.5	38	6	AR333673	AR333673	Sequence
C 893	10.4	49.5	38	6	AR331556	Sequence	966	10.4	49.5	38	6	AR333654	AR333654	Sequence
C 894	10.4	49.5	38	6	AR331584	Sequence	967	10.4	49.5	38	6	AR331854	AR331854	Sequence
C 895	10.4	49.5	38	6	AR331611	Sequence	968	10.4	49.5	38	6	AR331848	AR331848	Sequence

Query Match	Best Local	Similarity	Score	DB	Length	DB	Length	DB	Length
100.0%;	100.0%;	100.0%;	21;	DB 6;	Length 21;				
Best Local	Similarity	Score	DB	Length	DB	Length	DB	Length	DB
Matches	21;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

QY 1 CGGTCAATTAGACCGTACGCGA 21
 DB 21 CGGTCAATTAGACCGTACGCGA 1

RESULT 2
 BD181378 21 bp DNA linear PAT 15-MAY-2003
 LOCUS A method for determination of a nucleic acid using a control.
 DEFINITION BD181378
 ACCESSION BD181378.1 GI:30792296
 VERSION BD181378.1 GI:30792296
 KEYWORDS JP 2002335981-A/17.
 SOURCE synthetic construct
 ORGANISM Jaeger, S.
 1 (bases 1 to 21)
 REFERENCE A method for determination of a nucleic acid using a control
 AUTHORS Patent: JP 2002335981-A 17 26-NOV-2002;
 TITLE F. HOFFMANN LA ROCHE AG
 JOURNAL F. HOFFMANN LA ROCHE AG
 COMMENT OS Artificial Sequence
 PN JP 2002335981-A/17
 PD 26-NOV-2002
 PR 04-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
 PC C12N15/00
 CC Description of Artificial Sequence: artificial sequence to CC
 exemplify

ALIGNMENTS

RESULT 1
 BD181363 21 bp DNA linear PAT 15-MAY-2003
 LOCUS A method for determination of a nucleic acid using a control.
 DEFINITION BD181363
 ACCESSION BD181363.1 GI:30792281
 VERSION BD181363.1 GI:30792281
 KEYWORDS JP 2002335981-A/2.
 SOURCE synthetic construct
 ORGANISM Jaeger, S.
 1 (bases 1 to 21)
 REFERENCE A method for determination of a nucleic acid using a control
 AUTHORS Patent: JP 2002335981-A 2 26-NOV-2002;
 TITLE F. HOFFMANN LA ROCHE AG
 JOURNAL F. HOFFMANN LA ROCHE AG
 COMMENT OS Artificial Sequence
 PN JP 2002335981-A/2
 PD 26-NOV-2002
 PR 04-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
 PC C12N15/00
 CC Description of Artificial Sequence: artificial sequence to CC
 exemplify

RESULT 3
 AX523943 21 bp DNA linear PAT 21-NOV-2002
 LOCUS A method for determination of a nucleic acid using a control.
 DEFINITION AX523943
 ACCESSION AX523943.1 GI:25168874
 VERSION AX523943.1 GI:25168874
 KEYWORDS JP 2002335981-A/17.
 SOURCE synthetic construct
 ORGANISM Jaeger, S.
 1 (bases 1 to 21)
 REFERENCE A method for determination of a nucleic acid using a control
 AUTHORS Patent: EP 1236804-A 2 04-SEP-2002;
 TITLE F. HOFFMANN LA ROCHE AG
 JOURNAL F. HOFFMANN LA ROCHE AG
 COMMENT OS Artificial Sequence
 PN JP 2002335981-A/17
 PD 26-NOV-2002
 PR 04-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
 PC C12N15/00
 CC Description of Artificial Sequence: artificial sequence to CC
 exemplify

FEATURES
 source Location/Qualifiers
 1..21 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTCAATTAGACCGTACGCGA 21
 DB 21 CGGTCAATTAGACCGTACGCGA 1

RESULT 2
 BD181378 21 bp DNA linear PAT 15-MAY-2003
 LOCUS A method for determination of a nucleic acid using a control.
 DEFINITION BD181378
 ACCESSION BD181378.1 GI:30792296
 VERSION BD181378.1 GI:30792296
 KEYWORDS JP 2002335981-A/17.
 SOURCE synthetic construct
 ORGANISM Jaeger, S.
 1 (bases 1 to 21)
 REFERENCE A method for determination of a nucleic acid using a control
 AUTHORS Patent: JP 2002335981-A 17 26-NOV-2002;
 TITLE F. HOFFMANN LA ROCHE AG
 JOURNAL F. HOFFMANN LA ROCHE AG
 COMMENT OS Artificial Sequence
 PN JP 2002335981-A/17
 PD 26-NOV-2002
 PR 04-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
 PC C12N15/00
 CC Description of Artificial Sequence: artificial sequence to CC
 exemplify

ORIGIN
 Query Match 100.0%; Score 21; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTCAATTAGACCGTACGCGA 21
 DB 21 CGGTCAATTAGACCGTACGCGA 1

RESULT 3
 AX523943 21 bp DNA linear PAT 21-NOV-2002
 LOCUS A method for determination of a nucleic acid using a control.
 DEFINITION AX523943
 ACCESSION AX523943.1 GI:25168874
 VERSION AX523943.1 GI:25168874
 KEYWORDS JP 2002335981-A/17.
 SOURCE synthetic construct
 ORGANISM Jaeger, S.
 1 (bases 1 to 21)
 REFERENCE A method for determination of a nucleic acid using a control
 AUTHORS Patent: EP 1236804-A 2 04-SEP-2002;
 TITLE F. HOFFMANN LA ROCHE AG
 JOURNAL F. HOFFMANN LA ROCHE AG
 COMMENT OS Artificial Sequence
 PN JP 2002335981-A/17
 PD 26-NOV-2002
 PR 04-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
 PC C12N15/00
 CC Description of Artificial Sequence: artificial sequence to CC
 exemplify

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/db_xref="taxon:32630"
/note="artificial sequence to exemplify principle"
ORIGIN

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Query Match	100.0%	Score 21	DB 6	Length 21
Best Local Similarity	100.0%	Pred. No. 2.2		
Matches 21, Conservative	0	Mismatches	0	Gaps 0

Qy	1	CGGTCATTAGACCGGTACGCCA	21
Db	21	CGGTCATTAGACCGGTACGCCA	1

RESULT 4
AX524841/C
AX524841
LOCUS 21 bp
DNA
Linear
DATE 21-NOV-2002

ORGANISM synthetic construct
artificial sequences.

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/note="artificial sequence to exemplify principle"
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Query Match	100.0%	Score 21	DB 6	Length 21
Best Local Similarity	100.0%	Pred. NC	2.2	
Matches 21	Conservative 0	Mismatches 0	Indels 0	Gaps 0

RESULT	5
AX524856	
LOCUS	AM524856 21 bp DNA linear PAT 21-NOV-2002
DEFINITION	Sequence 17 from Patent EP1236805.
ACCESSION	AX524856
VERSION	AX524856.1 GI:25169950

ORGANISM synthetic construct
artificial sequences.

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TITLE      A method for the determination of a nucleic acid using a control
JOURNAL    Patent: EP 1236805-A 17 04-SEP-2002;
           Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
FEATURES   Location/Qualifiers
           1..21

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/u_w/are- cavou:3263v
 /note="artificial sequence to exemplify principle"
 ORIGIN

Db 1 CGGTCAITAGACCGTACGCGA 21

LOCUS	BD227377	29 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Secreted proteins and polynucleotides encoding them.				
ACCESSION	BD227377				
VERSION	BD227377.1	GI:33037147			
KEYWORDS	JP 2002522062-A/138.				
SOURCE	synthetic construct				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 29)	Jacobs, K., McCoy, J.M., Lavallie, E.R., Racle, L.A.C., Evans, C., Merberg, D., Treacy, M., Agostino, M.J., Li, R.Y.S., Spaulding, V., Wong, G.G., Clark, H.F. and Fechtel, K.	Secreterd proteins and polynucleotides encoding them	Patent: JP 2002522062-A 138 23-JUL-2002;	OS Artificial Sequence

FEATURES	Location/Qualifiers
source	1. .29

ORIGIN

Query Match	64.8%	Score 13.6	DB 6	Length 29
Best Local Similarity	80.0%	Pred. No. 2.9e+04		
Matches 16	Conservative 0	Mismatches 4	Indels 0	Gaps 0

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QY      2  GGTCAATTAGACCGTACGCCA  21
          ||||| ||||| ||| |
Db      5  GGTCAATAAGACAGTACTCCA  24
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RESULT 7			
AX752106/c			
LOCUS	AX752106	30 bp	DNA
DEFINITION	Sequence 5 from Patent WO03035876.		linear
			PAT 20-JUN-2003

VERSION	KEYWORDS	SOURCE	ORGANISM
AX752106.1	GI:32134216	Hepatitis C virus	Hepatitis C virus
		Viruses; ssRNA positive-strand viruses, no DNA stage: Flaviviridae;	

REFERENCE 1 Hepacivirus.
 AUTHORS Krebs, A., John, M., Schuppan, D., Limmer, S. and Kreutzner, R.
 TITLE Use of a double strand ribonucleic acid for treating an infection with a positive-strand rna-virus
 JOURNAL Patent: WO 03035876-A 5 01-MAY-2003;
 Ribopharma AG (DE)
 FEATURES Location/Qualifiers
 source 1..30
 /organism="Hepatitis C virus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:11103"

ORIGIN
 Query Match 61.0%; Score 12.8; DB 6; Length 30;
 Best Local Similarity 87.5%; Pred. No. 8.1e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTACG 18
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 30 GTCATTAGACGCTCCG 15

RESULT 8
 AX295474 20 bp DNA linear PAT 21-NOV-2001
 LOCUS Sequence 7236 from Patent WO0179548.
 DEFINITION AX295474
 ACCESSION AX295474
 VERSION AX295474.1 GI:17057163
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
 TITLE Method of designing addressable array for detection of nucleic acid
 JOURNAL Patent: WO 0179548-A 7236 25-OCT-2001;
 CORNELL RESEARCH FOUNDATION, INC. (US)
 FEATURES Location/Qualifiers
 source 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"

ORIGIN
 Query Match 60.0%; Score 12.6; DB 6; Length 20;
 Best Local Similarity 78.9%; Pred. No. 1.1e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACG 19
 |||||
 20 CCGTCACTAGACGACGCG 2

RESULT 9
 AX290841 24 bp DNA linear PAT 21-NOV-2001
 LOCUS Sequence 2603 from Patent WO0179548.
 DEFINITION AX290841
 ACCESSION AX290841
 VERSION AX290841.1 GI:17052524
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
 TITLE Method of designing addressable array for detection of nucleic acid
 JOURNAL Patent: WO 0179548-A 2603 25-OCT-2001;
 CORNELL RESEARCH FOUNDATION, INC. (US)
 FEATURES Location/Qualifiers

source 1..24
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"

ORIGIN
 Query Match 60.0%; Score 12.6; DB 6; Length 24;
 Best Local Similarity 78.9%; Pred. No. 1.1e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACG 19
 |||||
 20 CCGTCACTAGACGACGCG 2

RESULT 10
 BD260345 26 bp DNA linear PAT 17-JUL-2003
 LOCUS Methods.
 DEFINITION BD260345
 ACCESSION BD260345
 VERSION BD260345.1 GI:33070115
 KEYWORDS JP 2002542803-A/102.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Windase, J.D., Heaney, S.P., Renwick, A., Whitcombe, D.M., Little, S., Gibson, N.U., Theaker, J. and Stanger, C.P.
 TITLE Methods
 JOURNAL Patent: JP 2002542803-A 102 17-DEC-2002;
 SYNSENTA LTD
 COMMENT OS Artificial Sequence
 PN JP 2002542803-A/102
 PD 17-DEC-2002
 PF 26-APR-2000 JP 2000615395
 PR 30-APR-1999 GB 9910100.8, 13-MAR-2000 GB 0006004.6 PR
 P1 31-MAR-2000 GB 0007901.2
 PI JOHN DAVID WINDASS, STEPHEN PAUL HEANEY, ANNABEL RENWICK, PI
 DAVID MARK WHITCOMBE, STEPHEN LITTLE, NEIL JAMES GIBSON, JANE THEAKER.
 PI CAROLE PATRICIA STANGER
 PC C12N15/09, C07K14/37, C12O1/68, G01N33/566, G01N33/569, C12N15/00
 CC Description of Artificial Sequence: Primer
 FH Key
 FT source 1..26
 Location/Qualifiers
 /organism="Artificial Sequence".

FEATURES
 source 1..26
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 60.0%; Score 12.6; DB 6; Length 26;
 Best Local Similarity 78.9%; Pred. No. 1.1e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACG 20
 |||||
 20 GTCATTAGACGATACG 2

RESULT 11
 AX044290 26 bp DNA linear PAT 24-NOV-2000
 LOCUS AX044290
 DEFINITION AX044290
 ACCESSION AX044290
 VERSION AX044290.1 GI:11343168
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
AUTHORS Windase,J.D., Heaney,S.P., Renwick,A., Whitcombe,D.M., Little,S.,
Gibson,N.J., Theaker,J. and Stranger,C.P.
TITLE Method of detection of cytochrome b mutations in fungi leading to
JOURNAL resistance against anti-fungal agents
Patent: WO 006773-A 102 09-NOV-2000;
ZENBECA LIMITED (GB)
FEATURES Location/Qualifiers
SOURCE 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 26;
Best Local Similarity 78.9%; Pred.No.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTACGCG 20
DB 20 GGTCAATTGACCATACAGC 2
RESULT 12
LOCUS AR168721 31 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6287866.
ACCESSION AR168721
VERSION AR168721.1 GI:17904788
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Mukerji,P., Lemmel,S.A., Leonard,A.Eun,-Yeong. and Chaudhary,S.
TITLE beta-casein expressing constructs
JOURNAL Patent: US 6287866-A 17 11-SEP-2001;
FEATURES Location/Qualifiers
SOURCE 1..31
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 31;
Best Local Similarity 78.9%; Pred.No.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGGTCAATTAGACCGTACGCG 19
DB 30 CGGTCAATGACAGTACTC 12
RESULT 13
LOCUS AR047950 33 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 29 from patent US 5820866.
ACCESSION AR047950
VERSION AR047950.1 GI:5970293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kappler,J.W. and Marrack,P.
TITLE Product and process for T cell regulation
JOURNAL Patent: US 5820866-A 29 13-OCT-1998;
FEATURES Location/Qualifiers
SOURCE 1..33
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 33;
Best Local Similarity 78.9%; Pred.No.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGGTCAATTAGACCGTACGCG 19
DB 20 CGGTCAATGACAGTACTC 2
RESULT 14
LOCUS AR334533 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 11935 from patent US 6566127.
ACCESSION AR334533
VERSION AR334533.1 GI:33720341
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Payco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 11935 20-MAY-2003;
FEATURES Location/Qualifiers
SOURCE 1..38
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred.No.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTACGCGA 21
DB 16 GGCCGTTAGGCCGAGANGCGA 35
RESULT 15
LOCUS AR335779 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 13181 from patent US 6566127.
ACCESSION AR335779
VERSION AR335779.1 GI:33721587
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Payco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 13181 20-MAY-2003;
FEATURES Location/Qualifiers
SOURCE 1..38
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred.No.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTACGCGA 21
DB 16 GGCCGTTAGGCCGAGANGCGA 35
RESULT 16
LOCUS AR336409 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 13811 from patent US 6566127.

ACCESSION AR336409
VERSION AR336409.1 GI:33722217
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 656127-A 13811 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05; 5; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTAGCGGA 21
16 GGCCGTTAGCGCGAANGCGA 35
Db
RESULT 17
AR455837/c 38 bp DNA linear PAT 20-FEB-2004
LOCUS AR455837
DEFINITION Sequence 83 from patent US 6686154.
ACCESSION AR455837
VERSION AR455837.1 GI:42690729
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Nock,S. and Kassner,P.D.
TITLE Screening of phage displayed peptides without clearing of the cell culture
JOURNAL Patent: US 6686154-A 83 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTAGCGG 20
30 GGTCAATTACAAATGTCGCG 12
Db
RESULT 18
AX219207 38 bp RNA linear PAT 07-SEP-2001
LOCUS AX219207
DEFINITION Sequence 4649 from Patent WO0159103.
ACCESSION AX219207
VERSION AX219207.1 GI:15546931
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 4649 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
modified_base 31
/mod_base=i
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05; 5; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTAGCGGA 21
16 GGCCGTTAGCGCGAANGCGA 35
Db
RESULT 20
AX351248 38 bp DNA linear PAT 06-FEB-2002
LOCUS AX351248/c
DEFINITION Sequence 83 from Patent WO0194950.
ACCESSION AX351248
VERSION AX351248.1 GI:18616596
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Nock,S. and Kassner,P.D.
TITLE Screening of phage displayed peptides without clearing of the cell culture
JOURNAL Patent: WO 0194950-A 83 13-DEC-2001;
ZYOMYX, Inc. (US)
FEATURES Location/Qualifiers
source 1..38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
modified_base 31
/mod_base=i
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05; 5; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTAGCGGA 21
16 GGCCGTTAGCGCGAANGCGA 35
Db
RESULT 20
AX351248 38 bp DNA linear PAT 06-FEB-2002
LOCUS AX351248/c
DEFINITION Sequence 83 from Patent WO0194950.
ACCESSION AX351248
VERSION AX351248.1 GI:18616596
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Nock,S. and Kassner,P.D.
TITLE Screening of phage displayed peptides without clearing of the cell culture
JOURNAL Patent: WO 0194950-A 83 13-DEC-2001;
ZYOMYX, Inc. (US)
FEATURES Location/Qualifiers
source 1..38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="WVK24 primer"

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 20
|||||
30 GGTCAATTACATGTCGCG 12

Db

RESULT 21
AX424618 38 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 2954 from Patent WO0188124.
ACCESSION AX424618
VERSION AX424618.1 GI:21528000
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 2954 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
source
1..38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

misc_feature 31

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 21
|||||
16 GGCCGTTAGCCGCGAANGCGA 35

Db

RESULT 22
AX424731 38 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 3067 from Patent WO0188124.
ACCESSION AX424731
VERSION AX424731.1 GI:21528113
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 3067 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

misc_feature 31

/note="n strands for inosine"

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 21
|||||
16 GGCCGTTAGCCGCGAANGCGA 35

Db

RESULT 23
AX581188 38 bp RNA linear PAT 10-JAN-2003
LOCUS
DEFINITION Sequence 3026 from Patent WO0211674.
ACCESSION AX581188
VERSION AX581188.1 GI:27652998
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grube, A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 3026 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

modified_base 31
/mod_base=1

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 21
|||||
16 GGCCGTTAGCCGCGAANGCGA 35

Db

RESULT 24
AX581359 38 bp RNA linear PAT 10-JAN-2003
LOCUS
DEFINITION Sequence 3197 from Patent WO0211674.
ACCESSION AX581359
VERSION AX581359.1 GI:27653169
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grube, A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 3197 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES
source
1..38
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

modified_base 31
/mod_base=1

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTGATTAGACCGTAGCGGA 21
16 GGCGGTTAGCGCCGAGNCGGA 35

RESULT 25

A65234 42 bp DNA linear PAT 29-MAR-1999
LOCUS Sequence 5 from Patent WO9735011.
DEFINITION A65234
ACCESSION A65234
VERSION GI:4531029
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Silvestrini, M.C., Cutruzzola, F., Ciabatti, Iaria, Zennaro, E.,
Visco, C., Discepolo and Massimo.
RECOMBINANT PROCESS FOR THE PRODUCTION IN PSEUDOMONAS PUTIDA OF THE
CYTOCHROME C551 OF PSEUDOMONAS AERUGINOSA
Patent: WO 9735011-A 5 25-SEP-1997;
MINI RICERCA SCIENT TECNOLOG (IT)
Other publication IT MI960515 19970915.
Location/Qualifiers
1..42
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 42;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGGTCTTAGACCGTAGCGC 19
19 CGGTGATGAACCGTAGCGC 37

RESULT 26

AX295733/c 20 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 7495 from Patent WO0179548.
DEFINITION AX295733
ACCESSION AX295733
VERSION GI:17057422
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
Patent: WO 0179548-A 7495 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 ATTAGACCGTAGCGC 19
15 ATTAGACCGTAGCGC 2

RESULT 27
AX291100/c 24 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 2862 from Patent WO0179548.
DEFINITION AX291100
ACCESSION AX291100
VERSION GI:17052783
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
Patent: WO 0179548-A 2862 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 ATTAGACCGTAGCGC 19
15 ATTAGACCGTAGCGC 2

RESULT 28
AX464504/c 34 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 39 from Patent EP1219635.
DEFINITION AX464504
ACCESSION AX464504
VERSION GI:21899300
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Couture, F., Hamel, J., Brodeur, B.R. and Martin, D.
Chlamydia pneumoniae antigens
Patent: EP 1219635-A 39 03-JUL-2002;
SHIRE BIOCHEM INC. (CA)
Location/Qualifiers
1..34
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer"

ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 34;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CATTAGACCGTAGC 18
34 CATTAGACCGTAGC 21

RESULT 29

CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 24 BP; 7 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 24;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CGGTCAATGACCGTACGC 19
|||
DB 5 CGTCACTAGACGACGCG 23
|||
RESULT 15
ACI25753
ID ACI25753 standard; DNA; 25 BP.
XX
ACI25753;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 25744.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 25744; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX
SQ Sequence 25 BP; 5 A; 9 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CGGTCAATGACCGTACGC 19
|||
DB 7 CGTCCCTTAGACGACGCG 25
|||
RESULT 16
ACK18838/C
ID ACK18838 standard; DNA; 25 BP.
XX
ACK18838;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 118819.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 118819; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

Query Match 60.0%; Score 12.6; DB 9; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCAATTAGACCGTAGC 19
 21 CTGTCAATTCGACCGCACAC 3

Db

RESULT 17
 AC156057
 ID AC156057 standard; DNA; 25 BP.
 AC156057;
 13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 56048.
 EST; ss; probe; expressed sequence tag; microarray; gene expression;
 genetic variation; diallelic marker; polymorphism; human;
 cross-species comparison.

Homo sapiens.
 US2003104410-A1.
 05-JUN-2003.
 15-MAR-2002; 2002US-00098263.
 16-MAR-2001; 2001US-0276759P.
 (AFY-) AFFYMETRIX INC.
 Miltmann MP;
 MPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 56048; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying diallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 7 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 9; Length 25;

Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GTCAATTAGACCGTAGC 21
 6 GTCAATTACACCGTGTGCA 24

Db

RESULT 18
 ACK18839/C
 ID ACK18839 standard; DNA; 25 BP.
 ACK18839;
 14-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 118820.
 EST; ss; probe; expressed sequence tag; microarray; gene expression;
 genetic variation; diallelic marker; polymorphism; human;
 cross-species comparison.

Homo sapiens.
 US2003104410-A1.
 05-JUN-2003.
 15-MAR-2002; 2002US-00098263.
 16-MAR-2001; 2001US-0276759P.
 (AFY-) AFFYMETRIX INC.
 Miltmann MP;
 MPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 118820; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying diallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 9; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP, 2 A, 4 C, 8 G, 6 T, 0 U, 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 20;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DY 1 CGGTCTTAGACCGTAGCG 19
| | | | | | | | | | | | | | | | | | | | | |
DB 20 CCGTCTACTAGACCGAGCG 2
RESULT 13
AB187602/C
ID AB187602 standard; DNA; 24 BP.
XX
AC AB187602;
XX
DT 15-FEB-2002 (first entry)
DE Capture oligonucleotide Zip ID#2603 oligo #1.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic citrus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medialis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at a
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to

CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 24 BP, 2 A, 5 C, 10 G, 7 T, 0 U, 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 24;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DY 1 CGGTCTTAGACCGTAGCG 19
| | | | | | | | | | | | | | | | | | | | | |
DB 20 CCGTCTACTAGACCGAGCG 2
RESULT 14
AB187603
ID AB187603 standard; DNA; 24 BP.
XX
AC AB187603;
XX
DT 15-FEB-2002 (first entry)
DE Capture oligonucleotide Zip ID#2603 oligo #2.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic citrus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medialis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at a
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to

```

XX AC ADD12949;
XX DT 01-JAN-2004 (first entry)
XX DE HCV NS3 probe.
XX KW double-stranded RNA; dsRNA; infection; NS3 helicase; virucide;
XX KW antiinflammatory; hepatotropic; hepatitis C virus infection; ss; probe.
XX OS Hepatitis C virus.
XX FT Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /*mod_base= OTHER
XX FT /*note= "FAM labelled"
XX FT modified_base 30 /*tag= b
XX FT /*mod_base= OTHER
XX FT /*note= "TAMRA labelled"
XX PN WO2003035876-A1.
XX PD 01-MAY-2003.
XX PF 25-OCT-2002; 2002WO-BP011973.
XX PR 26-OCT-2001; 2001DE-01055280.
XX PR 29-NOV-2001; 2001DE-01058411.
XX PR 07-DEC-2001; 2001DE-01060151.
XX PR 09-JAN-2002; 2002WO-BP000151.
XX PR 09-JAN-2002; 2002WO-BP000152.
XX PR 02-AUG-2002; 2002DE-01035621.
XX PA (RIBO-) RIBOPHARMA AG.
XX PI Krebs A, John M, Schuppan D, Limmer S, Kreutzer R;
XX DR WPI; 2003-430419/40.
XX PT New double-stranded RNA for treating viral infections, useful especially
XX PT for hepatitis C infection, is complementary to a region of a positive-
XX PT strand RNA viral genome.
XX PS Disclosure; SEQ ID NO 5; 35pp; German.
XX CC This invention describes a novel use of a double-stranded RNA for
XX CC treating infections by a (+)-strand RNA virus, where one strand (S1) of
XX CC dsRNA includes a segment that is at least partly complementary to the
XX CC translatable region of the viral genome. dsRNA is directed against
XX CC hepatitis C virus (HCV) and inhibits expression of a polyprotein encoded
XX CC by the viral genome, preferably a protease or helicase and most
XX CC particularly the NS3 helicase, with the complementary region, in the
XX CC reading direction of viral RNA, being upstream of, or within, the
XX CC helicase coding region. dsRNA has, at least one end, an overhang of 1-4,
XX CC preferably 2-3 nucleotides particularly at the 3'-end of S1. The second
XX CC strand (S2) of dsRNA contains a 2-nucleotide overhang at the 3'-end of S1
XX CC but no overhang at the other end (blunt). A single overhang increases
XX CC inhibitory activity without causing significant loss of in vivo
XX CC stability. dsRNA is formulated with a conventional solvent (especially
XX CC phosphate-buffered saline) or it is incorporated into a micellar
XX CC structure, particularly a liposome, viral capsid, capsid or a polymeric
XX CC nano- or micro-capsule (or it is bound to such capsules). The products of
XX CC the invention have virucide, antiinflammatory and hepatotropic activity.
XX CC dsRNA is administered by inhalation, infusion or injection, or orally,
XX CC especially by intravenous or intraperitoneal injection or infusion. dsRNA
XX CC is specifically used for treatment of hepatitis C virus infections. dsRNA
XX CC permanently destroys the integrity of the viral genome. HHV-7 cells were
XX CC transfected with double-stranded RNA (dsRNA), directed against the NS3
XX CC coding region of the hepatitis C virus (HCV) genome and a fragment of the
XX CC HCV genome that replicated stably without formation of infectious
XX CC particles. Transfection with dsRNA resulted in a 60-fold inhibition of

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CC viral RNA production, relative to transfection with an irrelevant control
CC dsRNA. This sequence represents a probe used to detect the HCV NS3 gene.
XX CC
XX SQ Sequence 30 BP; 8 A; 8 C; 7 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 61.0%; Score 12.8; DB 10; Length 30;
XX Best Local Similarity 87.5%; Pred. No. 3.2e+03;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 GTCAATTGACCGTACG 18
XX |||||
XX DB 30 GTCAATTGACCGTCCG 15
XX
XX RESULT 12
XX AB195516/C
XX ID AB195516 standard; DNA; 20 BP.
XX AC AB195516;
XX DT 16-FEB-2002 (first entry)
XX DE Capture oligonucleotide Zip ID#2603 oligo #9.
XX DE
XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX KW oncogene; tumour suppressor; human papillomavirus; forensic;
XX KW environmental monitoring; food industry; feed industry; ss.
XX OS Synthetic.
XX OS WO200179548-A2.
XX PN 25-OCT-2001.
XX PD 04-APR-2001; 2001WO-US010958.
XX PF 14-APR-2000; 2000US-0197271P.
XX PR (CORR ) CORNELL RES FOUND INC.
XX PA Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;
XX PI WPI; 2002-034366/04.
XX DR
XX XX
XX XX Designing capture oligonucleotide probes for use on a support to which
XX XX complementary oligonucleotides hybridize with little mismatch.
XX XX
XX XX Example 5; Fig 29; 300pp; English.
XX PS
XX CC The present invention describes a method (M1) for designing capture
XX CC oligonucleotide probes (I) for use on a support to which complementary
XX CC oligonucleotide probes (II) will hybridise with little mismatch, where
XX CC (I) have melting temperatures within a narrow range. The method is useful
XX CC for detecting infectious diseases caused by bacterial infectious agents
XX CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
XX CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX CC Epstein-Barr virus and polio virus, and parasitic infectious agents
XX CC selected from Onchocerca volvulus, Entamoeba histolytica and Dicrocoelium
XX CC medinisae. The method is also useful for detecting genetic defects
XX CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX CC involved in DNA amplification, replication, recombination or repair, the
XX CC cancer is specifically associated with a gene selected from BRCA1 gene,
XX CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX CC method is also used for environmental monitoring, forensics and the food
XX CC and feed industry, detecting comprises scanning (using e.g. a scanning
XX CC electron microscope and infrared microscope) the support at the
XX CC particular sites and identifying if ligation of the oligonucleotide probe
XX CC sets occurred and correlating (using a computer) identified ligation to a
XX CC presence or absence of the target nucleotide sequences. AB182074 to

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DR WPI: 1998-523164/45.

XX Determination of gene expression levels - using combinations of different

PT CDNA samples tagged with different PCR adaptors.

XX Example 2; Page 10; 22pp; English.

XX The present sequence represents an adaptor which was used in the method

CC of the invention to determine the amount ratio between a cDNA coding for

CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney

CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene expression to be quantitatively determined,

CC and because internal standards are not required to prepare a calibration

CC curve, it is a quicker and less laborious process

XX

SEQ Sequence 35 BP; 8 A; 9 C; 9 G; 9 T; 0 U; 0 Other;

QY Query Match 62.9%; Score 13.2; DB 2; Length 35;

Best Local Similarity 83.3%; Pred. No. 1.9e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 GTCATTGACCGTACGCG 20

10 GTCGTTAGAACGACGCG 27

RESULT 7

ACN31831/C

ID ACN31831 standard; RNA; 37 BP.

XX ACN31831;

XX

DT 22-APR-2004 (first entry)

XX

DE MNV minus strand Zinzyme SEQ ID NO 31847.

XX

XX MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;

KW viruslike; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyme; ss.

XX

XX West Nile Virus.

OS

PN WO200268637-A2.

XX

PD 06-SEP-2002.

XX

PF 19-OCT-2001; 2001WO-US048350.

XX

PR 20-OCT-2000; 2000US-0242411P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLATT) BLATT L.

PA (MCSW/) MCSWIGEN J A.

XX

PI Blatt L, Mcswigen JA;

XX

XX WPI: 2002-706994/76.

DR

XX New nucleic acid molecule that modulates replication of West Nile Virus

PT (MNV), useful for treating a condition related to MNV infection e.g.

PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX

XX Claim 24; SEQ ID NO 31847; 495bp; English.

PS

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for

CC treating a condition related to MNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX

SEQ Sequence 37 BP; 13 A; 7 C; 12 G; 0 T; 5 U; 0 Other;

QY Query Match 62.9%; Score 13.2; DB 6; Length 37;

Best Local Similarity 83.3%; Pred. No. 1.9e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 GTCATTGACCGTACGCG 20

35 GTCATTGACCTCCTCG 18

RESULT 8

AAV61560/C

ID AAV61560 standard; DNA; 39 BP.

XX AAV61560;

XX

DT 08-DEC-1998 (first entry)

XX

DE Adaptor NNNN-CIGSR (- strand).

XX

XX Adaptor; quantitate; amount ratio; liver; kidney; apolipoprotein;

KW ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression;

KW internal standard; calibration curve; ss.

XX

XX Synthetic.

OS

OS Mus sp.

XX

XX EP870842-A2.

XX

XX 14-OCT-1998.

PD

XX 07-APR-1998; 98EP-00302726.

XX

PF 07-APR-1997; 97JP-00088495.

XX

PR 07-APR-1997; 97JP-00088495.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX

XX Kato K;

XX

XX WPI: 1998-523164/45.

DR

XX Determination of gene expression levels - using combinations of different

PT CDNA samples tagged with different PCR adaptors.

XX

XX Example 2; Page 10; 22pp; English.

PS

XX The present sequence represents an adaptor which was used in the method

CC of the invention to determine the amount ratio between a cDNA coding for

CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney

CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene expression to be quantitatively determined,

CC and because internal standards are not required to prepare a calibration

CC curve, it is a quicker and less laborious process

XX

SEQ Sequence 39 BP; 9 A; 9 C; 9 G; 8 T; 0 U; 4 Other;

QY Query Match 62.9%; Score 13.2; DB 2; Length 39;

Best Local Similarity 83.3%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 GTCATTGACCGTACGCG 20

30 GTCGTTAGAACGACGCG 13

RESULT 9

AC171602/c
ID AC171602 standard; DNA; 25 BP.

AC171602;

14-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 71593.

EST; ss; probe; expressed sequence tag; microarray; gene expression;

genetic variation; diallelic marker; polymorphism; human;

cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Miltmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in

Southern, Northern or dot-blot hybridization to identify or detect the

sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 71593; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying diallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 5 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 9; Length 25;

Best Local Similarity 76.2%; Pred. No. 2.4e+03; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 5;

1 CGGTCATTAGACCGTACGCGA 21

RESULT 10

AC171017
ID AC171017 standard; DNA; 25 BP.

AC171017;

14-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 71008.

EST; ss; probe; expressed sequence tag; microarray; gene expression;

genetic variation; diallelic marker; polymorphism; human;

cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Miltmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in

Southern, Northern or dot-blot hybridization to identify or detect the

sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 71008; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying diallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 9; Length 25;

Best Local Similarity 87.5%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2;

3 GTCATTAGACCGTACG 18

RESULT 11

ADD12949/c
ID ADD12949 standard; DNA; 30 BP.

XX Miltmann MP;
 PI
 XX
 DR MPI, 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1, SEQ ID NO 88853, 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 62.9%; Score 13.2; DB 9; Length 25;
 Best Local Similarity 83.3%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 TCATTAGACCGTAGCGGA 21
 Db |||||
 8 TCATATGACCTTACGGGA 25
 RESULT 5
 ACI88244 standard; DNA; 25 BP.
 XX
 AC ACI88244;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 88235.
 XX
 KW EST; ss: probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFY-) AFFMETRIX INC.
 XX
 PI Miltmann MP;
 XX

XX MPI, 2003-567953/53.
 DR
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1, SEQ ID NO 88235, 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 62.9%; Score 13.2; DB 9; Length 25;
 Best Local Similarity 83.3%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 TCATTAGACCGTAGCGGA 21
 Db |||||
 7 TCATATGACCTTACGGGA 24
 RESULT 6
 AAV61559 standard; DNA; 35 BP.
 XX
 ID AAV61559
 XX
 AC AAV61559;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE Adaptor NNNN-CIGSR (+ strand).
 XX
 KW Adaptor; quantitate; amount ratio; liver; kidney; apolipoprotein;
 KW ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression;
 KW internal standard; calibration curve; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN EP870842-A2.
 XX
 PD 14-OCT-1998.
 XX
 PF 07-APR-1998; 98EP-00302726.
 XX
 PR 07-APR-1997; 97JP-00088495.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Kato K;
 XX

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Meherberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;
 PI Wong GG, Clark HF, Fehnel K;
 DR WPI; 2000-205979/18.
 XX New polynucleotides encoding secreted proteins, which may have e.g.
 PT nutritional, chemokine, immune stimulating or suppressing, hematopoiesis
 PT regulating, tissue growth, activin/inhibin antiinflammatory or tumor
 PT inhibition activity.
 PS Disclosure; Page 631, 641pp; English.
 XX AA16618 to AA16697 encode the human secreted proteins given in AA16698
 CC to AA16698, isolated from human adult brain, adult thyroid, adult
 CC retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult
 CC placenta, adult testis, whole embryo, adult cartilage, kidney, foetal
 CC brain, adult thymus, foetal placenta, adult uterus, adult tumour, and
 CC adult bladder, cDNA libraries. The polynucleotides and proteins are
 CC predicted to have biological activities which would make them suitable
 CC for treating, preventing or ameliorating medical conditions in humans and
 CC animals. The polynucleotides can be used as markers for tissues in which
 CC the protein is preferentially expressed, as molecular weight markers on
 CC Southern gels, and as chromosome markers or tags to identify chromosomes
 CC or to map gene positions. The proteins can be used in the treatment of
 CC immune deficiencies and disorders, such as severe combined
 CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
 CC infections. These infections include human immunodeficiency virus (HIV),
 CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
 CC candidiasis. The proteins can be used to treat autoimmune disorders such
 CC as connective tissue disease, multiple sclerosis, systemic lupus
 CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
 CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
 CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
 CC autoimmune inflammatory eye disease. The proteins can also be used to
 CC treat allergic conditions, such as asthma. AA16698 to AA16774 represent
 CC probes for the human secreted proteins from the present invention
 CC XX
 SQ Sequence 29 BP; 7 A; 9 C; 6 G; 6 T; 0 U; 1 Other;
 Query Match 64.8%; Score 13.6; DB 3; Length 29;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 GGTCAATTAGACCGTAGCGGA 21
 Db 5 GGTCAATAGACAGTACTCCA 24
 RESULT 3
 AC109445/c
 ID AC109445 standard; DNA; 25 BP.
 XX AC109445;
 DT 13-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 9436.
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KM genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 XX Homo sapiens.
 OS
 PN US2003104410-A1.
 XX 05-JUN-2003.
 PD 15-MAR-2002; 2002US-00098263.
 XX 16-MAR-2001; 2001US-0276759P.
 PR

XX (AFFY-) AFFYMETRIX INC.
 PA Miltmann MP;
 PI WPI; 2003-567953/53.
 DR
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS Claim 1; SEQ ID NO 9436; 9pp; English.
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC XX
 SQ Sequence 25 BP; 11 A; 3 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 63.8%; Score 13.4; DB 9; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.4e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GTCATTAGACCGTAGAC 17
 Db 18 GTCATTAGACTGTAC 4
 RESULT 4
 AC188862
 ID AC188862 standard; DNA; 25 BP.
 XX AC188862;
 DT 14-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 88853.
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KM genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 XX Homo sapiens.
 OS
 PN US2003104410-A1.
 XX 05-JUN-2003.
 PD 15-MAR-2002; 2002US-00098263.
 XX 16-MAR-2001; 2001US-0276759P.
 PR (AFFY-) AFFYMETRIX INC.

533	11	52.4	36	6	ABX02836	Abx02836 HCV hamme	606	11	52.4	38	4	ABK05210	Abk05210 Human NOG
534	11	52.4	36	6	ABX02270	Abx02270 HCV hamme	607	11	52.4	38	4	ABK04785	Abk04785 Human NOG
535	11	52.4	36	6	ABX02731	Abx02731 HCV hamme	608	11	52.4	38	4	ABK04953	Abk04953 Human NOG
536	11	52.4	36	6	ABX02408	Abx02408 HCV hamme	609	11	52.4	38	4	ABK05212	Abk05212 Human NOG
537	11	52.4	36	6	ABX02198	Abx02198 HCV hamme	610	11	52.4	38	4	ABK03884	Abk03884 Human NOG
538	11	52.4	36	6	ABX02402	Abx02402 HCV hamme	611	11	52.4	38	4	ABK05178	Abk05178 Human NOG
539	11	52.4	36	6	ABX02026	Abx02026 HCV hamme	612	11	52.4	38	4	ABK08311	Abk08311 Human CD2
540	11	52.4	36	6	ABX02602	Abx02602 HCV hamme	613	11	52.4	38	4	ABK03825	Abk03825 Human NOG
541	11	52.4	36	6	ABX02319	Abx02319 HCV hamme	614	11	52.4	38	4	ABK04543	Abk04543 Human NOG
542	11	52.4	36	6	ABX01863	Abx01863 HCV hamme	615	11	52.4	38	4	ABK05160	Abk05160 Human NOG
543	11	52.4	36	6	ABX02404	Abx02404 HCV hamme	616	11	52.4	38	4	ABK08344	Abk08344 Human CD2
544	11	52.4	36	6	ABX02705	Abx02705 HCV hamme	617	11	52.4	38	4	ABK04527	Abk04527 Human NOG
545	11	52.4	36	6	ABX02219	Abx02219 HCV hamme	618	11	52.4	38	4	ABK04580	Abk04580 Human NOG
546	11	52.4	36	8	ACD56262	AcD56262 HBV enzym	619	11	52.4	38	4	ABK04691	Abk04691 Human NOG
547	11	52.4	36	8	ACD56358	AcD56358 HBV enzym	620	11	52.4	38	4	ABK04765	Abk04765 Human NOG
548	11	52.4	36	12	ADIS9388	AdiS9388 Inozyme S	621	11	52.4	38	4	ABK08356	Abk08356 Human CD2
549	11	52.4	36	12	ADIS9408	AdiS9408 Inozyme S	622	11	52.4	38	4	ABK04566	Abk04566 Human NOG
550	11	52.4	36	12	ADIS9410	AdiS9410 Inozyme S	623	11	52.4	38	4	ABK04583	Abk04583 Human NOG
551	11	52.4	36	12	ADIS9425	AdiS9425 Inozyme S	624	11	52.4	38	4	ABK04646	Abk04646 Human NOG
552	11	52.4	36	12	ADIS9437	AdiS9437 Inozyme S	625	11	52.4	38	4	ABK08260	Abk08260 Human CD2
553	11	52.4	36	12	ADIS9396	AdiS9396 Inozyme S	626	11	52.4	38	4	ABK08382	Abk08382 Human CD2
554	11	52.4	36	12	ADIS9457	AdiS9457 Inozyme S	627	11	52.4	38	4	ABK05112	Abk05112 Human NOG
555	11	52.4	37	3	AA264928	Aa264928 RPI motif	628	11	52.4	38	4	ABK07994	Abk07994 Human CD2
556	11	52.4	37	6	ABX03427	Abx03427 Ribozyme	629	11	52.4	38	4	ABK08174	Abk08174 Human CD2
557	11	52.4	37	6	ABK59352	AbK59352 Human CLC	630	11	52.4	38	4	ABK08243	Abk08243 Human CD2
558	11	52.4	37	6	ABK59388	AbK59388 Human CLC	631	11	52.4	38	4	ABK04529	Abk04529 Human NOG
559	11	52.4	37	6	ABK59340	AbK59340 Human CLC	632	11	52.4	38	4	ABK04985	Abk04985 Human NOG
560	11	52.4	37	6	ACN18895	Acn18895 MNV Zinzy	633	11	52.4	38	4	ABK05127	Abk05127 Human NOG
561	11	52.4	37	6	ACN18992	Acn18992 MNV Zinzy	634	11	52.4	38	4	ABK08277	Abk08277 Human CD2
562	11	52.4	37	6	ACN13108	Acn13108 MNV minis	635	11	52.4	38	4	ABK08316	Abk08316 Human CD2
563	11	52.4	37	6	ACN19493	Acn19493 MNV Zinzy	636	11	52.4	38	4	ABK03855	Abk03855 Human NOG
564	11	52.4	37	6	ACN19321	Acn19321 MNV Zinzy	637	11	52.4	38	4	ABK04698	Abk04698 Human NOG
565	11	52.4	37	6	ACN19329	Acn19329 MNV Zinzy	638	11	52.4	38	4	ABK04824	Abk04824 Human NOG
566	11	52.4	37	6	ACN19323	Acn19323 MNV Zinzy	639	11	52.4	38	4	ABK05306	Abk05306 Human NOG
567	11	52.4	37	6	ACN19355	Acn19355 MNV Zinzy	640	11	52.4	38	4	ABK08435	Abk08435 Human CD2
568	11	52.4	37	6	ACN19418	Acn19418 MNV Zinzy	641	11	52.4	38	4	ABK04862	Abk04862 Human NOG
569	11	52.4	37	6	ACN19889	Acn19889 MNV Zinzy	642	11	52.4	38	4	ABK04963	Abk04963 Human NOG
570	11	52.4	37	6	ACN31939	Acn31939 MNV minis	643	11	52.4	38	4	ABK05042	Abk05042 Human NOG
571	11	52.4	37	6	ACN19246	Acn19246 MNV Zinzy	644	11	52.4	38	4	ABK08305	Abk08305 Human CD2
572	11	52.4	37	6	ACN19519	Acn19519 MNV Zinzy	645	11	52.4	38	4	ABi47584	Abi47584 Human GRI
573	11	52.4	37	6	ACN37010	Acn37010 MNV enzym	646	11	52.4	38	4	ABi47630	Abi47630 Human GRI
574	11	52.4	37	6	ACN31978	Acn31978 MNV minis	647	11	52.4	38	4	ABi47555	Abi47555 Human GRI
575	11	52.4	37	6	ACN31928	Acn31928 MNV minis	648	11	52.4	38	4	ABi47620	Abi47620 Human GRI
576	11	52.4	37	6	ACN31151	Acn31151 MNV minis	649	11	52.4	38	4	ABi47500	Abi47500 Human GRI
577	11	52.4	37	6	ACN31700	Acn31700 MNV minis	650	11	52.4	38	4	ABi47479	Abi47479 Human GRI
578	11	52.4	37	6	ACN30899	Acn30899 MNV minis	651	11	52.4	38	4	ABi47551	Abi47551 Human GRI
579	11	52.4	37	8	ACA10034	ACA10034 Necrosis	652	11	52.4	38	4	ABi47475	Abi47475 Human GRI
580	11	52.4	37	8	ACA08160	ACA08160 Necrosis	653	11	52.4	38	4	ABi47530	Abi47530 Human GRI
581	11	52.4	37	8	ACA08072	ACA08072 Necrosis	654	11	52.4	38	6	ABQ72443	Abq72443 PCR prime
582	11	52.4	37	8	ACA10010	ACA10010 Necrosis	655	11	52.4	38	6	ABQ72448	Abq72448 PCR prime
583	11	52.4	37	8	ACA07927	ACA07927 Necrosis	656	11	52.4	38	6	ABQ72439	Abq72439 PCR prime
584	11	52.4	37	11	ADL75687	Adl75687 Human PTG	657	11	52.4	38	6	ABK19546	Abk19546 Human ERG
585	11	52.4	37	11	ADL52737	Adl52737 Human NOG	658	11	52.4	38	6	ABK20611	Abk20611 Human ERG
586	11	52.4	37	11	ADL54427	Adl54427 Human NOG	659	11	52.4	38	6	ABK20602	Abk20602 Human ERG
587	11	52.4	37	11	ADL75730	Adl75730 Human PTG	660	11	52.4	38	6	ABK20586	Abk20586 Human ERG
588	11	52.4	37	11	ADL54222	Adl54222 Human IXX	661	11	52.4	38	6	ABK20090	Abk20090 Human ERG
589	11	52.4	37	11	ADL73674	Adl73674 Human PKR	662	11	52.4	38	6	ABK20145	Abk20145 Human ERG
590	11	52.4	37	11	ADL75675	Adl75675 Human PTG	663	11	52.4	38	6	ABK20161	Abk20161 Human ERG
591	11	52.4	37	12	ADM64239	Adm64239 Hepatitis	664	11	52.4	38	6	ABK20303	Abk20303 Human ERG
592	11	52.4	37	12	ADM64143	Adm64143 Hepatitis	665	11	52.4	38	6	ABK19639	Abk19639 Human ERG
593	11	52.4	37	12	AD192342	Ad192342 Anti-HCV	666	11	52.4	38	6	ABK20081	Abk20081 Human ERG
594	11	52.4	38	4	AAH96508	Aah96508 Human Chk	667	11	52.4	38	6	ABK20415	Abk20415 Human ERG
595	11	52.4	38	4	AAH96651	Aah96651 Human Chk	668	11	52.4	38	6	ABK20181	Abk20181 Human ERG
596	11	52.4	38	4	AAH96621	Aah96621 Human Chk	669	11	52.4	38	6	ABK20216	Abk20216 Human ERG
597	11	52.4	38	4	AAH96520	Aah96520 Human Chk	670	11	52.4	38	6	ABK20559	Abk20559 Human ERG
598	11	52.4	38	4	AAH96453	Aah96453 Human Chk	671	11	52.4	38	6	ABK19485	Abk19485 Human ERG
599	11	52.4	38	4	ABK04658	Abk04658 Human NOG	672	11	52.4	38	6	ABK20075	Abk20075 Human ERG
600	11	52.4	38	4	ABK04965	Abk04965 Human NOG	673	11	52.4	38	6	ABK20275	Abk20275 Human ERG
601	11	52.4	38	4	ABK05131	Abk05131 Human NOG	674	11	52.4	38	6	ABK20379	Abk20379 Human ERG
602	11	52.4	38	4	ABK05154	Abk05154 Human NOG	675	11	52.4	38	6	ABK20563	Abk20563 Human ERG
603	11	52.4	38	4	ABK05066	Abk05066 Human NOG	676	11	52.4	38	6	ABK20267	Abk20267 Human ERG
604	11	52.4	38	4	ABK05101	Abk05101 Human NOG	677	11	52.4	38	6	ABK20126	Abk20126 Human ERG
605	11	52.4	38	4	ABK04871	Abk04871 Human NOG	678	11	52.4	38	6	ABK20391	Abk20391 Human ERG

679	11	52.4	38	6	ABK20483	Human	ERG	752	11	52.4	38	6	ACN18335	INVO	ACN18355	WNV	INVO
680	11	52.4	38	6	ABK20593	Human	ERG	753	11	52.4	38	6	ACN29005	WNV	ACN29005	WNV	min
681	11	52.4	38	6	ABK20087	Human	ERG	754	11	52.4	38	6	ACN29142	WNV	ACN29142	WNV	min
682	11	52.4	38	6	ABK20244	Human	ERG	755	11	52.4	38	6	ACN30123	WNV	ACN30123	WNV	min
683	11	52.4	38	6	ABK58122	Human	CLC	756	11	52.4	38	6	ACN30260	WNV	ACN30260	WNV	min
684	11	52.4	38	6	ABK58769	Human	CLC	757	11	52.4	38	6	ACN30315	WNV	ACN30315	WNV	min
685	11	52.4	38	6	ABK58447	Human	CLC	758	11	52.4	38	6	ACN16816	WNV	ACN16816	WNV	min
686	11	52.4	38	6	ABK58819	Human	CLC	759	11	52.4	38	6	ACN17288	WNV	ACN17288	WNV	min
687	11	52.4	38	6	ABK58841	Human	CLC	760	11	52.4	38	6	ACN18040	WNV	ACN18040	WNV	min
688	11	52.4	38	6	ABK58709	Human	CLC	761	11	52.4	38	6	ACN27900	WNV	ACN27900	WNV	min
689	11	52.4	38	6	ABK59011	Human	CLC	762	11	52.4	38	6	ACN27910	WNV	ACN27910	WNV	min
690	11	52.4	38	6	ABK58560	Human	CLC	763	11	52.4	38	6	ACN28758	WNV	ACN28758	WNV	min
691	11	52.4	38	6	ABK58624	Human	CLC	764	11	52.4	38	6	ACN29274	WNV	ACN29274	WNV	min
692	11	52.4	38	6	ABK58913	Human	CLC	765	11	52.4	38	6	ACN29354	WNV	ACN29354	WNV	min
693	11	52.4	38	6	ABK58753	Human	CLC	766	11	52.4	38	6	ACN29399	WNV	ACN29399	WNV	min
694	11	52.4	38	6	ABK58832	Human	CLC	767	11	52.4	38	6	ACN29677	WNV	ACN29677	WNV	min
695	11	52.4	38	6	ABK58745	Human	CLC	768	11	52.4	38	6	ACN30104	WNV	ACN30104	WNV	min
696	11	52.4	38	6	ABK58462	Human	CLC	769	11	52.4	38	6	ACN30273	WNV	ACN30273	WNV	min
697	11	52.4	38	6	ABK58485	Human	CLC	770	11	52.4	38	6	ACN16820	WNV	ACN16820	WNV	min
698	11	52.4	38	6	ABK58667	Human	CLC	771	11	52.4	38	6	ACN17460	WNV	ACN17460	WNV	min
699	11	52.4	38	6	ABK16957	WNV	Inoxy	772	11	52.4	38	6	ACN18547	WNV	ACN18547	WNV	min
700	11	52.4	38	6	ACN17961	WNV	Inoxy	773	11	52.4	38	6	ACN26565	WNV	ACN26565	WNV	min
701	11	52.4	38	6	ACN18702	WNV	Inoxy	774	11	52.4	38	6	ACN27006	WNV	ACN27006	WNV	min
702	11	52.4	38	6	ACN18702	WNV	Inoxy	775	11	52.4	38	6	ACN28084	WNV	ACN28084	WNV	min
703	11	52.4	38	6	ACN26995	WNV	min	776	11	52.4	38	6	ACN28733	WNV	ACN28733	WNV	min
704	11	52.4	38	6	ACN28105	WNV	min	777	11	52.4	38	6	ACN28773	WNV	ACN28773	WNV	min
705	11	52.4	38	6	ACN28136	WNV	min	778	11	52.4	38	6	ACN29740	WNV	ACN29740	WNV	min
706	11	52.4	38	6	ACN28157	WNV	min	779	11	52.4	38	6	ACN30517	WNV	ACN3051		

825	11	52.4	38	6	ACN28443	ACN28443	WNV minus	898	11	52.4	38	8	ACA07471	ACA07471	Necrosis
826	11	52.4	38	6	ACN28810	ACN28810	WNV minus	899	11	52.4	38	8	ACA07599	ACA07599	Necrosis
827	11	52.4	38	6	ACN28885	ACN28885	WNV minus	900	11	52.4	38	8	ACA07377	ACA07377	Necrosis
828	11	52.4	38	6	ACN29256	ACN29256	WNV minus	901	11	52.4	38	8	ACA07332	ACA07332	Necrosis
829	11	52.4	38	6	ACN29522	ACN29522	WNV minus	902	11	52.4	38	8	ACA07457	ACA07457	Necrosis
830	11	52.4	38	6	ACN29553	ACN29553	WNV minus	903	11	52.4	38	8	ACA07558	ACA07558	Necrosis
831	11	52.4	38	6	ACN30579	ACN30579	WNV minus	904	11	52.4	38	8	ACA06952	ACA06952	Necrosis
832	11	52.4	38	6	ACN17136	ACN17136	WNV Inoxy	905	11	52.4	38	8	ACA06968	ACA06968	Necrosis
833	11	52.4	38	6	ACN17634	ACN17634	WNV Inoxy	906	11	52.4	38	8	ACA07582	ACA07582	Necrosis
834	11	52.4	38	6	ACN17918	ACN17918	WNV Inoxy	907	11	52.4	38	8	ACA07274	ACA07274	Necrosis
835	11	52.4	38	6	ACN18044	ACN18044	WNV Inoxy	908	11	52.4	38	8	ACA07171	ACA07171	Necrosis
836	11	52.4	38	6	ACN18084	ACN18084	WNV Inoxy	909	11	52.4	38	8	ACA06932	ACA06932	Necrosis
837	11	52.4	38	6	ACN28708	ACN28708	WNV minus	910	11	52.4	38	8	ACA07132	ACA07132	Necrosis
838	11	52.4	38	6	ACN28738	ACN28738	WNV minus	911	11	52.4	38	8	ACA07486	ACA07486	Necrosis
839	11	52.4	38	6	ACN28907	ACN28907	WNV minus	912	11	52.4	38	8	ACA07208	ACA07208	Necrosis
840	11	52.4	38	6	ACN29169	ACN29169	WNV minus	913	11	52.4	38	8	ACA07211	ACA07211	Necrosis
841	11	52.4	38	6	ACN29180	ACN29180	WNV minus	914	11	52.4	38	8	ACA07386	ACA07386	Necrosis
842	11	52.4	38	6	ACN29563	ACN29563	WNV minus	915	11	52.4	38	8	ACA07091	ACA07091	Necrosis
843	11	52.4	38	6	ACN30084	ACN30084	WNV minus	916	11	52.4	38	8	ACA07247	ACA07247	Necrosis
844	11	52.4	38	6	ACN16310	ACN16310	WNV Hamme	917	11	52.4	38	8	ACA07263	ACA07263	Necrosis
845	11	52.4	38	6	ACN17199	ACN17199	WNV Inoxy	918	11	52.4	38	8	ACA07568	ACA07568	Necrosis
846	11	52.4	38	6	ACN17556	ACN17556	WNV Inoxy	919	11	52.4	38	8	ACD52556	ACD52556	HBV Inoxy
847	11	52.4	38	6	ACN17661	ACN17661	WNV Inoxy	920	11	52.4	38	8	ACD52259	ACD52259	HBV Inoxy
848	11	52.4	38	6	ACN18473	ACN18473	WNV Inoxy	921	11	52.4	38	8	ACD52146	ACD52146	HBV Inoxy
849	11	52.4	38	6	ACN29017	ACN29017	WNV minus	922	11	52.4	38	8	ACD52647	ACD52647	HBV Inoxy
850	11	52.4	38	6	ACN29109	ACN29109	WNV minus	923	11	52.4	38	8	ACD51846	ACD51846	HBV Inoxy
851	11	52.4	38	6	ACN29662	ACN29662	WNV minus	924	11	52.4	38	8	ACD51853	ACD51853	HBV Inoxy
852	11	52.4	38	6	ACN29849	ACN29849	WNV minus	925	11	52.4	38	8	ACD52059	ACD52059	HBV Inoxy
853	11	52.4	38	6	ACN30114	ACN30114	WNV minus	926	11	52.4	38	8	ACD52884	ACD52884	HBV Inoxy
854	11	52.4	38	6	ACN30291	ACN30291	WNV minus	927	11	52.4	38	8	ACD53068	ACD53068	HBV Inoxy
855	11	52.4	38	6	ACN30347	ACN30347	WNV minus	928	11	52.4	38	8	ACD51000	ACD51000	HBV Inoxy
856	11	52.4	38	6	ACN15696	ACN15696	WNV Hamme	929	11	52.4	38	8	ACD52977	ACD52977	HBV Inoxy
857	11	52.4	38	6	ACN16680	ACN16680	WNV Hamme	930	11	52.4	38	8	ACD50914	ACD50914	HBV Inoxy
858	11	52.4	38	6	ACN17566	ACN17566	WNV Inoxy	931	11	52.4	38	8	ACD51754	ACD51754	HBV Inoxy
859	11	52.4	38	6	ACN17785	ACN17785	WNV Inoxy	932	11	52.4	38	8	ACD52661	ACD52661	HBV Inoxy
860	11	52.4	38	6	ACN18063	ACN18063	WNV Inoxy	933	11	52.4	38	8	ACD50997	ACD50997	HBV Inoxy
861	11	52.4	38	6	ACN18465	ACN18465	WNV Inoxy	934	11	52.4	38	8	ACD51642	ACD51642	HBV Inoxy
862	11	52.4	38	6	ACN28121	ACN28121	WNV minus	935	11	52.4	38	8	ACD52243	ACD52243	HBV Inoxy
863	11	52.4	38	6	ACN28284	ACN28284	WNV minus	936	11	52.4	38	8	ACD52637	ACD52637	HBV Inoxy
864	11	52.4	38	6	ACN28574	ACN28574	WNV minus	937	11	52.4	38	8	ACD52664	ACD52664	HBV Inoxy
865	11	52.4	38	6	ACN29324	ACN29324	WNV minus	938	11	52.4	38	8	ACD52673	ACD52673	HBV Inoxy
866	11	52.4	38	6	ACN29616	ACN29616	WNV minus	939	11	52.4	38	8	ACD52981	ACD52981	HBV Inoxy
867	11	52.4	38	6	ACN29697	ACN29697	WNV minus	940	11	52.4	38	8	ACD51940	ACD51940	HBV Inoxy
868	11	52.4	38	6	ACN29765	ACN29765	WNV minus	941	11	52.4	38	8	ACD53074	ACD53074	HBV Inoxy
869	11	52.4	38	6	ACN30340	ACN30340	WNV minus	942	11	52.4	38	8	ACD52268	ACD52268	HBV Inoxy
870	11	52.4	38	6	ACN15599	ACN15599	WNV Hamme	943	11	52.4	38	8	ACD52343	ACD52343	HBV Inoxy
871	11	52.4	38	6	ACN17500	ACN17500	WNV Inoxy	944	11	52.4	38	8	ACD52959	ACD52959	HBV Inoxy
872	11	52.4	38	6	ACN17782	ACN17782	WNV Inoxy	945	11	52.4	38	8	ACD52460	ACD52460	HBV Inoxy
873	11	52.4	38	6	ACN26162	ACN26162	WNV minus	946	11	52.4	38	8	ACD52646	ACD52646	HBV Inoxy
874	11	52.4	38	6	ACN28211	ACN28211	WNV minus	947	11	52.4	38	8	ACD53152	ACD53152	HBV Inoxy
875	11	52.4	38	6	ACN28291	ACN28291	WNV minus	948	11	52.4	38	8	ACD52548	ACD52548	HBV Inoxy
876	11	52.4	38	6	ACN29165	ACN29165	WNV minus	949	11	52.4	38	8	ACD52775	ACD52775	HBV Inoxy
877	11	52.4	38	6	ACN30093	ACN30093	WNV minus	950	11	52.4	38	8	ACD51858	ACD51858	HBV Inoxy
878	11	52.4	38	6	ACN30562	ACN30562	WNV minus	951	11	52.4	38	8	ACD53141	ACD53141	HBV Inoxy
879	11	52.4	38	6	ACN15580	ACN15580	WNV Hamme	952	11	52.4	38	11	ADL52282	ADL52282	Human NOG
880	11	52.4	38	6	ACN17255	ACN17255	WNV Inoxy	953	11	52.4	38	11	ADL53719	ADL53719	Human IKK
881	11	52.4	38	6	ACN17935	ACN17935	WNV Inoxy	954	11	52.4	38	11	ADL53750	ADL53750	Human IKK
882	11	52.4	38	6	ACN18449	ACN18449	WNV Inoxy	955	11	52.4	38	11	ADL53761	ADL53761	Human IKK
883	11	52.4	38	6	ACN18450	ACN18450	WNV Inoxy	956	11	52.4	38	11	ADL53913	ADL53913	Human IKK
884	11	52.4	38	6	ACN18506	ACN18506	WNV Inoxy	957	11	52.4	38	11	ADL54077	ADL54077	Human IKK
885	11	52.4	38	6	ACN28560	ACN28560	WNV minus	958	11	52.4	38	11	ADL75070	ADL75070	Human PTG
886	11	52.4	38	6	ACN28668	ACN28668	WNV minus	959	11	52.4	38	11	ADL52399	ADL52399	Human NOG
887	11	52.4	38	6	ACN28716	ACN28716	WNV minus	960	11	52.4	38	11	ADL74977	ADL74977	Human PTG
888	11	52.4	38	6	ACN29218	ACN29218	WNV minus	961	11	52.4	38	11	ADL75375	ADL75375	Human PTG
889	11	52.4	38	6	ACN29611	ACN29611	WNV minus	962	11	52.4	38	11	ADL52036	ADL52036	Human NOG
890	11	52.4	38	6	ACA07220	ACA07220	Necrosis	963	11	52.4	38	11	ADL52435	ADL52435	Human NOG
891	11	52.4	38	8	ACA07476	ACA07476	Necrosis	964	11	52.4	38	11	ADL53838	ADL53838	Human IKK
892	11	52.4	38	8	ACA07410	ACA07410	Necrosis	965	11	52.4	38	11	ADL75222	ADL75222	Human PTG
893	11	52.4	38	8	ACA07570	ACA07570	Necrosis	966	11	52.4	38	11	ADL52135	ADL52135	Human NOG
894	11	52.4	38	8	ACA07379	ACA07379	Necrosis	967	11	52.4	38	11	ADL52228	ADL52228	Human NOG
895	11	52.4	38	8	ACA06956	ACA06956	Necrosis	968	11	52.4	38	11	ADL52407	ADL52407	Human NOG
896	11	52.4	38	8	ACA07113	ACA07113	Necrosis	969	11	52.4	38	11	ADL53997	ADL53997	Human IKK
897	11	52.4	38	8	ACA07319	ACA07319	Necrosis	970	11	52.4	38	11	ADL54011	ADL54011	Human IKK

ADL54087	Human	IKK
971	11	52.4
972	11	52.4
973	11	52.4
974	11	52.4
975	11	52.4
976	11	52.4
977	11	52.4
978	11	52.4
979	11	52.4
980	11	52.4
981	11	52.4
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983	11	52.4
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985	11	52.4
986	11	52.4
987	11	52.4
988	11	52.4
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991	11	52.4
992	11	52.4
993	11	52.4
994	11	52.4
995	11	52.4
996	11	52.4
997	11	52.4
998	11	52.4
999	11	52.4
1000	11	52.4

ALIGNMENTS

RESULT 1

ACIS6056

ID ACIS6056 standard; DNA; 25 BP.

ACIS6056;

13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 56047.

EST; ss; probe; expressed sequence tag; microarray; gene expression;

genetic variation; biallelic marker; polymorphism; human;

cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Mittmann MP;

WPI, 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in

Southern, Northern or dot-blot hybridization to identify or detect the

sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 56047; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic

acid probes including one of 2,018,500 fully defined sequences, or its

perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping or detecting the sequence or specific mutations of any gene, in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 7 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 67.6%; Score 14.2; DB 9; Length 25;

Best Local Similarity 84.2%; Pred. No. 5.1e+02; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;

3 GTCATTAGACCGTACGCA 21

6 GTCATTAGACCGTACGCA 24

AAAL6755

ID AAAL6755 standard; DNA; 29 BP.

AAAL6755;

16-JUN-2000 (first entry)

Human secreted protein clone LL89_3 probe SEQ ID NO:218.

Human; secreted protein; immunostimulant; immunosuppressant; vitruide;

antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;

antidiabetic; antiaesthetic; antiarthritic; antirheumatic; protozoicide;

antithyroid; immune deficiency; severe combined immunodeficiency; SCID;

infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;

connective tissue disease; multiple sclerosis; erythematosis;

rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;

Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;

insulin dependent diabetes mellitus; graft-versus-host-disease;

autoimmune inflammatory eye disease; allergy; hybridisation; probe; ss.

Homo sapiens.

WO200009552-A1.

24-FEB-2000.

13-AUG-1999; 99WO-US018298.

14-AUG-1998; 98US-0096622P.

17-AUG-1998; 98US-0096815P.

04-SEP-1998; 98US-0099229P.

23-OCT-1998; 98US-0105368P.

08-JAN-1999; 99US-0115234P.

12-FEB-1999; 99US-0119931P.

18-FEB-1999; 99US-0120575P.

30-APR-1999; 99US-0132020P.

11-AUG-1999; 99US-0148424P.

(GEM) GENETICS INST INC.

C 387	11.2	53.3	25	9	ACH60892	ACH60892 DNA large	C 460	11	52.4	24	10	ADC57939	ADC57939 Human PRO
C 388	11.2	53.3	25	10	ABZ84510	ABZ84510 Toxicology	C 461	11	52.4	24	10	ADC55303	ADC55303 Human PRO
C 389	11.2	53.3	28	2	AAT73081	Aat73081 un snRNA	C 462	11	52.4	24	10	ADC12170	ADC12170 Human PRO
C 390	11.2	53.3	28	12	ADO11376	Ado11376 Single mu	C 463	11	52.4	24	10	ADC56592	ADC56592 Human PRO
C 391	11.2	53.3	28	12	ADO11426	Ado11426 Single mu	C 464	11	52.4	24	10	ADC07647	ADC07647 Human PRO
C 392	11.2	53.3	29	6	ABO82513	Abq82513 Promoter	C 465	11	52.4	24	10	ADC11637	ADC11637 Human PRO
C 393	11.2	53.3	30	10	ADC83961	Adc83961 Human pap	C 466	11	52.4	24	10	ADC14759	ADC14759 Novel hum
C 394	11.2	53.3	30	10	ADP43834	Adp43834 HPV 39 de	C 467	11	52.4	24	10	ADC08291	ADC08291 Human sec
C 395	11.2	53.3	31	2	AAT35700	Aat35700 3' VK pri	C 468	11	52.4	24	10	ADC82116	ADC82116 Human PRO
C 396	11.2	53.3	31	2	AAK62513	Aak62513 Granule ol	C 469	11	52.4	24	10	ADC07758	ADC07758 Human sec
C 397	11.2	53.3	34	3	AAK62282	Aak62282 Sample ol	C 470	11	52.4	24	10	ADC82649	ADC82649 Human PRO
C 398	11.2	53.3	37	6	ABK59294	Abk59294 Human CLC	C 471	11	52.4	24	10	ADC08829	ADC08829 Human sec
C 399	11.2	53.3	37	6	ACN19390	Acn19390 WNV Zinzy	C 472	11	52.4	24	10	ADC07078	ADC07078 Human sec
C 400	11.2	53.3	37	6	ACN30875	Acn30875 WNV minus	C 473	11	52.4	24	10	ADC83325	ADC83325 Human PRO
C 401	11.2	53.3	37	6	ACN19673	Acn19673 WNV Zinzy	C 474	11	52.4	24	10	ADC62014	ADC62014 Human PRO
C 402	11.2	53.3	37	6	ACN18820	Acn18820 WNV Zinzy	C 475	11	52.4	24	10	ADC62015	ADC62015 Plasmodu
C 403	11.2	53.3	37	6	ACN30634	Acn30634 WNV minus	C 476	11	52.4	24	10	ADC55432	ADC55432 Human PRO
C 404	11.2	53.3	37	6	ACN31064	Acn31064 WNV minus	C 477	11	52.4	24	10	ADC56390	ADC56390 Human PRO
C 405	11.2	53.3	37	6	ACN31914	Acn31914 WNV minus	C 478	11	52.4	24	10	ADC54828	ADC54828 Human PRO
C 406	11.2	53.3	37	6	ACN30941	Acn30941 WNV minus	C 479	11	52.4	24	10	ADC26982	ADC26982 Novel hum
C 407	11.2	53.3	37	6	ACN31346	Acn31346 WNV minus	C 480	11	52.4	24	10	ADC26449	ADC26449 Novel hum
C 408	11.2	53.3	37	8	ACA08020	ACA08020 Necrosis	C 481	11	52.4	24	10	ADP67386	ADP67386 Human CDN
C 409	11.2	53.3	37	8	ACA08100	ACA08100 Necrosis	C 482	11	52.4	24	10	ADP35640	ADP35640 Human PRO
C 410	11.2	53.3	38	6	ABQ72429	Abq72429 PCR prime	C 483	11	52.4	24	10	ADP100133	ADP100133 Novel hum
C 411	11.2	53.3	39	10	ADC46944	Adc46944 Primer fo	C 484	11	52.4	24	10	ABX78017	ABX78017 Human PRO
C 412	11.2	53.3	40	2	AAT87214	Aat87214 Interleuk	C 485	11	52.4	24	10	ABX80429	ABX80429 Human sec
C 413	11.2	53.3	40	6	ABZ21788	Abz21788 Human ery	C 486	11	52.4	24	10	ACA69335	ACA69335 Human sec
C 414	11.2	53.3	40	6	ABZ21789	Abz21789 Human ery	C 487	11	52.4	24	10	ABX90406	ABX90406 Human sec
C 415	11.2	53.3	45	4	AA513391	AA513391 Alantine s	C 488	11	52.4	24	10	ABX64252	ABX64252 Human PRO
C 416	11.2	53.3	50	6	ABZ06239	Abz06239 Human leu	C 489	11	52.4	24	12	ADP35585	ADP35585 Human PRO
C 417	11.2	52.4	16	3	AAZ47286	AAZ47286 C-myc pro	C 490	11	52.4	24	12	ADG11835	ADG11835 Human PRO
C 418	11.2	52.4	17	2	AAK75296	AAK75296 Mouse flt	C 491	11	52.4	24	12	ADH119705	ADH119705 Human PRO
C 419	11.2	52.4	17	2	AAK75297	AAK75297 Mouse flt	C 492	11	52.4	24	12	ADH21198	ADH21198 Human PRO
C 420	11.2	52.4	20	2	AAK72519	AAK72519 PCR prime	C 493	11	52.4	24	12	ADH20238	ADH20238 Human PRO
C 421	11.2	52.4	20	3	AAZ72519	AAZ72519 Human bia	C 494	11	52.4	24	12	ADP37421	ADP37421 M. tuberc
C 422	11.2	52.4	21	12	ADM92428	Adm92428 Panceracti	C 495	11	52.4	25	9	ACI74364	ACI74364 Human mtc
C 423	11.2	52.4	22	6	ABL59233	Ab159233 Antisense	C 496	11	52.4	25	9	ACI31851	ACI31851 Human mtc
C 424	11.2	52.4	22	12	ADP6451	Adp6451 Mouse GAP	C 497	11	52.4	25	9	ACI14671	ACI14671 Human mtc
C 425	11.2	52.4	23	4	AAO07923	Aao07923 Human G-P	C 498	11	52.4	25	9	ACI90851	ACI90851 Human mtc
C 426	11.2	52.4	24	2	AAO92089	Aao92089 Human rec	C 499	11	52.4	25	9	ACI28866	ACI28866 Human mtc
C 427	11.2	52.4	24	2	AAK35264	AAK35264 PCR prime	C 500	11	52.4	25	9	ACI04993	ACI04993 Human mtc
C 428	11.2	52.4	24	3	AAK58316	AAK58316 Human PRO	C 501	11	52.4	25	9	ACI86887	ACI86887 Human mtc
C 429	11.2	52.4	24	5	AA517470	AA517470 P. viwax	C 502	11	52.4	25	9	ACI16955	ACI16955 Human mtc
C 430	11.2	52.4	24	5	AAAF4420	AAAF4420 Human PRO	C 503	11	52.4	25	9	ACK00553	ACK00553 Human mtc
C 431	11.2	52.4	24	6	ABK87485	Abk87485 Synthetic	C 504	11	52.4	25	9	ACI28682	ACI28682 Human mtc
C 432	11.2	52.4	24	6	ABK87486	Abk87486 Synthetic	C 505	11	52.4	25	9	ACI94261	ACI94261 Human mtc
C 433	11.2	52.4	24	6	ABQ03239	Abq03239 Oligonuci	C 506	11	52.4	25	9	ACT119780	ACT119780 Human mtc
C 434	11.2	52.4	24	6	ABQ79141	Abq79141 Primer #1	C 507	11	52.4	25	9	ACK12417	ACK12417 Human mtc
C 435	11.2	52.4	24	8	ACA64474	ACA64474 Novel hum	C 508	11	52.4	25	9	ACT15267	ACT15267 Human mtc
C 436	11.2	52.4	24	8	ABX80933	Abx80933 Human sec	C 509	11	52.4	25	9	ACI25752	ACI25752 Human mtc
C 437	11.2	52.4	24	8	ACD44442	Abcd44442 Human PRO	C 510	11	52.4	25	9	ACT96369	ACT96369 Human mtc
C 438	11.2	52.4	24	8	ABX79613	Abx79613 Human sec	C 511	11	52.4	25	9	ACH64101	ACH64101 DNA large
C 439	11.2	52.4	24	8	ACA93634	ACA93634 Novel hum	C 512	11	52.4	25	9	ACH64227	ACH64227 DNA large
C 440	11.2	52.4	24	8	ABX81316	Abx81316 Human sec	C 513	11	52.4	25	12	ADK72525	ADK72525 Streptomy
C 441	11.2	52.4	24	8	ACA93132	ACA93132 Novel hum	C 514	11	52.4	28	2	ADL71141	Adl71141 Interleuk
C 442	11.2	52.4	24	8	ABX17216	Abx17216 Human PRO	C 515	11	52.4	28	2	AAQ46856	Aaq46856 Streptomy
C 443	11.2	52.4	24	9	ACA88071	ACA88071 Novel hum	C 516	11	52.4	28	6	ABR54214	ABR54214 Pantocis
C 444	11.2	52.4	24	9	ACA88520	ACA88520 Human sec	C 517	11	52.4	31	4	AAI29879	AAI29879 Human bin
C 445	11.2	52.4	24	9	ACD82027	ACD82027 Human PRO	C 518	11	52.4	32	3	AAA99084	AAA99084 UBQ10 gen
C 446	11.2	52.4	24	9	ADA71970	Ada71970 Human sec	C 519	11	52.4	33	3	AAZ64927	AAZ64927 Control R
C 447	11.2	52.4	24	9	ADA21656	Ada21656 Human PRO	C 520	11	52.4	33	6	ABX03349	ABX03349 Ribozyme
C 448	11.2	52.4	24	9	ADA10443	Ada10443 Human PRO	C 521	11	52.4	33	12	ADP84085	ADP84085 Small nuc
C 449	11.2	52.4	24	9	ADA17987	Ada17987 Human PRO	C 522	11	52.4	34	10	ADP13553	ADP13553 SPV1 gene
C 450	11.2	52.4	24	9	ADA28095	Ada28095 Human PRO	C 523	11	52.4	35	6	ABK54214	ABK54214 Pantocis
C 451	11.2	52.4	24	9	ADA94675	Ada94675 Human PRO	C 524	11	52.4	35	8	ACH10009	ACH10009 Necrosis
C 452	11.2	52.4	24	9	ADA38900	Ada38900 Human PRO	C 525	11	52.4	35	8	ACH10011	ACH10011 Necrosis
C 453	11.2	52.4	24	9	ADA93021	Ada93021 Human PRO	C 526	11	52.4	36	2	AAV11874	AAV11874 Synthetic
C 454	11.2	52.4	24	9	ACH65588	ACH65588 Human PRO	C 527	11	52.4	36	2	AAV19025	AAV19025 Plasmid p
C 455	11.2	52.4	24	9	ADA22582	Ada22582 Human sec	C 528	11	52.4	36	6	ABX01900	ABX01900 HCV hamme
C 456	11.2	52.4	24	9	ADC039578	Adc039578 Human PRO	C 529	11	52.4	36	6	ABX02596	ABX02596 HCV hamme
C 457	11.2	52.4	24	9	ADA06748	Ada06748 Human sec	C 530	11	52.4	36	6	ABX02112	ABX02112 HCV hamme
C 458	11.2	52.4	24	9	ADA39441	Ada39441 Human PRO	C 531	11	52.4	36	6	ABX02392	ABX02392 HCV hamme
C 459	11.2	52.4	24	9	ADB96467	ADB96467 Human PRO	C 532	11	52.4	36	6	ABX02676	ABX02676 HCV hamme

241	11.6	55.2	38	6	ACN16944	ACN16944	WNV	Inozy	C 314	11.4	54.3	20	2	AAQ45350	AAQ45350 PCR prime
242	11.6	55.2	38	6	ACN18309	ACN18309	WNV	Inozy	C 315	11.4	54.3	22	6	ABJ31902	ABJ31902 Human CYP
243	11.6	55.2	38	6	ACN18573	ACN18573	WNV	Inozy	C 316	11.4	54.3	23	8	ABV75861	ABV75861 Arabidops
244	11.6	55.2	38	6	ACN17194	ACN17194	WNV	Inozy	C 317	11.4	54.3	23	9	ABZ81234	ABZ81234 Arabidops
245	11.6	55.2	38	6	ACN28445	ACN28445	WNV	minus	C 318	11.4	54.3	23	10	ADH35553	ADH35553 H+-ATPase
246	11.6	55.2	38	6	ACN30165	ACN30165	WNV	minus	C 319	11.4	54.3	23	10	ADH18214	ADH18214 H+-ATPase
247	11.6	55.2	38	6	ACN18467	ACN18467	WNV	Inozy	C 320	11.4	54.3	24	6	ABO08710	ABO08710 Oligonuc1
248	11.6	55.2	38	6	ACN18695	ACN18695	WNV	Inozy	C 321	11.4	54.3	24	6	ABO02374	ABO02374 Oligonuc1
249	11.6	55.2	38	6	ACN18695	ACN18695	WNV	Inozy	C 322	11.4	54.3	24	6	ABO08669	ABO08669 Oligonuc1
250	11.6	55.2	38	6	ACN28523	ACN28523	WNV	minus	C 323	11.4	54.3	24	6	ABO08669	ABO08669 Oligonuc1
251	11.6	55.2	38	6	ACN29692	ACN29692	WNV	minus	C 324	11.4	54.3	24	6	AB184227	AB184227 Capture o
252	11.6	55.2	38	6	ACN29692	ACN29692	WNV	minus	C 325	11.4	54.3	24	6	AB184226	AB184226 Capture o
253	11.6	55.2	38	6	ACN28657	ACN28657	WNV	minus	C 326	11.4	54.3	25	9	ACI56633	ACI56633 Human m1c
254	11.6	55.2	38	6	ACN29459	ACN29459	WNV	minus	C 327	11.4	54.3	25	9	ACI189575	ACI189575 Human m1c
255	11.6	55.2	38	6	ACN29488	ACN29488	WNV	minus	C 328	11.4	54.3	25	9	ACI89574	ACI89574 Human m1c
256	11.6	55.2	38	6	ACN30357	ACN30357	WNV	minus	C 329	11.4	54.3	25	9	ACI169299	ACI169299 Human m1c
257	11.6	55.2	38	6	ACN18644	ACN18644	WNV	Inozy	C 330	11.4	54.3	25	9	ACI171603	ACI171603 Human m1c
258	11.6	55.2	38	6	ACN29655	ACN29655	WNV	minus	C 331	11.4	54.3	25	9	ACI34741	ACI34741 Human m1c
259	11.6	55.2	38	6	ACN29671	ACN29671	WNV	minus	C 332	11.4	54.3	25	9	ACI34741	ACI34741 Human m1c
260	11.6	55.2	38	6	ACN17594	ACN17594	WNV	Inozy	C 333	11.4	54.3	25	9	ACR04457	ACR04457 Human m1c
261	11.6	55.2	38	6	ACN29252	ACN29252	WNV	minus	C 334	11.4	54.3	25	9	ACR21465	ACR21465 Human m1c
262	11.6	55.2	38	6	ACN17438	ACN17438	WNV	Inozy	C 335	11.4	54.3	25	9	ACI69299	ACI69299 Human m1c
263	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 336	11.4	54.3	25	9	ACI61541	ACI61541 DNA targe
264	11.6	55.2	38	6	ACN16983	ACN16983	WNV	Inozy	C 337	11.4	54.3	25	9	ACH64299	ACH64299 Human targe
265	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 338	11.4	54.3	26	6	ABT11741	ABT11741 DNA targe
266	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 339	11.4	54.3	26	6	ABT11741	ABT11741 DNA targe
267	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 340	11.4	54.3	27	8	ABT11785	ABT11785 Transcrip
268	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 341	11.4	54.3	27	10	ADC60797	ADC60797 Cis eleme
269	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 342	11.4	54.3	27	10	ADC60796	ADC60796 Cis eleme
270	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 343	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
271	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 344	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
272	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 345	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
273	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 346	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
274	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 347	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
275	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 348	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
276	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 349	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
277	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 350	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
278	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 351	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
279	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 352	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
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302	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 375	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
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307	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 380	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
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310	11.6	55.2	38	6	ACN17890	ACN17890	WNV	Inozy	C 383	11.4	54.3	27	10	ADP48567	ADP48567 Cis-eleme
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312	11.4	54.3	15	3	AAZ64069	AAZ64069	Substrate		C 385	11.2	53.3	25	9	ACH59775	ACH59775 DNA targe
313	11.4	54.3	15	3	ABX01122	ABX01122	Hepatitis		C 386	11.2	53.3	25	9	ACH60780	ACH60780 DNA targe

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Db 21 CATTGACCTTAGCGA 5

RESULT 34
LOCUS AX392054/c
DEFINITION Sequence 13 from Patent WO0215920.
ACCESSION AX392054
VERSION AX392054.1 GI:19700558
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Ward,S.B., Bavik,C.B., Cork,M.B. and Tazi-Ahmini,R.B.
TITLE Treatment of hyperproliferative diseases
JOURNAL Patent: WO 0215920-A 13 28-FEB-2002;
THE UNIVERSITY OF SHEFFIELD (GB)
FEATURES
source 1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTAGCG 19
18 GTCATTAGACCGTAGCG 2

Db 18 GTCATTAGACCGTAGCG 2

RESULT 35
LOCUS AX755148
DEFINITION Sequence 29 from Patent WO03025003.
ACCESSION AX755148
VERSION AX755148.1 GI:32167628
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van Wely,C.A.
TITLE Vaccines
JOURNAL Patent: WO 03025003-A 29 27-MAR-2003;
GLAXO GROUP LIMITED (GB)
FEATURES
source 1..32
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

ORIGIN

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QY 5 CATTAGACCGTAGCGCA 21
1 CATTAGACCGCGCGCA 17

Db 1 CATTAGACCGCGCGCA 17

RESULT 36
LOCUS AX755156
DEFINITION Sequence 37 from Patent WO03025003.
32 bp DNA linear PAT 23-JUN-2003

ACCESSION AX755156
VERSION AX755156.1 GI:32167636
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van Wely,C.A.
TITLE Vaccines
JOURNAL Patent: WO 03025003-A 37 27-MAR-2003;
GLAXO GROUP LIMITED (GB)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

ORIGIN

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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATTAGACCGTAGCGCA 21
1 CATTAGACCGCGCGCA 17

Db 1 CATTAGACCGCGCGCA 17

RESULT 37
LOCUS AX351239/c
DEFINITION Sequence 74 from Patent WO0194950.
ACCESSION AX351239
VERSION AX351239.1 GI:18616587
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Nock,S. and Kassner,P.D.
TITLE Screening of phage displayed peptides without clearing of the cell culture
JOURNAL Patent: WO 0194950-A 74 13-DEC-2001;
Zyomyx, Inc. (US)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="WVK15 primer"

ORIGIN

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Best Local Similarity 73.7%; Pred. No. 1.7e+05;
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30 GGTCATCASAATGTCGCG 12

Db 30 GGTCATCASAATGTCGCG 12

RESULT 38
LOCUS AX581788/c
DEFINITION Sequence 3626 from Patent WO0211674.
ACCESSION AX581788
VERSION AX581788.1 GI:27653598
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1

AR046887/c
LOCUS AR046887 38 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1680 from patent US 5817796.
ACCESSION AR046887
VERSION AR046887.1 GI:5968352
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylyate residues
JOURNAL Patent: US 5817796-A 1680 06-OCT-1996;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
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ORIGIN
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Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTAC 17
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15 TCATCAGACCGTAC 2

RESULT 30
153939/c 153939 38 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 1680 from patent US 5646042.
DEFINITION 153939
ACCESSION 153939.1 GI:2475142
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1680 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
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ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
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QY 4 TCATTAGACCGTAC 17
|||||
15 TCATCAGACCGTAC 2

RESULT 31
AX220204/c 38 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 5646 from Patent W00159103.
DEFINITION AX220204
ACCESSION AX220204
VERSION AX220204.1 GI:15547928
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 5646 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..38
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
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Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCATTAGACCGT 15
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37 GGCATTAGACCTT 24

RESULT 32
AR314417/c 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 4954 from patent US 6559294.
DEFINITION AR314417
ACCESSION AR314417
VERSION AR314417.1 GI:31707843
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Hoiseh,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
TITLE Sankaran,B. and Fletcher,J.D.
JOURNAL Chlamydia pneumoniae polynucleotides and uses thereof
FEATURES Patent: US 6559294-A 4954 06-MAY-2003;
Location/Qualifiers
source 1..20
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ORIGIN
Query Match 58.1%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTACCG 20
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18 TCATTATAGCGTCCGC 2

RESULT 33
AR364921/c 21 bp DNA linear PAT 03-SEP-2003
LOCUS Sequence 8 from patent US 5451502.
DEFINITION AR364921
ACCESSION AR364921
VERSION AR364921.1 GI:34428117
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS George,A.L., Jr.
TITLE Restriction amplification assay
JOURNAL Patent: US 5451502-A 8 19-SEP-1995;
FEATURES Location/Qualifiers
source 1..21
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ORIGIN
Query Match 58.1%; Score 12.2; DB 6; Length 21;
Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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96	12	57.1	36	6	ABX02155	Abx02155 HCV hamme	169	11.6	55.2	25	9	ACT188245	Act188245 Human m1c
97	12	57.1	36	6	ABX02284	Abx02284 HCV hamme	170	11.6	55.2	25	9	ACT97085	Act97085 Human m1c
98	12	57.1	37	6	ABK59280	Abk59280 WNV Zinzv	171	11.6	55.2	26	4	AAc97064	Aac97064 Cytochrom
99	12	57.1	37	6	ACN19032	Acn19032 WNV Zinzv	172	11.6	55.2	32	12	AD059622	Ad059622 HCV RNA P
100	12	57.1	37	6	ACN30898	Acn30898 WNV Zinzv	173	11.6	55.2	32	12	AD059629	Ad059629 HCV RNA P
101	12	57.1	37	6	ACN18884	Acn18884 WNV Zinzv	174	11.6	55.2	32	12	AD059633	Ad059633 HCV RNA P
102	12	57.1	37	6	ACN18893	Acn18893 WNV Zinzv	175	11.6	55.2	32	12	AD059625	Ad059625 HCV RNA P
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105	12	57.1	37	6	ACN19720	Acn19720 WNV Zinzv	178	11.6	55.2	32	12	AD059632	Ad059632 HCV RNA P
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109	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	182	11.6	55.2	32	12	AD059633	Ad059633 HCV RNA P
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116	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	189	11.6	55.2	35	12	AD159444	AD159444 Inozyme 8
117	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	190	11.6	55.2	37	5	AAH41019	Aah41019 PCR prime
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120	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	193	11.6	55.2	37	6	ABK59311	Abk59311 Human CLC
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122	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	195	11.6	55.2	37	6	ACN30995	Acn30995 WNV m1nus
123	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	196	11.6	55.2	37	6	ACN31582	Acn31582 WNV m1nus
124	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	197	11.6	55.2	37	6	ACN30780	Acn30780 WNV m1nus
125	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	198	11.6	55.2	37	6	ACN31436	Acn31436 WNV m1nus
126	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	199	11.6	55.2	37	6	ACN31709	Acn31709 WNV m1nus
127	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	200	11.6	55.2	37	6	ACN31816	Acn31816 WNV m1nus
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129	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	202	11.6	55.2	37	6	AD154295	AD154295 Human m1c
130	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	203	11.6	55.2	38	4	ABK04713	Abk04713 Human NOG
131	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	204	11.6	55.2	38	4	ABK04713	Abk04713 Human NOG
132	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	205	11.6	55.2	38	4	ABK04626	Abk04626 Human NOG
133	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	206	11.6	55.2	38	4	ABK05292	Abk05292 Human NOG
134	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	207	11.6	55.2	38	4	ABK04620	Abk04620 Human NOG
135	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	208	11.6	55.2	38	4	ABK04722	Abk04722 Human NOG
136	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	209	11.6	55.2	38	4	ABK04634	Abk04634 Human NOG
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138	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	211	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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140	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	213	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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145	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	218	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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147	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	220	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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149	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	222	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
150	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	223	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
151	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	224	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
152	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	225	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
153	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	226	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
154	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	227	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
155	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	228	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
156	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	229	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
157	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	230	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
158	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	231	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
159	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	232	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
160	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	233	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
161	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	234	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
162	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	235	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
163	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	236	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
164	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	237	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
165	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	238	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
166	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	239	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
167	12	57.1	37	6	ACN11240	Acn11240 WNV Zinzv	240	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG

OY 1 CGGTCATTAGACCGTACGC 19
|||
Db 21 CTGTCATTGACCGACAC 3

RESULT 19
AAC97127/c
ID AAC97127 standard; DNA; 26 BP.

XX AAC97127;

XX 26-FEB-2001 (first entry)

XX Cytochrome b PCR primer; SEQ ID 102.

XX Mutation detection; fungi; cytochrome b; strobilurin analogue resistance;
KW single nucleotide polymorphism; PCR primer; fungal resistance; crop;
KW fruit; vegetable; ss.

XX Venturia inaequalis.

XX WO20066773-A2.

XX 09-NOV-2000.

XX 26-APR-2000; 2000WO-GB001620.

XX 30-APR-1999; 99GB-00010100.

XX 13-MAR-2000; 2000GB-00006004.

XX 31-MAR-2000; 2000GB-00007901.

XX (ZENE) ZENECA LTD.

XX Windass JD, Heaney SP, Renwick A, Whitcombe DM, Little S;
PI Gibson NJ, Theaker J, Stanger CP;

XX WPI; 2001-007234/01.

PT Detecting a cytochrome b mutation which leads to resistance to
PT strobilurin analogs or compounds in the same resistance group in fungal
PT nucleic acid using a single nucleotide polymorphism detection technique.

PS Disclosure; Page 35; 173pp; English.

XX The present invention relates to a method for detecting mutations in
CC fungal cytochrome b coding sequences which give rise to resistance to
CC strobilurin analogues. The method uses a single nucleotide polymorphism
CC (SNP) detection technique. The present sequence is a PCR primer used in
CC the method of the present invention. The method is suitable for
CC monitoring fungal resistance to a strobilurin analogue or a compound in
CC the same cross resistance group in crops such as cereals, fruit and
CC vegetables such as canola, sunflower, tobacco, sugarbeet, cotton, soya,
CC wheat, barley, rice, sorghum, tomatoes, mangoes, peaches, apples,
CC pears, strawberries, bananas, melons, potatoes and carrot

XX Sequence 26 BP; 7 A; 4 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 4; Length 26;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GGTGATTAGACCGTACGC 20
|||
Db 20 GGTGATTAGACCGTACGC 2

RESULT 20
AA250914/c
ID AA250914 standard; DNA; 31 BP.
XX AA250914;
XX

DT 31-MAY-2000 (first entry)
XX PCR primer RO204 to amplify Prac promoter.

KW Plasmid pRAB-84-69; recombinant; beta-casein; PCR primer; Prac promoter;
KW casein kinase II alpha subunit; casein kinase II beta subunit;
KW kanamycin resistance marker; iminopeptidase; genetic stability;
KW pharmaceutical; nutritional composition; vaccine formulation; ss.

XX Unidentified.

XX WO200008174-A1.

XX 17-FEB-2000.

XX 06-AUG-1999; 99WO-US017873.

XX 07-AUG-1998; 98US-00131028.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Lemmel SA, Leonard AB, Chaudhary S;

XX WPI; 2000-205721/18.

PT Recombinant construct useful for producing human milk protein, edible
PT plant protein, antibody, antigen or hormone, comprises nucleotide
PT sequences expressing beta-casein protein.

PS Example 1; Page 11; 73pp; English.

XX The patent discloses a method of producing human milk protein, edible
CC plant protein, antibody or an antigen in a host cell. It involves
CC transforming host cells with a vector comprising the gene of interest
CC linked to a promoter and nucleotide sequences encoding subunits of a
CC kinase, resistance marker and a peptidase. This method is useful for
CC improving the genetic stability of a plasmid-containing cell during
CC fermentation. Proteins produced may be used in pharmaceutical or
CC nutritional compositions and in vaccine formulations. The present
CC sequence is that of PCR primer RO204, used to amplify Prac promoter with
CC multiple cloning site and rmbp1B2 terminator from plasmid pK223-3. The
CC PCR product is used for construction of plasmid pRAB-84-69. pRAB-84-69
CC construct comprises genes encoding human beta-casein, casein kinase II
CC alpha and beta subunits, bacterial kanamycin resistance marker and
CC iminopeptidase

XX Sequence 31 BP; 7 A; 6 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 3; Length 31;
Best Local Similarity 78.9%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGGTCATTAGACCGTACGC 19
|||
Db 30 CGGTCATTAGACCGTACGC 12

RESULT 21
AAT04264/c
ID AAT04264 standard; DNA; 33 BP.

XX AAT04264;

XX 16-APR-1996 (first entry)

XX Primer #259 for IA beta chain gene.

XX Polymerase chain reaction; PCR; primer; amplify;
KW major histocompatibility complex; MHC; T-cell receptor; TCR;
KW autoimmune disease; immunodeficiency disease; immune response;
KW immunoproliferation disease; graft-host rejection; therapy; ss.
XX Synthetic.

XX MO9523814-A1.
 XX 08-SEP-1995.
 XX 03-MAR-1995; 95WO-US002689.
 XX 04-MAR-1994; 94US-00207481.
 XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX Kappeler JM, Marrack P;
 XX WPI; 1995-320543/41.
 XX Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
 PT - useful as reagents for the treatment of diseases including auto-immune
 PT diseases, immuno-stimulatory diseases or graft-host rejection.

XX Example 1; Page 54; 94pp; English.

XX The sequences represented by AAT04263 and AAT04264 are amplification
 CC primers for a fragment of the IA beta chain gene (fragment 333-259). This
 CC fragment was used in the construction of a hybrid IA alpha beta dimer
 CC containing the OVA peptide, and a linker. The encoded protein (pIAD-OVA)
 CC was found to be more stable than the IA alpha beta dimer. The stability
 CC was decreased by the addition of a MHC groove specific binding peptide
 CC (e.g. see AAR82527, AAR82528 and AAR82531), compared to an increase seen
 CC on the addition of a MHC binding peptide to IE k/d-MHC. These complexes
 CC may be used to regulate an immune response. The complexes are capable of
 CC being recognised by a TCR alone or in combination with additional MHC
 CC proteins. These complexes are useful for therapeutic purposes and
 CC experimental purposes. They can also be used as reagents for the
 CC treatment of diseases including autoimmune diseases, immunodeficiency
 CC diseases, immunoproliferation diseases, and graft-host rejection

XX Sequence 33 BP; 9 A; 8 C; 12 G; 4 T; 0 U; 0 Other;
 SQ
 XX Query Match 60.0%; Score 12.6; DB 2; Length 33;
 XX Best Local Similarity 78.9%; Pred. No. 4.2e+03;
 XX Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCAATTAGACCGTACGC 19
 |||||
 Db 20 CGTTCATTGCTTGTGACGC 2

RESULT 22

ACAI0066/C
 ID ACAI0066 standard; RNA; 36 BP.

XX ACAI0066;

XX 03-JUN-2003 (first entry)

XX Necrosis factor kappa B (NFkB) sub-unit modulating zinzyme #16.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 XX G-cleaver; amberzyme; cancer; RBL-A activity; breast cancer; lung cancer;
 XX prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
 XX stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
 XX head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
 XX multidrug resistant cancer; RBL-A-specific inhibitor; chemotherapy;
 XX paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;
 XX doxorubicin; fluorouracil carboplatin; edatrexate; gemcitabine;
 XX radiation therapy; inflammatory disease; asthma; diabetes;
 XX rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 XX transplant/graft rejection; reperfusion injury; glomerulonephritis;
 XX allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX Synthetic.

PN US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-0077916.

XX (STIN/) STINGCOMB D T.

XX (MCSW/) MCSWINGEN J.

XX (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswigen J, Draper KG;
 XX WPI; 2003-340953/32.

XX Claim 2; SEQ ID NO 3885; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating RBL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of RBL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of RBL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, lymphoma, glioma or
 CC cervical, head and neck, ovarian cancer, melanoma, bladder, pancreatic,
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC cyclophosphamide, docetaxel, cisplatin, methotrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents an enzymatic nucleic acid used to
 CC modulate the function of a necrosis factor kappa B sub-unit

XX Sequence 36 BP; 10 A; 8 C; 13 G; 0 T; 4 U; 1 Other;
 SQ
 XX Query Match 60.0%; Score 12.6; DB 8; Length 36;
 XX Best Local Similarity 78.9%; Pred. No. 4.3e+03;
 XX Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGC 20
 |||||
 Db 35 GGCATTAGACCTCACTCG 17

RESULT 23
 ACD66384
 ID ACD66384 standard; RNA; 36 BP.

XX ACD66384;

XX 23-SEP-2003 (first entry)

XX Anti-HCV nucleic acid molecule #232.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 XX RNA stability; RNA expression; RNA synthesis; antisense;
 XX

KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
 KM amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KM HBV reverse transcriptase; Enhancer I region; anti-HCV;
 KM viral replication; degenerative; disease state; HBV infection;
 KM HCV infection; cirrhosis; liver failure; hepatocellular carcinoma;
 KM hepatotropic; cytostatic; virucide; antiinflammatory; ss.
 OS Hepatitis C virus.
 XX
 FN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 PF
 XX 26-MAR-2001; 2001US-00817879.
 PR
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-035059P.
 PR 05-DEC-2001; 2001US-037055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAYC/) PAYCO P.
 PA (LEBP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Payco P, Lee P;
 PI Draper K, Roberts E;
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 XX Claim 1; Page 322; 387pp; English.
 PS
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents one of the anti-HCV nucleic
 CC acid molecules disclosed in the present invention
 XX
 SQ Sequence 36 BP; 10 A; 6 C; 14 G; 0 T; 5 U; 1 Other;
 QY
 Query Match 60.0%; Score 12.6; DB 8; Length 36;
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 2 GGTCATTAGACCGTAGCGCA 21
 Db 15 GGCCGUAAGCGCCGANGCGA 34
 RESULT 24
 ACN19551/c

ID ACN19551 standard; RNA; 37 BP.
 XX
 AC ACN19551;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV Zinzyme SEQ ID NO 19567.
 XX
 KM WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KM encephalitis; myocarditis; meningitis; infection; hepatitis;
 KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KM Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 XX
 PI Blatt L, Mcswigen JA;
 XX
 DR WPI; 2002-706994/76.
 XX
 PT New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 24; SEQ ID NO 19567; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 37 BP; 11 A; 8 C; 13 G; 0 T; 5 U; 0 Other;
 QY
 Query Match 60.0%; Score 12.6; DB 6; Length 37;
 Best Local Similarity 78.9%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 2 GGTCATTAGACCGTAGCGC 20
 Db 36 GGTCAGTACGACTACTCG 18
 RESULT 25
 ACN31602/c
 ID ACN31602 standard; RNA; 37 BP.
 XX
 AC ACN31602;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV minus strand Zinzyme SEQ ID NO 31618.

XX MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
 KW viraemia; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 OS West Nile Virus.
 XX WO200268637-A2.
 XX 06-SEP-2002.
 XX 19-OCT-2001; 2001MO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGEN J A.
 XX Blatt L, Mcswigen JA;
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (MNV), useful for treating a condition related to MNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT Claim 24; SEQ ID NO 31618; 495bp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 XX treating a condition related to MNV infection e.g. pancreatitis,
 XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 XX molecule is selected from the group of ribozymes consisting of
 XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 XX nucleic acid molecules further comprise at least five ribose residues, at
 XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 XX least three of the 5' terminal nucleotides and a 3' end modification of a
 XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 XX in the specification. The present sequence is that of a nucleic acid
 XX molecule of the invention
 SQ Sequence 37 BP; 9 A; 9 C; 13 G; 0 T; 6 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 6; Length 37;
 Best Local Similarity 78.9%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 GGTCAATTAGACCTAGCG 20
 Db 36 GGTCACTAGACCTCACTCG 18
 RESULT 26
 ACN19001/c
 ID ACN19001 standard; RNA; 37 BP.
 XX ACN19001;
 XX 22-APR-2004 (first entry)
 XX MNV Zinzyme SEQ ID NO 19017.
 XX MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
 KW viraemia; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX

OS West Nile Virus.
 XX WO200268637-A2.
 XX 06-SEP-2002.
 XX 19-OCT-2001; 2001MO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGEN J A.
 XX Blatt L, Mcswigen JA;
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (MNV), useful for treating a condition related to MNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT Claim 24; SEQ ID NO 19017; 495bp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 XX treating a condition related to MNV infection e.g. pancreatitis,
 XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 XX molecule is selected from the group of ribozymes consisting of
 XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 XX nucleic acid molecules further comprise at least five ribose residues, at
 XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 XX least three of the 5' terminal nucleotides and a 3' end modification of a
 XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 XX in the specification. The present sequence is that of a nucleic acid
 XX molecule of the invention
 SQ Sequence 37 BP; 10 A; 6 C; 15 G; 0 T; 6 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 6; Length 37;
 Best Local Similarity 78.9%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 GGTCAATTAGACCTAGCG 20
 Db 36 GGTCACTAGACCTCACTCG 18
 RESULT 27
 ACA07993/c
 ID ACA07993 standard; RNA; 37 BP.
 XX ACA07993;
 XX 03-JUN-2003 (first entry)
 XX Necrosis factor kappa B (NFkB) sub-unit modulating zinzyme #97.
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; RBL-A activity; breast cancer; lung cancer;
 KW prostate cancer; colorectal cancer; brain cancer; esophageal cancer;
 KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
 KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
 KW multidrug resistant cancer; RBL-A-specific inhibitor; chemotherapeutic;
 KW paclitaxel; docetaxel; cisplatin; edatrexate; cyclophosphamide;
 KW doxorubicin; fluorouracil carboplatin; edatrexate; gemcitabine;
 KW radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; resensitis; Crohn's disease; obesity; ischemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 KW

XX OS Synthetic.
 XX PN US2002177568-A1.
 XX PD 28-NOV-2002.
 XX PF 23-MAY-2001; 2001US-00864785.
 XX PR 07-DEC-1992; 92US-00987132.
 XX PR 18-MAY-1994; 94US-00245466.
 XX PR 15-AUG-1994; 94US-00291932.
 XX PR 23-DEC-1996; 96US-00777916.
 XX PA (STIN/) STINGHOMB D T.
 XX PA (MCSW/) MCSWIGEN J.
 XX PA (DRAP/) DRAPER K G.
 XX PI Stinchcomb DT, Mcswigen J, Draper KG;
 XX WPI; 2003-340953/32.
 XX DR WPI; 2003-340953/32.
 XX XX
 PT Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 PS Claim 2; Page 39; 72pp; English.
 CC The invention describes an enzymatic nucleic acid molecule (1) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (1) is an inozyme, zinczyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (1) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, or
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemtobine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, resectosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents an enzymatic nucleic acid used to
 CC modulate the function of a necrosis factor kappa B sub-unit
 XX
 SO Sequence 37 BP; 11 A; 9 C; 13 G; 0 T; 4 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 8; Length 37;
 Best Local Similarity 78.9%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGCTATTAGACCGTACGCG 20
 |||||||||
 DB 36 GGCCATTAGACCTCACTCG 18

RESULT 28
 ABRK04673
 ID ABRK04673 standard; RNA; 38 BP.
 AC ABRK04673;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX Human NOGO inozyme substrate sequence #150.

XX Human; ss; antisense therapy; cytosolic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200159103-A2.
 XX PN 16-AUG-2001.
 XX PD
 XX PF 09-FEB-2001; 2001WO-US004273.
 XX PR 11-FEB-2000; 2000US-0181797P.
 XX PR 28-FEB-2000; 2000US-0185516P.
 XX PR 06-MAR-2000; 2000US-0187128P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (BLAT/) BLATT L.
 XX PA (MCSW/) MCSWIGEN J.
 XX PA (CHOW/) CHOWRIRA B M.
 XX PI Blatt L, Mcswigen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX DR WPI; 2001-607195/69.
 XX XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 89; Page 80; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA motif) or
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present

CC Sequence is a substrate sequence for a nucleic acid of the invention
CC based on the human NOGO sequence
XX
SQ Sequence 38 BP; 9 A; 8 C; 14 G; 0 T; 6 U; 1 Other;
Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTAGCGCA 21
DB 16 GGCCGUUAGGCCGANGCGA 35
RESULT 29
ABK04649
ID ABK04649 standard; RNA; 38 BP.
AC ABK04649;
XX
XX
XX
XX
XX 12-MAR-2002 (first entry)
DE Human NOGO Inozyme substrate sequence #126.
XX
XX
XX Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;
XX cerebrioprotective; neuroprotective; antiparkinsonian;
XX muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
XX DNAzyme; Inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
XX MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
XX inflammatory arthropathy; central nervous system injury;
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSM/) MCSMIRGEN J.
XX PA (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 89; Page 80; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NOGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
XX DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
XX an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
XX based on the human NOGO sequence
SQ Sequence 38 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 1 Other;
Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGTCAATTAGACCGTAGCGCA 21
DB 16 GGCCGUUAGGCCGANGCGA 35
RESULT 30
ABQ72447/C
ID ABQ72447 standard; DNA; 38 BP.
XX
XX AC ABQ72447;
XX
XX 30-AUG-2002 (first entry)
XX
XX PCR primer MKV24 for ScFv and Fab library generation.
XX
XX PCR; primer; replicable genetic package; phage display; scFv; Fab;
XX heavy chain variable region; light chain variable region; HPe002; HPe025;
XX HPe054; ss.
XX
XX Synthetic.
XX
XX WO200194950-A2.
XX
XX 13-DEC-2001.
XX
XX 05-JUN-2001; 2001WO-US018421.
XX
XX 05-JUN-2000; 2000US-0209503P.
XX 04-JUN-2001; 2001US-00874547.
XX
XX (ZYOM-) ZYOMYX INC.
XX
XX Nock S, Kassner PD;
XX
XX WPI; 2002-519063/55.
XX
XX Screening phase displayed peptides, for obtaining a replicable genetic
XX package (RGP) that displays a fusion protein that binds to a target
XX molecule, comprises contacting the molecule with an uncleared cell
XX culture comprising the RGPs.
XX

PS Example 1; Page 20; 39pp; English.
XX
CC The present invention relates to a method for screening replicable
CC genetic packages (RGP) to obtain RGP that display on their surface a
CC fusion protein that specifically binds to a target molecule. The method
CC comprises contacting a target molecule with an uncloned cell culture
CC having: (i) RGPs, each displaying a fusion protein having a surface-
CC displayed RGP polypeptide and a potential binding polypeptide; and (ii)
CC cells in which RGP were amplified. Phage displaying antibody fragments
CC scFvs or Fab's were generated by PCR amplification of cDNA corresponding
CC to the heavy and light chain variable regions from the H6002, H6025,
CC and H6054 hybridomas. The regions were amplified using the PCR primers
CC ABQ72365-ABQ72448
XX
SQ Sequence 38 BP; 8 A; 13 C; 7 G; 10 T; 0 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 78.9%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 GGTCAATTGACCGTACGCCG 20
Db 30 GGTCAATTGACCGTACGCCG 12
RESULT 31
ABK20307
ID ABK20307 standard; RNA; 38 BP.
XX
AC ABK20307;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG inozyme, Seq ID No 2954.
XX
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; vitruicide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kipfel-Trenauay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
XX WO200188124-A2.
XX
XX 22-NOV-2001.
XX
XX 16-MAY-2001; 2001WO-US015866.
XX
XX 16-MAY-2000; 2000US-00572021.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (GLAX) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswigen JA, McLaughlin F, Randi AM,
XX WPI, 2002-082995/11.
XX
XX Novel polynucleotide which down regulates expression of Ets-related gene,
XX useful for treating cancer, diabetic retinopathy, macular degeneration,
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
XX Claim 5; Page 74; 149pp; English.
XX
XX The invention relates to a nucleic acid molecule (I) which down regulates
XX expression of an Ets-related gene (ERG). (I) is useful for treating
XX conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
XX tumour angiogenesis, diabetic retinopathy, macular degeneration,
XX neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kipfel-Trenauay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 38 BP; 7 A; 10 C; 14 G; 0 T; 6 U; 1 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 65.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY 2 GGTCAATTGACCGTACGCCG 21
Db 16 GGCGCGUAGCGCGGAMGCCG 35
RESULT 32
ABK20420
ID ABK20420 standard; RNA; 38 BP.
XX
AC ABK20420;
XX
DT 09-APR-2002 (first entry)
XX
XX Human ERG inozyme, Seq ID No 3067.
XX
DE Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; vitruicide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kipfel-Trenauay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
XX WO200188124-A2.
XX
XX 22-NOV-2001.
XX
XX 16-MAY-2001; 2001WO-US015866.
XX
XX 16-MAY-2000; 2000US-00572021.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (GLAX) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswigen JA, McLaughlin F, Randi AM,
XX WPI, 2002-082995/11.
XX
XX Novel polynucleotide which down regulates expression of Ets-related gene,
XX useful for treating cancer, diabetic retinopathy, macular degeneration,
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 5; Page 76; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (ClCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of ClCA1 in a cell or
CC tissue. The sequences are useful for reducing ClCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of ClCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ClCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 38 BP; 9 A; 9 C; 12 G; 0 T; 7 U; 1 Other;
XX
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 65.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
XX
QY 2 GGTCAATTGACCGTAGCGCA 21
DB 16 GGCCGUVAGCCGAGNCGCA 35
XX
RESULT 35
ACN17900
ID ACN17900 standard; RNA; 38 BP.
XX
AC ACN17900;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV Inozyme SEQ ID NO 17916.
XX
XX MNV, West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PE 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
PI Blatt L, Mcswigen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 24; SEQ ID NO 17916; 495pp; English.
XX

CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 38 BP; 7 A; 9 C; 12 G; 0 T; 9 U; 1 Other;
XX
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 65.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
XX
QY 2 GGTCAATTGACCGTAGCGCA 21
DB 16 GGCCGUVAGCCGAGNCGCA 35
XX
RESULT 36
ACN17240
ID ACN17240 standard; RNA; 38 BP.
XX
AC ACN17240;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV Inozyme SEQ ID NO 17243.
XX
XX MNV, West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PE 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
PI Blatt L, Mcswigen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 24; SEQ ID NO 17243; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX
 SQ Sequence 38 BP; 6 A; 6 C; 15 G; 0 T; 10 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTAGCCGA 21
 16 GGCCGUUAGGCCGAGANGCGA 35

DB

RESULT 37
 ACN16711
 ID ACN16711 standard; RNA; 38 BP.
 XX
 AC ACN16711;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX MNV Inozyme SEQ ID NO 16714.
 DE
 XX MNV; West Nile Virus; antiinflammatory; cytosratic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 XX
 PI Blatt L, Mcswigen JA;
 XX
 PS Claim 24; SEQ ID NO 16714; 495pp; English.
 DR
 XX WPI; 2002-706994/76.
 PT
 PT New nucleic acid molecule that modulates replication of West Nile Virus
 (MNV), useful for treating a condition related to MNV infection e.g.
 pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 24; SEQ ID NO 16714; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 CC treating a condition related to MNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX
 SQ Sequence 38 BP; 9 A; 11 C; 11 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTAGCCGA 21
 16 GGCCGUUAGGCCGAGANGCGA 35

DB

RESULT 38
 ACN30373
 ID ACN30373 standard; RNA; 38 BP.
 XX
 AC ACN30373;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX MNV minus strand Inozyme SEQ ID NO 30389.
 DE
 XX MNV; West Nile Virus; antiinflammatory; cytosratic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 XX
 PI Blatt L, Mcswigen JA;
 XX
 PS Claim 24; SEQ ID NO 30389; 495pp; English.
 DR
 XX WPI; 2002-706994/76.
 PT
 PT New nucleic acid molecule that modulates replication of West Nile Virus
 (MNV), useful for treating a condition related to MNV infection e.g.
 pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 24; SEQ ID NO 30389; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 CC treating a condition related to MNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX
 SQ Sequence 38 BP; 8 A; 9 C; 13 G; 0 T; 7 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATGACCGTAGCGCA 21
|||::|||
Db 16 GGCCGUNAGCCGAGNCGCA 35

RESULT 39

ACN29690 standard; RNA; 38 BP.

ACN29690;

22-APR-2004 (first entry)

MNV minus strand Inozyme SEQ ID NO 29706.

MNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic; viruslike; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme; Amberzyme; Zinzyme; ss.

West Nile Virus.

WO200268637-A2.

06-SEP-2002.

19-OCT-2001; 2001WO-US048350.

20-OCT-2000; 2000US-0242411P.

(RIBO-) RIBOZYME PHARM INC.

(BLAT/) BLATT L.

(MCSW/) MCSWIGEN J A.

Blatt L, Mcswigen JA;

WPI; 2002-706994/76.

New nucleic acid molecule that modulates replication of West Nile Virus (MNV), useful for treating a condition related to MNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 24; SEQ ID NO 29706; 495bp; English.

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (MNV). The nucleic acid molecules are useful for treating a condition related to MNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

Sequence 38 BP; 7 A; 11 C; 13 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 65.0%; Pred. No. 4.3e+03;

Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

2 GGTCAATGACCGTAGCGCA 21
|||::|||
16 GGCCGUNAGCCGAGNCGCA 35

RESULT 40
ACN27931

ID ACN27931 standard; RNA; 38 BP.

ACN27931;

22-APR-2004 (first entry)

MNV minus strand Inozyme SEQ ID NO 27947.

MNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic; viruslike; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme; Amberzyme; Zinzyme; ss.

West Nile Virus.

WO200268637-A2.

06-SEP-2002.

19-OCT-2001; 2001WO-US048350.

20-OCT-2000; 2000US-0242411P.

(RIBO-) RIBOZYME PHARM INC.

(BLAT/) BLATT L.

(MCSW/) MCSWIGEN J A.

Blatt L, Mcswigen JA;

WPI; 2002-706994/76.

New nucleic acid molecule that modulates replication of West Nile Virus (MNV), useful for treating a condition related to MNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 24; SEQ ID NO 27947; 495bp; English.

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (MNV). The nucleic acid molecules are useful for treating a condition related to MNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

Sequence 38 BP; 11 A; 8 C; 12 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 65.0%; Pred. No. 4.3e+03;

Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

2 GGTCAATGACCGTAGCGCA 21
|||::|||
16 GGCCGUNAGCCGAGNCGCA 35

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Job time : 113.708 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 24.3034 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631b-17
Perfect score: 21
Sequence: 1 cgcgcatacagccgtacgcga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	13.2	62.9	39 3	US-09-056-052-13 Sequence 13, Appl
3	12.6	60.0	31 3	US-09-131-028A-17 Sequence 17, Appl
4	12.6	60.0	33 1	US-08-207-481-29 Sequence 29, Appl
5	12.6	60.0	33 5	PCT-US95-02689-31 Sequence 31, Appl
6	12.6	60.0	38 4	US-09-371-772B-11935 Sequence 11935, A
7	12.6	60.0	38 4	US-09-371-772B-13181 Sequence 13181, A
8	12.6	60.0	38 4	US-09-371-772B-13811 Sequence 13811, A
9	12.6	60.0	38 4	US-09-874-547-83 Sequence 83, Appl
10	12.4	59.0	38 1	US-08-373-124A-1680 Sequence 1680, Ap
11	12.4	59.0	38 1	US-08-433-628-1680 Sequence 1680, Ap
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14	12.2	58.1	41 4	US-09-313-221A-19 Sequence 19, Appl
15	12.2	57.1	25 2	US-08-860-882A-75 Sequence 75, Appl
16	12.2	57.1	25 4	US-09-011-769A-61 Sequence 61, Appl
17	12.2	57.1	29 4	US-09-814-351-25 Sequence 25, Appl
18	12.2	57.1	32 4	US-09-709-103-34 Sequence 34, Appl
19	12.2	57.1	32 4	US-09-439-410A-34 Sequence 34, Appl
20	12.2	57.1	38 4	US-09-371-772B-7357 Sequence 7357, Ap
21	12.2	57.1	38 4	US-09-371-772B-7797 Sequence 7797, Ap
22	12.2	57.1	38 4	US-09-371-772B-8104 Sequence 8104, Ap
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26	12.2	57.1	38 4	US-09-371-772B-9974 Sequence 9974, Ap
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50	11.4	54.3	43 1	US-08-802-985-5 Sequence 5, Appl
51	11.4	54.3	44 1	US-08-452-083-17 Sequence 17, Appl
52	11.4	54.3	44 1	US-08-452-083-18 Sequence 18, Appl
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55	11.2	53.3	31 3	US-08-679-645-388 Sequence 388, App
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57	11.2	53.3	34 4	US-10-038-520-3 Sequence 3, Appl
58	11.2	53.3	38 4	US-09-874-547-65 Sequence 65, Appl
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105	11	52.4	38	4	US-09-371-772B-11401	Sequence 11401, A	178	11	52.4	40	4	US-09-949-109-5	Sequence 5, Appl
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107	11	52.4	38	4	US-09-371-772B-11674	Sequence 11674, A	180	11	52.4	42	1	US-08-433-124A-238	Sequence 238, App
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114	11	52.4	38	4	US-09-371-772B-11897	Sequence 11897, A	187	10.8	51.4	27	3	US-08-584-040-1315	Sequence 1315, Ap
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139	11	52.4	38	4	US-09-371-772B-12598	Sequence 12598, A	212	10.8	51.4	45	6	5467963-19	Patent No. 5467963
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146	11	52.4	38	4	US-09-371-772B-13218	Sequence 13218, A	219	10.6	50.5	30	4	US-09-293-427-8	Sequence 2, Appl
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149	11	52.4	38	4	US-09-371-772B-13421	Sequence 13421, A	222	10.6	50.5	36	1	US-08-074-121-11	Sequence 11, Appl
150	11	52.4	38	4	US-09-371-772B-13421	Sequence 13421, A	223	10.6	50.5	36	5	PCT-US94-06447-11	Sequence 11, Appl
151	11	52.4	38	4	US-09-371-772B-13487	Sequence 13487, A	224	10.6	50.5	37	1	US-08-411-796-517	Sequence 517, App
152	11	52.4	38	4	US-09-371-772B-13518	Sequence 13518, A	225	10.6	50.5	37	3	US-08-471-033-517	Sequence 517, App
153	11	52.4	38	4	US-09-371-772B-13529	Sequence 13529, A	226	10.6	50.5	37	3	US-08-559-390-517	Sequence 517, App
154	11	52.4	38	4	US-09-371-772B-13559	Sequence 13559, A	227	10.6	50.5	37	5	PCT-US93-11198-517	Sequence 517, App
155	11	52.4	38	4	US-09-371-772B-13591	Sequence 13591, A	228	10.6	50.5	38	4	US-09-371-772B-11237	Sequence 11237, A
156	11	52.4	38	4	US-09-371-772B-13633	Sequence 13633, A	229	10.6	50.5	38	4	US-09-371-772B-11239	Sequence 11239, A
157	11	52.4	38	4	US-09-371-772B-13652	Sequence 13652, A	230	10.6	50.5	38	4	US-09-371-772B-11295	Sequence 11295, A
158	11	52.4	38	4	US-09-371-772B-13669	Sequence 13669, A	231	10.6	50.5	38	4	US-09-371-772B-11305	Sequence 11305, A
159	11	52.4	38	4	US-09-371-772B-13681	Sequence 13681, A	232	10.6	50.5	38	4	US-09-371-772B-11315	Sequence 11315, A
160	11	52.4	38	4	US-09-371-772B-13710	Sequence 13710, A	233	10.6	50.5	38	4	US-09-371-772B-11418	Sequence 11418, A
161	11	52.4	38	4	US-09-371-772B-13740	Sequence 13740, A	234	10.6	50.5	38	4	US-09-371-772B-11448	Sequence 11448, A
162	11	52.4	38	4	US-09-371-772B-13758	Sequence 13758, A	235	10.6	50.5	38	4	US-09-371-772B-11514	Sequence 11514, A
163	11	52.4	38	4	US-09-371-772B-13760	Sequence 13760, A	236	10.6	50.5	38	4	US-09-371-772B-11600	Sequence 11600, A
164	11	52.4	38	4	US-09-371-772B-13805	Sequence 13805, A	237	10.6	50.5	38	4	US-09-371-772B-11647	Sequence 11647, A
165	11	52.4	38	4	US-09-371-772B-13816	Sequence 13816, A	238	10.6	50.5	38	4	US-09-371-772B-11650	Sequence 11650, A
166	11	52.4	38	4	US-09-371-772B-13833	Sequence 13833, A	239	10.6	50.5	38	4	US-09-371-772B-11689	Sequence 11689, A
167	11	52.4	38	4	US-09-371-772B-13867	Sequence 13867, A	240	10.6	50.5	38	4	US-09-371-772B-11700	Sequence 11700, A
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169	11	52.4	38	4	US-09-371-772B-13931	Sequence 13931, A	242	10.6	50.5	38	4	US-09-371-772B-11773	Sequence 11773, A
170	11	52.4	38	4	US-09-371-772B-13974	Sequence 13974, A	243	10.6	50.5	38	4	US-09-371-772B-11796	Sequence 11796, A
171	11	52.4	38	4	US-09-371-772B-13985	Sequence 13985, A	244	10.6	50.5	38	4	US-09-371-772B-11798	Sequence 11798, A
172	11	52.4	38	4	US-09-371-772B-14014	Sequence 14014, A	245	10.6	50.5	38	4	US-09-371-772B-11818	Sequence 11818, A
173	11	52.4	38	4	US-09-874-547-75	Sequence 75, Appl	246	10.6	50.5	38	4	US-09-371-772B-11818	Sequence 11818, A

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249	10.6	50.5	38	4	US-09-371-772B-11849	Sequence 11849, A	322	10.6	50.5	47	4	US-09-422-978-195	Sequence 2156, App
250	10.6	50.5	38	4	US-09-371-772B-11851	Sequence 11851, A	323	10.4	49.5	18	3	US-08-642-807A-11	Sequence 11, Appl
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252	10.6	50.5	38	4	US-09-371-772B-11957	Sequence 11957, A	325	10.4	49.5	21	4	US-09-501-612A-27	Sequence 27, Appl
253	10.6	50.5	38	4	US-09-371-772B-11973	Sequence 11973, A	326	10.4	49.5	22	4	US-09-527-030G-151	Sequence 151, App
254	10.6	50.5	38	4	US-09-371-772B-11983	Sequence 11983, A	327	10.4	49.5	24	1	US-08-470-179-197	Sequence 197, App
255	10.6	50.5	38	4	US-09-371-772B-12007	Sequence 12007, A	328	10.4	49.5	24	3	US-07-876-288-12	Sequence 12, Appl
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257	10.6	50.5	38	4	US-09-371-772B-12038	Sequence 12038, A	330	10.4	49.5	27	1	US-08-513-764-6	Sequence 6, Appl
258	10.6	50.5	38	4	US-09-371-772B-12049	Sequence 12049, A	331	10.4	49.5	29	3	US-09-118-841B-20	Sequence 20, Appl
259	10.6	50.5	38	4	US-09-371-772B-12053	Sequence 12053, A	332	10.4	49.5	29	3	US-09-414-439-20	Sequence 20, Appl
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261	10.6	50.5	38	4	US-09-371-772B-12117	Sequence 12117, A	334	10.4	49.5	33	3	US-09-303-064-42	Sequence 42, Appl
262	10.6	50.5	38	4	US-09-371-772B-12178	Sequence 12178, A	335	10.4	49.5	33	3	US-09-086-503-42	Sequence 42, Appl
263	10.6	50.5	38	4	US-09-371-772B-12180	Sequence 12180, A	336	10.4	49.5	33	4	US-09-301-533-16	Sequence 16, Appl
264	10.6	50.5	38	4	US-09-371-772B-12184	Sequence 12184, A	337	10.4	49.5	34	1	US-08-044-621D-16	Sequence 16, Appl
265	10.6	50.5	38	4	US-09-371-772B-12192	Sequence 12192, A	338	10.4	49.5	34	1	US-08-044-621D-16	Sequence 22, Appl
266	10.6	50.5	38	4	US-09-371-772B-12210	Sequence 12210, A	339	10.4	49.5	34	1	US-08-803-973-8	Sequence 8, Appl
267	10.6	50.5	38	4	US-09-371-772B-12224	Sequence 12224, A	340	10.4	49.5	34	1	US-08-803-972-8	Sequence 8, Appl
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269	10.6	50.5	38	4	US-09-371-772B-12241	Sequence 12241, A	342	10.4	49.5	35	4	US-09-165-868-9	Sequence 9, Appl
270	10.6	50.5	38	4	US-09-371-772B-12270	Sequence 12270, A	343	10.4	49.5	36	2	US-08-292-620A-806	Sequence 806, App
271	10.6	50.5	38	4	US-09-371-772B-12286	Sequence 12286, A	344	10.4	49.5	36	2	US-08-292-620A-815	Sequence 815, App
272	10.6	50.5	38	4	US-09-371-772B-12368	Sequence 12368, A	345	10.4	49.5	36	2	US-08-292-620A-1147	Sequence 1147, App
273	10.6	50.5	38	4	US-09-371-772B-12368	Sequence 12368, A	346	10.4	49.5	36	2	US-08-292-620A-1195	Sequence 1195, App
274	10.6	50.5	38	4	US-09-371-772B-12387	Sequence 12387, A	347	10.4	49.5	36	2	US-08-292-620A-1225	Sequence 1225, App
275	10.6	50.5	38	4	US-09-371-772B-12404	Sequence 12404, A	348	10.4	49.5	36	2	US-08-292-620A-1289	Sequence 1289, App
276	10.6	50.5	38	4	US-09-371-772B-12424	Sequence 12424, A	349	10.4	49.5	36	2	US-08-292-620A-1289	Sequence 1289, App
277	10.6	50.5	38	4	US-09-371-772B-12428	Sequence 12428, A	350	10.4	49.5	36	2	US-08-292-620A-1346	Sequence 1346, App
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279	10.6	50.5	38	4	US-09-371-772B-12471	Sequence 12471, A	352	10.4	49.5	36	3	US-09-071-845-815	Sequence 815, App
280	10.6	50.5	38	4	US-09-371-772B-12584	Sequence 12584, A	353	10.4	49.5	36	3	US-09-071-845-1147	Sequence 1147, App
281	10.6	50.5	38	4	US-09-371-772B-12690	Sequence 12690, A	354	10.4	49.5	36	3	US-09-071-845-1186	Sequence 1186, App
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283	10.6	50.5	38	4	US-09-371-772B-13197	Sequence 13197, A	356	10.4	49.5	36	3	US-09-071-845-1225	Sequence 1225, App
284	10.6	50.5	38	4	US-09-371-772B-13238	Sequence 13238, A	357	10.4	49.5	36	3	US-09-071-845-1289	Sequence 1289, App
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287	10.6	50.5	38	4	US-09-371-772B-13435	Sequence 13435, A	360	10.4	49.5	38	4	US-09-371-772B-12201	Sequence 7201, App
288	10.6	50.5	38	4	US-09-371-772B-13452	Sequence 13452, A	361	10.4	49.5	38	4	US-09-371-772B-12293	Sequence 7293, App
289	10.6	50.5	38	4	US-09-371-772B-13455	Sequence 13455, A	362	10.4	49.5	38	4	US-09-371-772B-1344	Sequence 7344, App
290	10.6	50.5	38	4	US-09-371-772B-13501	Sequence 13501, A	363	10.4	49.5	38	4	US-09-371-772B-1348	Sequence 7348, App
291	10.6	50.5	38	4	US-09-371-772B-13522	Sequence 13522, A	364	10.4	49.5	38	4	US-09-371-772B-1364	Sequence 7364, App
292	10.6	50.5	38	4	US-09-371-772B-13525	Sequence 13525, A	365	10.4	49.5	38	4	US-09-371-772B-1364	Sequence 7364, App
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295	10.6	50.5	38	4	US-09-371-772B-13611	Sequence 13611, A	368	10.4	49.5	38	4	US-09-371-772B-1401	Sequence 7401, App
296	10.6	50.5	38	4	US-09-371-772B-13617	Sequence 13617, A	369	10.4	49.5	38	4	US-09-371-772B-1428	Sequence 7428, App
297	10.6	50.5	38	4	US-09-371-772B-13626	Sequence 13626, A	370	10.4	49.5	38	4	US-09-371-772B-1441	Sequence 7441, App
298	10.6	50.5	38	4	US-09-371-772B-13645	Sequence 13645, A	371	10.4	49.5	38	4	US-09-371-772B-1482	Sequence 7482, App
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303	10.6	50.5	38	4	US-09-371-772B-13684	Sequence 13684, A	376	10.4	49.5	38	4	US-09-371-772B-1556	Sequence 7556, App
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307	10.6	50.5	38	4	US-09-371-772B-13764	Sequence 13764, A	380	10.4	49.5	38	4	US-09-371-772B-1619	Sequence 7619, App
308	10.6	50.5	38	4	US-09-371-772B-13838	Sequence 13838, A	381	10.4	49.5	38	4	US-09-371-772B-1652	Sequence 7652, App
309	10.6	50.5	38	4	US-09-371-772B-13853	Sequence 13853, A	382	10.4	49.5	38	4	US-09-371-772B-1656	Sequence 7656, App
310	10.6	50.5	38	4	US-09-371-772B-13882	Sequence 13882, A	383	10.4	49.5	38	4	US-09-371-772B-1738	Sequence 7738, App
311	10.6	50.5	38	4	US-09-371-772B-13907	Sequence 13907, A	384	10.4	49.5	38	4	US-09-371-772B-1788	Sequence 7788, App
312	10.6	50.5	38	4	US-09-371-772B-13934	Sequence 13934, A	385	10.4	49.5	38	4	US-09-371-772B-1792	Sequence 7792, App
313	10.6	50.5	38	4	US-09-371-772B-13970	Sequence 13970, A	386	10.4	49.5	38	4	US-09-371-772B-1973	Sequence 7973, App
314	10.6	50.5	38	4	US-09-371-772B-13976	Sequence 13976, A	387	10.4	49.5	38	4	US-09-371-772B-8031	Sequence 8031, App
315	10.6	50.5	38	4	US-09-371-772B-14021	Sequence 14021, A	388	10.4	49.5	38	4	US-09-371-772B-8084	Sequence 8084, App
316	10.6	50.5	38	4	US-09-874-547-67	Sequence 67, Appl	389	10.4	49.5	38	4	US-09-371-772B-8105	Sequence 8105, App
317	10.6	50.5	39	4	US-09-060-299-189	Sequence 189, App	390	10.4	49.5	38	4	US-09-371-772B-8166	Sequence 8166, App
318	10.6	50.5	39	4	US-09-402-923A-189	Sequence 189, App	391	10.4	49.5	38	4	US-09-371-772B-8168	Sequence 8168, App
319	10.6	50.5	45	1	US-08-681-935-13	Sequence 13, Appl	392	10.4	49.5	38	4	US-09-371-772B-8173	Sequence 8173, App

393	10.4	49.5	38	4	US-09-371-772B-8209	Sequence 8209, Ap
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397	10.4	49.5	38	4	US-09-371-772B-8549	Sequence 8549, Ap
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433	10.4	49.5	38	4	US-09-371-772B-9949	Sequence 9949, Ap
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435	10.4	49.5	38	4	US-09-371-772B-10011	Sequence 10011, A
436	10.4	49.5	38	4	US-09-371-772B-10017	Sequence 10053, A
437	10.4	49.5	38	4	US-09-371-772B-10053	Sequence 10053, A
438	10.4	49.5	38	4	US-09-371-772B-10055	Sequence 10064, A
439	10.4	49.5	38	4	US-09-371-772B-10065	Sequence 10068, A
440	10.4	49.5	38	4	US-09-371-772B-10068	Sequence 10172, A
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446	10.4	49.5	38	4	US-09-371-772B-10317	Sequence 10317, A
447	10.4	49.5	38	4	US-09-371-772B-10325	Sequence 10325, A
448	10.4	49.5	38	4	US-09-371-772B-10356	Sequence 10356, A
449	10.4	49.5	38	4	US-09-371-772B-10363	Sequence 10363, A
450	10.4	49.5	38	4	US-09-371-772B-10365	Sequence 10365, A
451	10.4	49.5	38	4	US-09-371-772B-10368	Sequence 10368, A
452	10.4	49.5	38	4	US-09-371-772B-10368	Sequence 10382, A
453	10.4	49.5	38	4	US-09-371-772B-10368	Sequence 10403, A
454	10.4	49.5	38	4	US-09-371-772B-10382	Sequence 10431, A
455	10.4	49.5	38	4	US-09-371-772B-10403	Sequence 10437, A
456	10.4	49.5	38	4	US-09-371-772B-10431	Sequence 10439, A
457	10.4	49.5	38	4	US-09-371-772B-10437	Sequence 10459, A
458	10.4	49.5	38	4	US-09-371-772B-10449	Sequence 10467, A
459	10.4	49.5	38	4	US-09-371-772B-10459	Sequence 10467, A
460	10.4	49.5	38	4	US-09-371-772B-10467	Sequence 10485, A
461	10.4	49.5	38	4	US-09-371-772B-10485	Sequence 10491, A
462	10.4	49.5	38	4	US-09-371-772B-10485	Sequence 10518, A
463	10.4	49.5	38	4	US-09-371-772B-10491	Sequence 10518, A
464	10.4	49.5	38	4	US-09-371-772B-10518	Sequence 10518, A
465	10.4	49.5	38	4	US-09-371-772B-10518	Sequence 10518, A

C 539	10.2	48.6	20	3	US-09-048-810-6	Sequence 6, Appli	c 612	10.2	48.6	45	4	US-09-096-700-305	Sequence 305, App
C 540	10.2	48.6	20	3	US-09-167-151-4	Sequence 4, Appli	c 613	10.2	48.6	45	4	US-09-903-603A-305	Sequence 305, App
C 541	10.2	48.6	20	4	US-09-980-052-64	Sequence 64, Appli	c 614	10.2	48.6	47	4	US-09-422-978-3195	Sequence 3195, Ap
C 542	10.2	48.6	20	4	US-09-842-347A-4	Sequence 4, Appli	c 615	10.2	48.6	48	1	US-08-604-913B-9	Sequence 9, Appli
C 543	10.2	48.6	21	4	US-09-622-166A-30	Sequence 30, Appli	c 616	10.2	48.6	49	4	US-09-538-709-122	Sequence 122, App
C 544	10.2	48.6	21	4	US-09-657-472-350	Sequence 350, App	c 617	10.2	48.6	49	4	US-09-538-709-1285	Sequence 1285, Ap
C 545	10.2	48.6	22	3	US-09-037-327-11	Sequence 11, Appli	c 618	10.2	48.6	50	4	US-09-470-661A-36	Sequence 36, Appli
C 546	10.2	48.6	24	4	US-09-360-545-9	Sequence 9, Appli	c 619	10	47.6	17	3	US-08-584-040-3963	Sequence 3963, Ap
C 547	10.2	48.6	24	4	US-10-142-231-78	Sequence 78, Appli	c 620	10	47.6	17	3	US-08-584-040-3964	Sequence 3964, Ap
C 548	10.2	48.6	25	2	US-08-631-751A-7	Sequence 7, Appli	c 621	10	47.6	17	4	US-09-371-772B-1730	Sequence 1730, Ap
C 549	10.2	48.6	26	3	US-08-986-837-5	Sequence 5, Appli	c 622	10	47.6	17	4	US-09-371-772B-1731	Sequence 1731, Ap
C 550	10.2	48.6	26	4	US-09-809-592-5	Sequence 5, Appli	c 623	10	47.6	17	4	US-09-371-772B-6370	Sequence 6370, Ap
C 551	10.2	48.6	27	3	US-08-584-040-666	Sequence 666, App	c 624	10	47.6	18	3	US-08-584-040-4467	Sequence 4467, Ap
C 552	10.2	48.6	27	3	US-08-584-040-1419	Sequence 1419, Ap	c 625	10	47.6	18	4	US-09-371-772B-2180	Sequence 2180, Ap
C 553	10.2	48.6	27	3	US-08-584-040-3300	Sequence 3300, Ap	c 626	10	47.6	20	1	US-07-767-135-15	Sequence 15, Appli
C 554	10.2	48.6	27	3	US-08-584-040-6284	Sequence 6284, Ap	c 627	10	47.6	20	1	US-07-841-652-22	Sequence 22, Appli
C 555	10.2	48.6	27	3	US-08-584-040-6348	Sequence 6348, Ap	c 628	10	47.6	20	4	US-09-422-978-9310	Sequence 9310, Ap
C 556	10.2	48.6	29	3	US-08-612-973-94	Sequence 94, Appli	c 629	10	47.6	20	4	US-09-198-452A-3752	Sequence 3752, Ap
C 557	10.2	48.6	29	3	US-08-927-537-94	Sequence 94, Appli	c 630	10	47.6	21	3	US-09-203-231B-87	Sequence 87, Appli
C 558	10.2	48.6	31	4	US-09-530-157B-5	Sequence 5, Appli	c 631	10	47.6	22	1	US-08-482-577B-29	Sequence 29, Appli
C 559	10.2	48.6	33	1	US-08-624-545-11	Sequence 11, Appli	c 632	10	47.6	22	2	US-08-288-508C-20	Sequence 20, Appli
C 560	10.2	48.6	33	3	US-09-168-406A-12	Sequence 12, Appli	c 633	10	47.6	22	3	US-08-289-222E-33	Sequence 33, Appli
C 561	10.2	48.6	35	3	US-08-507-426C-12	Sequence 12, Appli	c 634	10	47.6	22	3	US-09-218-176-12	Sequence 12, Appli
C 562	10.2	48.6	35	4	US-09-705-014-12	Sequence 12, Appli	c 635	10	47.6	22	3	US-09-054-526B-33	Sequence 33, Appli
C 563	10.2	48.6	35	4	US-08-894-799-30	Sequence 30, Appli	c 636	10	47.6	22	3	US-08-943-731-238	Sequence 238, App
C 564	10.2	48.6	36	1	US-08-604-913B-5	Sequence 5, Appli	c 637	10	47.6	24	4	US-09-386-4500-20	Sequence 20, Appli
C 565	10.2	48.6	36	1	US-08-604-913B-8	Sequence 8, Appli	c 638	10	47.6	24	1	US-08-117-329-1	Sequence 1, Appli
C 566	10.2	48.6	36	3	US-08-358-627F-27	Sequence 27, Appli	c 639	10	47.6	24	3	US-09-016-542-6	Sequence 6, Appli
C 567	10.2	48.6	36	4	US-08-465-712C-27	Sequence 27, Appli	c 640	10	47.6	24	3	US-09-540-699-2	Sequence 2, Appli
C 568	10.2	48.6	36	4	US-09-552-733-27	Sequence 27, Appli	c 641	10	47.6	24	3	US-09-540-699-3	Sequence 3, Appli
C 569	10.2	48.6	36	4	US-09-293-427-33	Sequence 33, Appli	c 642	10	47.6	24	4	US-09-404-448-4	Sequence 4, Appli
C 570	10.2	48.6	36	4	US-09-349-925-27	Sequence 27, Appli	c 643	10	47.6	27	1	US-08-400-256-10	Sequence 10, Appli
C 571	10.2	48.6	37	1	US-08-276-852-133	Sequence 133, App	c 644	10	47.6	27	1	US-08-578-649-9	Sequence 9, Appli
C 572	10.2	48.6	37	1	US-08-276-852-134	Sequence 134, App	c 645	10	47.6	27	2	US-08-997-080-131	Sequence 131, App
C 573	10.2	48.6	37	1	US-08-899-575-133	Sequence 133, App	c 646	10	47.6	27	2	US-08-997-362-131	Sequence 131, App
C 574	10.2	48.6	37	1	US-08-899-575-134	Sequence 134, App	c 647	10	47.6	27	3	US-08-975-365-10	Sequence 10, Appli
C 575	10.2	48.6	37	1	US-08-899-575-133	Sequence 133, App	c 648	10	47.6	27	3	US-09-055-855-131	Sequence 131, App
C 576	10.2	48.6	37	1	US-08-899-575-134	Sequence 134, App	c 649	10	47.6	27	3	US-09-324-542-131	Sequence 131, App
C 577	10.2	48.6	37	3	US-08-961-083-310	Sequence 310, App	c 650	10	47.6	27	4	US-09-205-426-131	Sequence 131, App
C 578	10.2	48.6	37	4	US-09-470-661A-31	Sequence 31, Appli	c 651	10	47.6	30	1	US-08-545-562A-54	Sequence 54, Appli
C 579	10.2	48.6	37	4	US-09-536-784-310	Sequence 310, App	c 652	10	47.6	31	2	US-08-145-061-15	Sequence 15, Appli
C 580	10.2	48.6	37	5	PCT-US95-08743-133	Sequence 133, App	c 653	10	47.6	33	1	US-08-184-607-3	Sequence 3, Appli
C 581	10.2	48.6	37	5	PCT-US95-08743-134	Sequence 134, App	c 654	10	47.6	33	1	US-08-184-607-4	Sequence 4, Appli
C 582	10.2	48.6	38	1	US-08-373-124A-957	Sequence 957, App	c 655	10	47.6	33	4	US-09-813-781-127	Sequence 127, App
C 583	10.2	48.6	38	1	US-08-435-628-957	Sequence 957, App	c 656	10	47.6	35	2	US-08-965-780-2	Sequence 2, Appli
C 584	10.2	48.6	38	4	US-09-474-432B-1045	Sequence 1045, App	c 657	10	47.6	35	3	US-08-458-237-1	Sequence 1, Appli
C 585	10.2	48.6	38	4	US-09-371-772B-7784	Sequence 7784, Ap	c 658	10	47.6	35	3	US-08-458-237-3	Sequence 3, Appli
C 586	10.2	48.6	38	4	US-09-371-772B-8516	Sequence 8516, Ap	c 659	10	47.6	35	3	US-08-458-237-4	Sequence 4, Appli
C 587	10.2	48.6	38	4	US-09-371-772B-8869	Sequence 8869, App	c 660	10	47.6	35	3	US-08-458-237-5	Sequence 5, Appli
C 588	10.2	48.6	38	4	US-09-371-772B-10175	Sequence 10175, A	c 661	10	47.6	35	3	US-08-458-237-6	Sequence 6, Appli
C 589	10.2	48.6	38	4	US-09-371-772B-10234	Sequence 10234, A	c 662	10	47.6	35	3	US-08-458-237-7	Sequence 7, Appli
C 590	10.2	48.6	38	4	US-09-371-772B-11439	Sequence 11439, A	c 663	10	47.6	35	3	US-08-458-237-8	Sequence 8, Appli
C 591	10.2	48.6	38	4	US-09-371-772B-13916	Sequence 13916, A	c 664	10	47.6	35	3	US-08-458-237-9	Sequence 9, Appli
C 592	10.2	48.6	38	4	US-09-476-387-1044	Sequence 1044, App	c 665	10	47.6	35	3	US-08-458-237-10	Sequence 10, Appli
C 593	10.2	48.6	38	4	US-09-874-547-66	Sequence 66, Appli	c 666	10	47.6	35	3	US-08-458-237-11	Sequence 11, Appli
C 594	10.2	48.6	38	4	US-09-874-547-77	Sequence 77, Appli	c 667	10	47.6	35	3	US-08-458-237-12	Sequence 12, Appli
C 595	10.2	48.6	39	5	PCT-US95-03866-26	Sequence 26, Appli	c 668	10	47.6	35	3	US-08-458-237-13	Sequence 13, Appli
C 596	10.2	48.6	40	1	US-07-931-473B-153	Sequence 153, App	c 669	10	47.6	35	3	US-09-149-727-28	Sequence 28, Appli
C 597	10.2	48.6	40	1	US-07-714-131C-153	Sequence 153, App	c 670	10	47.6	35	4	US-09-270-957-67	Sequence 67, Appli
C 598	10.2	48.6	40	1	US-08-412-110-153	Sequence 153, App	c 671	10	47.6	35	4	US-08-459-340-2	Sequence 2, Appli
C 599	10.2	48.6	40	1	US-08-409-442A-153	Sequence 153, App	c 672	10	47.6	35	4	US-08-459-340-3	Sequence 3, Appli
C 600	10.2	48.6	40	2	US-08-469-609A-153	Sequence 153, App	c 673	10	47.6	35	4	US-08-459-340-4	Sequence 4, Appli
C 601	10.2	48.6	40	2	US-08-324-362-1	Sequence 1, Appli	c 674	10	47.6	35	4	US-08-459-340-5	Sequence 5, Appli
C 602	10.2	48.6	40	2	US-08-324-362-2	Sequence 2, Appli	c 675	10	47.6	35	4	US-08-459-340-6	Sequence 6, Appli
C 603	10.2	48.6	40	3	US-09-143-190-153	Sequence 153, App	c 676	10	47.6	35	4	US-08-459-340-7	Sequence 7, Appli
C 604	10.2	48.6	40	3	US-09-448-478-12	Sequence 12, Appli	c 677	10	47.6	35	4	US-08-459-340-8	Sequence 8, Appli
C 605	10.2	48.6	40	3	US-09-502-344-153	Sequence 153, App	c 678	10	47.6	35	4	US-08-459-340-9	Sequence 9, Appli
C 606	10.2	48.6	44	3	US-09-448-478-11	Sequence 11, Appli	c 679	10	47.6	35	4	US-08-459-340-10	Sequence 10, Appli
C 607	10.2	48.6	45	3	US-09-177-268-2	Sequence 2, Appli	c 680	10	47.6	35	4	US-08-459-340-11	Sequence 11, Appli
C 608	10.2	48.6	45	4	US-09-656-010-2	Sequence 2, Appli	c 681	10	47.6	35	4	US-08-459-340-12	Sequence 12, Appli
C 609	10.2	48.6	45	4	US-09-907-794A-305	Sequence 305, App	c 682	10	47.6	35	4	US-08-459-340-13	Sequence 13, Appli
C 610	10.2	48.6	45	4	US-09-905-125A-305	Sequence 305, App	c 683	10	47.6	35	5	PCT-US93-07603-12	Sequence 12, Appli
C 611	10.2	48.6	45	4	US-09-902-775A-305	Sequence 305, App	c 684	10	47.6	35	5	PCT-US93-07603-13	Sequence 13, Appli

685	10	47.6	10	47.6	10	758	10	47.6	38	4	US-09-371-772B-9051	Sequence 9051, Ap
686	10	47.6	10	47.6	10	759	10	47.6	38	4	US-09-371-772B-9092	Sequence 9092, Ap
c 687	10	47.6	10	47.6	10	760	10	47.6	38	4	US-09-371-772B-9093	Sequence 9093, Ap
c 688	10	47.6	10	47.6	10	761	10	47.6	38	4	US-09-371-772B-9099	Sequence 9099, Ap
c 689	10	47.6	10	47.6	10	762	10	47.6	38	4	US-09-371-772B-9111	Sequence 9111, Ap
c 690	10	47.6	10	47.6	10	763	10	47.6	38	4	US-09-371-772B-9141	Sequence 9141, Ap
691	10	47.6	10	47.6	10	764	10	47.6	38	4	US-09-371-772B-9166	Sequence 9166, Ap
692	10	47.6	10	47.6	10	765	10	47.6	38	4	US-09-371-772B-9195	Sequence 9195, Ap
693	10	47.6	10	47.6	10	766	10	47.6	38	4	US-09-371-772B-9196	Sequence 9196, Ap
694	10	47.6	10	47.6	10	767	10	47.6	38	4	US-09-371-772B-9255	Sequence 9255, Ap
695	10	47.6	10	47.6	10	768	10	47.6	38	4	US-09-371-772B-9273	Sequence 9273, Ap
696	10	47.6	10	47.6	10	769	10	47.6	38	4	US-09-371-772B-9283	Sequence 9283, Ap
697	10	47.6	10	47.6	10	770	10	47.6	38	4	US-09-371-772B-9304	Sequence 9304, Ap
698	10	47.6	10	47.6	10	771	10	47.6	38	4	US-09-371-772B-9369	Sequence 9369, Ap
699	10	47.6	10	47.6	10	772	10	47.6	38	4	US-09-371-772B-9381	Sequence 9381, Ap
700	10	47.6	10	47.6	10	773	10	47.6	38	4	US-09-371-772B-9389	Sequence 9389, Ap
701	10	47.6	10	47.6	10	774	10	47.6	38	4	US-09-371-772B-9390	Sequence 9390, Ap
702	10	47.6	10	47.6	10	775	10	47.6	38	4	US-09-371-772B-9404	Sequence 9404, Ap
703	10	47.6	10	47.6	10	776	10	47.6	38	4	US-09-371-772B-9429	Sequence 9429, Ap
704	10	47.6	10	47.6	10	777	10	47.6	38	4	US-09-371-772B-9470	Sequence 9470, Ap
c 705	10	47.6	10	47.6	10	778	10	47.6	38	4	US-09-371-772B-9477	Sequence 9477, Ap
706	10	47.6	10	47.6	10	779	10	47.6	38	4	US-09-371-772B-9496	Sequence 9496, Ap
707	10	47.6	10	47.6	10	780	10	47.6	38	4	US-09-371-772B-9503	Sequence 9503, Ap
708	10	47.6	10	47.6	10	781	10	47.6	38	4	US-09-371-772B-9504	Sequence 9504, Ap
709	10	47.6	10	47.6	10	782	10	47.6	38	4	US-09-371-772B-9557	Sequence 9557, Ap
710	10	47.6	10	47.6	10	783	10	47.6	38	4	US-09-371-772B-9593	Sequence 9593, Ap
711	10	47.6	10	47.6	10	784	10	47.6	38	4	US-09-371-772B-9594	Sequence 9594, Ap
712	10	47.6	10	47.6	10	785	10	47.6	38	4	US-09-371-772B-9597	Sequence 9597, Ap
713	10	47.6	10	47.6	10	786	10	47.6	38	4	US-09-371-772B-9630	Sequence 9630, Ap
714	10	47.6	10	47.6	10	787	10	47.6	38	4	US-09-371-772B-9639	Sequence 9639, Ap
715	10	47.6	10	47.6	10	788	10	47.6	38	4	US-09-371-772B-9659	Sequence 9659, Ap
716	10	47.6	10	47.6	10	789	10	47.6	38	4	US-09-371-772B-9663	Sequence 9663, Ap
717	10	47.6	10	47.6	10	790	10	47.6	38	4	US-09-371-772B-9712	Sequence 9712, Ap
718	10	47.6	10	47.6	10	791	10	47.6	38	4	US-09-371-772B-9717	Sequence 9717, Ap
719	10	47.6	10	47.6	10	792	10	47.6	38	4	US-09-371-772B-9770	Sequence 9770, Ap
720	10	47.6	10	47.6	10	793	10	47.6	38	4	US-09-371-772B-9777	Sequence 9777, Ap
721	10	47.6	10	47.6	10	794	10	47.6	38	4	US-09-371-772B-9782	Sequence 9782, Ap
722	10	47.6	10	47.6	10	795	10	47.6	38	4	US-09-371-772B-9788	Sequence 9788, Ap
723	10	47.6	10	47.6	10	796	10	47.6	38	4	US-09-371-772B-9798	Sequence 9798, Ap
724	10	47.6	10	47.6	10	797	10	47.6	38	4	US-09-371-772B-9833	Sequence 9833, Ap
725	10	47.6	10	47.6	10	798	10	47.6	38	4	US-09-371-772B-9876	Sequence 9876, Ap
726	10	47.6	10	47.6	10	799	10	47.6	38	4	US-09-371-772B-9891	Sequence 9891, Ap
727	10	47.6	10	47.6	10	800	10	47.6	38	4	US-09-371-772B-9898	Sequence 9898, Ap
728	10	47.6	10	47.6	10	801	10	47.6	38	4	US-09-371-772B-9901	Sequence 9901, Ap
729	10	47.6	10	47.6	10	802	10	47.6	38	4	US-09-371-772B-9923	Sequence 9923, Ap
730	10	47.6	10	47.6	10	803	10	47.6	38	4	US-09-371-772B-9960	Sequence 9960, Ap
731	10	47.6	10	47.6	10	804	10	47.6	38	4	US-09-371-772B-9968	Sequence 9968, Ap
732	10	47.6	10	47.6	10	805	10	47.6	38	4	US-09-371-772B-9970	Sequence 9970, Ap
733	10	47.6	10	47.6	10	806	10	47.6	38	4	US-09-371-772B-9978	Sequence 9978, Ap
734	10	47.6	10	47.6	10	807	10	47.6	38	4	US-09-371-772B-9987	Sequence 9987, Ap
735	10	47.6	10	47.6	10	808	10	47.6	38	4	US-09-371-772B-10010	Sequence 10010, A
736	10	47.6	10	47.6	10	809	10	47.6	38	4	US-09-371-772B-10023	Sequence 10023, A
737	10	47.6	10	47.6	10	810	10	47.6	38	4	US-09-371-772B-10035	Sequence 10035, A
738	10	47.6	10	47.6	10	811	10	47.6	38	4	US-09-371-772B-10035	Sequence 10035, A
739	10	47.6	10	47.6	10	812	10	47.6	38	4	US-09-371-772B-10178	Sequence 10178, A
740	10	47.6	10	47.6	10	813	10	47.6	38	4	US-09-371-772B-10178	Sequence 10178, A
741	10	47.6	10	47.6	10	814	10	47.6	38	4	US-09-371-772B-10231	Sequence 10231, A
742	10	47.6	10	47.6	10	815	10	47.6	38	4	US-09-371-772B-10249	Sequence 10249, A
743	10	47.6	10	47.6	10	816	10	47.6	38	4	US-09-371-772B-10266	Sequence 10266, A
744	10	47.6	10	47.6	10	817	10	47.6	38	4	US-09-371-772B-10271	Sequence 10271, A
745	10	47.6	10	47.6	10	818	10	47.6	38	4	US-09-371-772B-10290	Sequence 10290, A
746	10	47.6	10	47.6	10	819	10	47.6	38	4	US-09-371-772B-10320	Sequence 10320, A
747	10	47.6	10	47.6	10	820	10	47.6	38	4	US-09-371-772B-10338	Sequence 10338, A
748	10	47.6	10	47.6	10	821	10	47.6	38	4	US-09-371-772B-10420	Sequence 10420, A
749	10	47.6	10	47.6	10	822	10	47.6	38	4	US-09-371-772B-10452	Sequence 10452, A
750	10	47.6	10	47.6	10	823	10	47.6	38	4	US-09-371-772B-10464	Sequence 10464, A
751	10	47.6	10	47.6	10	824	10	47.6	38	4	US-09-371-772B-10495	Sequence 10495, A
752	10	47.6	10	47.6	10	825	10	47.6	38	4	US-09-371-772B-10513	Sequence 10513, A
753	10	47.6	10	47.6	10	826	10	47.6	38	4	US-09-371-772B-10525	Sequence 10525, A
754	10	47.6	10	47.6	10	827	10	47.6	38	4	US-09-371-772B-10548	Sequence 10548, A
755	10	47.6	10	47.6	10	828	10	47.6	38	4	US-09-371-772B-10551	Sequence 10551, A
756	10	47.6	10	47.6	10	829	10	47.6	38	4	US-09-371-772B-10553	Sequence 10553, A
757	10	47.6	10	47.6	10	830	10	47.6	38	4	US-09-371-772B-10554	Sequence 10554, A

831	10	47.6	38	4	US-09-371-772B-10621	A	Sequence 10621	A	904	10	47.6	38	4	US-09-371-772B-12011	A	Sequence 12011
832	10	47.6	38	4	US-09-371-772B-10642	A	Sequence 10642	A	905	10	47.6	38	4	US-09-371-772B-12015	A	Sequence 12015
833	10	47.6	38	4	US-09-371-772B-10651	A	Sequence 10651	A	906	10	47.6	38	4	US-09-371-772B-12058	A	Sequence 12058
834	10	47.6	38	4	US-09-371-772B-10661	A	Sequence 10661	A	907	10	47.6	38	4	US-09-371-772B-12064	A	Sequence 12064
835	10	47.6	38	4	US-09-371-772B-10672	A	Sequence 10672	A	908	10	47.6	38	4	US-09-371-772B-12071	A	Sequence 12071
836	10	47.6	38	4	US-09-371-772B-10685	A	Sequence 10685	A	909	10	47.6	38	4	US-09-371-772B-12076	A	Sequence 12076
837	10	47.6	38	4	US-09-371-772B-10687	A	Sequence 10687	A	910	10	47.6	38	4	US-09-371-772B-12077	A	Sequence 12077
838	10	47.6	38	4	US-09-371-772B-10703	A	Sequence 10703	A	911	10	47.6	38	4	US-09-371-772B-12085	A	Sequence 12085
839	10	47.6	38	4	US-09-371-772B-10719	A	Sequence 10719	A	912	10	47.6	38	4	US-09-371-772B-12087	A	Sequence 12087
840	10	47.6	38	4	US-09-371-772B-10727	A	Sequence 10727	A	913	10	47.6	38	4	US-09-371-772B-12089	A	Sequence 12089
841	10	47.6	38	4	US-09-371-772B-10765	A	Sequence 10765	A	914	10	47.6	38	4	US-09-371-772B-12091	A	Sequence 12091
842	10	47.6	38	4	US-09-371-772B-10771	A	Sequence 10771	A	915	10	47.6	38	4	US-09-371-772B-12103	A	Sequence 12103
843	10	47.6	38	4	US-09-371-772B-10775	A	Sequence 10775	A	916	10	47.6	38	4	US-09-371-772B-12104	A	Sequence 12104
844	10	47.6	38	4	US-09-371-772B-10834	A	Sequence 10834	A	917	10	47.6	38	4	US-09-371-772B-12112	A	Sequence 12112
845	10	47.6	38	4	US-09-371-772B-10838	A	Sequence 10838	A	918	10	47.6	38	4	US-09-371-772B-12125	A	Sequence 12125
846	10	47.6	38	4	US-09-371-772B-10848	A	Sequence 10848	A	919	10	47.6	38	4	US-09-371-772B-12149	A	Sequence 12149
847	10	47.6	38	4	US-09-371-772B-10893	A	Sequence 10893	A	920	10	47.6	38	4	US-09-371-772B-12153	A	Sequence 12153
848	10	47.6	38	4	US-09-371-772B-10916	A	Sequence 10916	A	921	10	47.6	38	4	US-09-371-772B-12157	A	Sequence 12157
849	10	47.6	38	4	US-09-371-772B-10928	A	Sequence 10928	A	922	10	47.6	38	4	US-09-371-772B-12175	A	Sequence 12175
850	10	47.6	38	4	US-09-371-772B-10934	A	Sequence 10934	A	923	10	47.6	38	4	US-09-371-772B-12196	A	Sequence 12196
851	10	47.6	38	4	US-09-371-772B-10937	A	Sequence 10937	A	924	10	47.6	38	4	US-09-371-772B-12218	A	Sequence 12218
852	10	47.6	38	4	US-09-371-772B-10979	A	Sequence 10979	A	925	10	47.6	38	4	US-09-371-772B-12275	A	Sequence 12275
853	10	47.6	38	4	US-09-371-772B-10984	A	Sequence 10984	A	926	10	47.6	38	4	US-09-371-772B-12318	A	Sequence 12318
854	10	47.6	38	4	US-09-371-772B-10986	A	Sequence 10986	A	927	10	47.6	38	4	US-09-371-772B-12356	A	Sequence 12356
855	10	47.6	38	4	US-09-371-772B-10994	A	Sequence 10994	A	928	10	47.6	38	4	US-09-371-7		

Sequence 13998, A
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Sequence 62, Appl
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Sequence 69, Appl
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Sequence 80, Appl
Sequence 12, Appl
Sequence 25, Appl
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Sequence 25, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 1188, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 2881, Appl

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10 47.6 38 4 US-09-874-547-62
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10 47.6 38 4 US-09-874-547-80
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10 47.6 39 3 US-09-136-574A-12
10 47.6 40 1 US-08-422-101-25
10 47.6 40 1 US-08-422-091-25
10 47.6 40 2 US-08-422-092-25
10 47.6 40 3 US-08-422-093-25
10 47.6 40 3 US-08-422-112-25
10 47.6 40 3 US-09-416-050A-62
10 47.6 40 3 US-09-664-800-62
10 47.6 40 3 US-09-665-309-62
10 47.6 40 3 US-09-661-569-62
10 47.6 40 4 US-09-538-709-1188
10 47.6 49 1 US-07-615-448A-9
10 47.6 49 1 US-08-196-361-9
10 47.6 49 2 US-08-446-934-9
10 47.6 49 2 US-08-448-128-9
10 47.6 49 3 US-08-948-703-9
10 47.6 50 4 US-08-956-171E-2881

ALIGNMENTS

RESULT 1
US-09-056-052-12
; Sequence 12, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-056-052-12

Query Match 62.9%; Score 13.2; DB 3; Length 35;
Best Local Similarity 83.3%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTACGCG 20
||| ||||| |||||
Db 10 GTCGTTAGAACGACGCG 27

RESULT 2
US-09-056-052-13/c
; Sequence 13, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; NAME/KEY: misc feature
; LOCATION: (1)..(4)
; OTHER INFORMATION: 'n' can be any base A, T, G, or C
US-09-056-052-13

Query Match 62.9%; Score 13.2; DB 3; Length 39;
Best Local Similarity 83.3%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTACGCG 20
||| ||||| |||||
Db 30 GTCGTTAGAACGACGCG 13

RESULT 3
US-09-131-028A-17/c
; Sequence 17, Application US/09131028A
; Patent No. 6287866
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Lemmer, Steven A.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Chaudhary, Sunita
; TITLE OF INVENTION: BETA-CASEIN EXPRESSING CONSTRUCTS
; FILE REFERENCE: 6004.US.P1
; CURRENT APPLICATION NUMBER: US/09/131,028A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: US 08/064,440
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer RO204
US-09-131-028A-17

Query Match 60.0%; Score 12.6; DB 3; Length 31;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGCG 19
||| ||||| |||||
Db 30 CGCTCATGAGACAGTACTC 12

RESULT 4
US-08-207-481-29/c
; Sequence 29, Application US/08207481
; Patent No. 5820866
; GENERAL INFORMATION:
; APPLICANT: Kappler, John W.
; APPLICANT: Marrack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL
; TITLE OF INVENTION: REGULATION
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA

```
;
;
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,481
; FILING DATE: 04-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-207-481-29

Query Match 60.0%; Score 12.6; DB 1; Length 33;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCAATTAGACCGTACGC 19
Db 20 CGTTCATTGTTCTGTCACGC 2

RESULT 5
PCT-US95-02689-31/c
; Sequence 31, Application PC/TUS9502689
; GENERAL INFORMATION:
; APPLICANT: National Jewish Center for Immunology and
; APPLICANT: Respiratory Medicine
; APPLICANT: Kappler, John W.
; APPLICANT: Marrack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02689
; FILING DATE: 03-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PCT-US95-02689-31

Query Match 60.0%; Score 12.6; DB 5; Length 33;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCAATTAGACCGTACGC 19
Db 20 CGTTCATTGTTCTGTCACGC 2

RESULT 6
US-09-371-772B-11935
; Sequence 11935, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11935
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
; US-09-371-772B-11935

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21
Db 16 GGCCGUUAGGCCGAANGCGA 35

RESULT 7
US-09-371-772B-13181
; Sequence 13181, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
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FILE REFERENCE: 020144-001110US
CURRENT APPLICATION NUMBER: US/09/874,547
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/209,503
PRIOR FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 83
LENGTH: 38
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (31)-(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-13181

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21
||| :||| ||| ||| |||
Db 16 GGCCGUAGGCCGAANGCGA 35

RESULT 8

US-09-371-772B-13811
Sequence 13811, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MH800,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13811
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc feature
LOCATION: (31)-(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-13811

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21
||| :||| ||| ||| |||
Db 16 GGCCGUAGGCCGAANGCGA 35

RESULT 9

US-09-874-547-83/C
Sequence 83, Application US/09874547
Patent No. 6686154
GENERAL INFORMATION:
APPLICANT: No. 6686154k, Steffen
APPLICANT: Kassner, Paul D.
APPLICANT: Zyomvix, Inc.
TITLE OF INVENTION: Screening of Phage Displayed Peptides
TITLE OF INVENTION: Without Clearing of the Cell Culture

FILE REFERENCE: 020144-001110US
CURRENT APPLICATION NUMBER: US/09/874,547
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/209,503
PRIOR FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 83
LENGTH: 38
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primers for ScFv and Fab library generation (Table
OTHER INFORMATION: I) - MVK24
US-09-874-547-83

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 78.9%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCG 20
||| ||| ||| ||| ||| |||
Db 30 GGTCATTACATGTCGCG 12

RESULT 10

US-08-373-124A-1680/c
Sequence 1680, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1680:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;
Best Local Similarity 92.9%; Pred. No. 8.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTAC 17
|||||
Db 15 TCATCAGACCGTAC 2

RESULT 11

US-08-435-628-1680/c

; Sequence 1680, Application US/08435628

; Patent No. 5817796

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Draper, Kenneth

; APPLICANT: McSwiggen, James

; APPLICANT: Jarvis, Thale

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

; TITLE OF INVENTION: CANCER USING RIBOZYMES

; NUMBER OF SEQUENCES: 2627

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/435,628

; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/373,124

; FILING DATE: January 13, 1995

; APPLICATION NUMBER: 08/245,466

; FILING DATE: May 18, 1994

; APPLICATION NUMBER: 08/192,943

; FILING DATE: February 7, 1994

; APPLICATION NUMBER: 07/987,132

; FILING DATE: December 7, 1992

; APPLICATION NUMBER: 07/936,422

; FILING DATE: August 26, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/035

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1680:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-435-628-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;
Best Local Similarity 92.9%; Pred. No. 8.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTAC 17
|||||
Db 15 TCATCAGACCGTAC 2

RESULT 12

US-09-198-452A-4954/c

; Sequence 4954, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4954

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4954

Query Match 58.1%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTACGCG 20
|||||
Db 18 TCATTATAGCGTCCGCG 2

RESULT 13

5451502-8/c

; Patent No. 5451502

; APPLICANT: GEORGE JR., ALBERT L.

; TITLE OF INVENTION: RESTRICTION AMPLIFICATION ASSAY

; NUMBER OF SEQUENCES: 18

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/114,997

; FILING DATE: 31-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 998,644

; FILING DATE: 16-DEC-1992

; APPLICATION NUMBER: 790,174

; FILING DATE: 12-NOV-1991

; APPLICATION NUMBER: 519,146

; FILING DATE: 04-MAY-1990

; SEQ ID NO:8:

; LENGTH: 21

5451502-8

Query Match 58.1%; Score 12.2; DB 6; Length 21;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATTAGACCGTACGCGA 21
|||||
Db 21 CATTGACCTTATCGGA 5

RESULT 14

US-09-313-221A-19

; Sequence 19, Application US/09313221A

; Patent No. 6468743

; GENERAL INFORMATION:

; APPLICANT: Thomas L. Romick (Inventor)

APPLICANT: Mark S. Fraser (Inventor)
 TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
 TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
 FILE REFERENCE: HUNT-042784
 CURRENT APPLICATION NUMBER: US/09/313,221A
 PRIOR FILING DATE: 1999-05-17
 PRIOR APPLICATION NUMBER: US 60/086,025
 PRIOR FILING DATE: 1998-05-18
 NUMBER OF SEQ ID NOS: 145
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 19
 LENGTH: 41
 TYPE: DNA
 ORGANISM: Escherichia coli
 US-09-313-221A-19

Query Match 58.1%; Score 12.2; DB 4; Length 41;
 Best Local Similarity 82.4%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATTAGACCGTACGCGA 21
 ||||| ||||| |||||
 Db 8 CATTATACCGTCCCGA 24

RESULT 15
 US-08-860-882A-75
 Sequence 75, Application US/08860882A
 Patent No. 5985281
 GENERAL INFORMATION:

APPLICANT: TAYLORSON, CHRISTOPHER JOHN
 APPLICANT: EGGELTE, HENDRIKUS JOHANNES
 APPLICANT: TARRAGONA-FIOL, ANTONIO
 APPLICANT: RABIN, BRIAN ROBERT
 APPLICANT: BOYLE, FRANCIS THOMAS
 APPLICANT: HENNAM, JOHN FREDERICK
 APPLICANT: BLAKELY, DAVID CHARLES
 APPLICANT: MARSHAM, PETER ROBERT
 APPLICANT: HEATON, DAVID WILLIAM
 APPLICANT: DAVIES, DAVID HUW
 TITLE OF INVENTION: CHEMICAL COMPOUNDS
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:

ADDRESS: PILLSBURY, MADISON & SUTRO
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/860.882A
 FILING DATE: JUNE 23, 1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: DONALD J. BIRD
 REGISTRATION NUMBER: 25,323
 REFERENCE/DOCKET NUMBER: 9901/238653
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3027
 TELEFAX: (202) 822-0944
 TELEX: 6174627 CUSH

INFORMATION FOR SEQ ID NO: 75:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-860-882A-75

Query Match 57.1%; Score 12; DB 2; Length 25;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCGA 21
 ||||| ||||| |||||
 Db 1 GGTCATAAGCCCGTACGCGA 20

RESULT 16
 US-09-011-769A-61
 Sequence 61, Application US/09011769A
 Patent No. 6436691
 GENERAL INFORMATION:
 APPLICANT: SLATER, Anthony M.
 APPLICANT: BLAKLEY, David C.
 APPLICANT: DAVIES, David H.
 APPLICANT: HENNAM, John F.
 APPLICANT: HENNEQUIN, Laurent F.A.
 APPLICANT: MARSHAM, Peter R.
 APPLICANT: DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds
 NUMBER OF SEQUENCES: 87
 CORRESPONDENCE ADDRESS:
 ADDRESS: Pillsbury Madison & Sutro, LLP
 STREET: 1100 New York Ave., N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: 1.44 Mb disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/011,769A
 FILING DATE: 13-Feb-1998
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB96/01975
 FILING DATE: 13-AUG-1996
 APPLICATION NUMBER: GB 9612295.7
 FILING DATE: 12-JUN-1996
 APPLICATION NUMBER: GB 9611019.2
 FILING DATE: 25-MAY-1996
 APPLICATION NUMBER: GB 9516810.0
 FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 SEQUENCE DESCRIPTION: SEQ ID NO: 61:
 US-09-011-769A-61

Query Match 57.1%; Score 12; DB 4; Length 25;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCGA 21
 ||||| ||||| |||||
 Db 1 GGTCATAAGCCCGTACGCGA 20

RESULT 17
 US-09-814-351-25
 Sequence 25, Application US/09814351
 Patent No. 6692736
 GENERAL INFORMATION:

APPLICANT: Yu, De-Chao
APPLICANT: Li, Yuanhao
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
FILE REFERENCE: 348022001700
CURRENT APPLICATION NUMBER: US/09/814,351
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/192,156
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human UPII (PCR primer 127.2.1)
US-09-814-351-25

Query Match 57.1%; Score 12; DB 4; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACCGC 20
Db 6 CGGTCATTATAGGCGACCG 25

RESULT 18

US-09-709-103-34
Sequence 34, Application US/09709103
Patent No. 6733991
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
FILE REFERENCE: 60388-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/709,103
CURRENT FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Probe/Primer
US-09-709-103-34

Query Match 57.1%; Score 12; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACCGCA 21
Db 2 GGTCAATGAACCTGGCGCGCA 21

RESULT 19

US-09-439-410A-34
Sequence 34, Application US/09439410A
Patent No. 6746852
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: 1919/60388-B
CURRENT APPLICATION NUMBER: US/09/439,410A
CURRENT FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34

LENGTH: 32
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Probe/Primer
US-09-439-410A-34

Query Match 57.1%; Score 12; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACCGCA 21
Db 2 GGTCAATGAACCTGGCGCGCA 21

RESULT 20

US-09-371-772B-7357
Sequence 7357, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
FILE REFERENCE: MEHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7357
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7357

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACCGCA 21
Db 16 GGCGGUAGGCGCGAAGCGCA 35

RESULT 21

US-09-371-772B-7797
Sequence 7797, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
FILE REFERENCE: MEHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08

```
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7797
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7797

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCGA 21
   |||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 22
US-09-371-772B-8104
; Sequence 8104, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8104
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8104

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCGA 21
   |||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 23
US-09-371-772B-8341
; Sequence 8341, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
```

```
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8341
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8341

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCGA 21
   |||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 24
US-09-371-772B-9392
; Sequence 9392, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9392
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9392

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCGA 21
   |||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 25
US-09-371-772B-9781
; Sequence 9781, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
```


; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9781
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9781

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21
|||::|||
Db 16 GGCCGUUAGCGCGAAGCGA 35

RESULT 26
US-09-371-772B-9974
; Sequence 9974, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9974
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9974

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21
|||::|||
Db 16 GGCCGUUAGCGCGAAGCGA 35

RESULT 27
US-09-371-772B-10321
; Sequence 10321, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10321
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10321

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21
|||::|||
Db 16 GGCCGUUAGCGCGAAGCGA 35

RESULT 28
US-09-371-772B-10352
; Sequence 10352, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10352
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10352

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21
|||::|||
Db 16 GGCCGUUAGCGCGAAGCGA 35

RESULT 29
US-09-371-772B-10512
; Sequence 10512, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/1198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10512
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10512

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTAGCGGA 21
|||:|||||
Db 16 GGCCGUUAGCGCAAGGAG 35

RESULT 30
US-09-172-045-20/c
; Sequence 20, Application US/09172045
; Patent No. 6277594
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Nakata, Katsunori
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: Hiraki-03497
; CURRENT APPLICATION NUMBER: US/09/172,045
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: JP98/86979
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP98/121456
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-172-045-20

Query Match 55.2%; Score 11.6; DB 3; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTAGCGG 20
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Db 20 GTCATTACCGCAAGGAG 3

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; Sequence 20, Application US/09342325C
; Patent No. 6500637
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko

; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Katsunori, Nakata
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: HIRAKI-03814
; CURRENT APPLICATION NUMBER: US/09/342,325C
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: JP98/86979
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: JP98/121456
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 09/172,045
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 64
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-342-325C-20

Query Match 55.2%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTAGCGG 20
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Db 20 GTCATTACCGCAAGGAG 3

RESULT 32
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; Sequence 10, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-056-052-10

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Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTAGCGG 20
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Db 10 GTCGTTAGACGCACTCG 27

RESULT 33
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; Sequence 10, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamamouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332

; APPLICANT: Escobedo, Jaime

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Best Local Similarity	63.2%;	Pred. No. 2.4e+03;		
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RESULT 38
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 ; Sequence 12396, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
 ; FILE REFERENCE: MBHH00, 876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 12396
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ; NAME/KEY: misc feature
 ; LOCATION: (31)..(31)
 ; OTHER INFORMATION: n stands for inosine
 ; US-09-371-772B-12396
 Query Match 55.2%; Score 11.6; DB 4; Length 38;

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Best Local Similarity	63.2%	Pred No. 2	4e+03	
Matches	12	Conservative	2	Mismatches 5; Indels 0; Gaps 0
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ph	16	GGCCGUAAGCCGAANGCG	34	

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; Sequence 13450, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases of Con
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHE900, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13450
; LENGTH: 38
; TYPE: RNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13450

Query Match 55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 63.2%; Pred. NO. 2.4e+03;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCG 20
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Db 16 GGCCGUAGCCGAANGCG 34

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Job time : 25.3034 secs

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OM nucleic - nucleic search, using sw model

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Title: US-10-087-631b-17

Perfect score: 21

Sequence: 1 cggtcattagaccgtacgcga 21

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	21	100.0	21	15	US-10-419-022-17
C 5	14.2	67.6	25	15	US-10-098-263B-56047
C 6	13.6	64.8	29	10	US-09-374-046A-218
C 7	13.6	64.8	29	16	US-10-616-263-218
C 8	13.6	64.8	37	16	US-10-138-674-20182
C 9	13.6	64.8	37	16	US-10-138-674-20479
C 10	13.6	64.8	37	17	US-10-287-949A-20182
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25	15	US-10-098-263B-88853	Sequence 88853, A
25	15	US-10-098-263B-71593	Sequence 71593, A
25	15	US-10-098-263B-71008	Sequence 71008, A
25	15	US-10-098-263B-25744	Sequence 25744, A
25	15	US-10-098-263B-56048	Sequence 56048, A
25	15	US-10-098-263B-118819	Sequence 118819, A
25	15	US-10-098-263B-118820	Sequence 118820, A
36	9	US-09-864-785-3885	Sequence 3885, Ap
37	9	US-09-864-785-1812	Sequence 1812, Ap
37	10	US-09-740-332-9583	Sequence 9583, Ap
37	10	US-09-817-879-9583	Sequence 9583, Ap
37	16	US-10-138-674-18225	Sequence 18225, A
37	16	US-10-138-674-18462	Sequence 18462, A
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37	17	US-10-287-949A-18462	Sequence 18462, A
37	17	US-10-287-949A-20525	Sequence 20525, A
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38	9	US-09-874-547-83	Sequence 83, Appl
38	9	US-09-864-785-1169	Sequence 1169, Ap
38	10	US-09-780-533A-3557	Sequence 3557, Ap
38	10	US-09-780-533A-3581	Sequence 3581, Ap
38	10	US-09-927-046-3026	Sequence 3026, Ap
38	10	US-09-927-046-3197	Sequence 3197, Ap
38	10	US-09-877-478-3764	Sequence 3764, Ap
38	10	US-09-848-754A-5094	Sequence 5094, Ap
38	10	US-09-848-754A-5300	Sequence 5300, Ap
38	15	US-10-230-006-911	Sequence 911, App
38	15	US-10-230-006-1011	Sequence 1011, Ap
38	15	US-10-230-006-1101	Sequence 1101, Ap
38	16	US-10-342-902-3468	Sequence 3468, Ap
38	16	US-10-342-902-3764	Sequence 3764, Ap
38	16	US-10-138-674-14212	Sequence 14212, A
38	16	US-10-138-674-15458	Sequence 15458, A
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38	17	US-10-287-949A-15458	Sequence 15458, A
38	17	US-10-287-949A-16088	Sequence 16088, A
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38	17	US-10-712-672-3746	Sequence 3746, Ap
38	17	US-10-712-672-4185	Sequence 4185, Ap
38	17	US-10-669-841-8359	Sequence 8359, Ap
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37	10	US-09-927-046-3631	Sequence 3631, Ap
37	10	US-09-927-046-3664	Sequence 3664, Ap
37	10	US-09-848-754A-5959	Sequence 5959, Ap
37	10	US-09-848-754A-6388	Sequence 6388, Ap
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25	15	US-10-308-343-2	Sequence 2, Appli
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25	15	US-10-098-263B-3824	Sequence 3824, Ap
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25	15	US-10-098-263B-122296	Sequence 122296, A
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29	10	US-09-814-357-25	Sequence 25, Appl
29	10	US-09-814-351-25	Sequence 25, Appl
32	17	US-10-804-491-34	Sequence 34, Appl

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93	12	57.1	36	9	US-09-274-553D-2066	Sequence 2066, Ap	166	11.6	55.2	25	15	US-10-098-263B-88236	Sequence 88236, A
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c 108	12	57.1	38	10	US-09-927-046-2466	Sequence 2466, Ap	c 181	11.6	55.2	37	16	US-10-138-674-20309	Sequence 20309, A
c 109	12	57.1	38	10	US-09-877-478-2875	Sequence 2875, Ap	c 182	11.6	55.2	37	16	US-10-138-674-20416	Sequence 20416, A
c 110	12	57.1	38	10	US-09-848-754A-4055	Sequence 4055, Ap	c 183	11.6	55.2	37	16	US-10-138-674-20440	Sequence 20440, A
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c 129	12	57.1	38	17	US-10-287-949A-10074	Sequence 10074, A	203	11.6	55.2	38	10	US-09-780-533A-4158	Sequence 4158, Ap
c 130	12	57.1	38	17	US-10-287-949A-10381	Sequence 10381, A	204	11.6	55.2	38	10	US-09-780-533A-4200	Sequence 4200, Ap
c 131	12	57.1	38	17	US-10-287-949A-10618	Sequence 10618, A	205	11.6	55.2	38	10	US-09-927-046-2935	Sequence 2935, Ap
c 132	12	57.1	38	17	US-10-287-949A-11669	Sequence 11669, A	206	11.6	55.2	38	10	US-09-927-046-2993	Sequence 2993, Ap
c 133	12	57.1	38	17	US-10-287-949A-12058	Sequence 12058, A	207	11.6	55.2	38	10	US-09-927-046-3354	Sequence 3354, Ap
c 134	12	57.1	38	17	US-10-287-949A-12251	Sequence 12251, A	208	11.6	55.2	38	10	US-09-927-046-3450	Sequence 3450, Ap
c 135	12	57.1	38	17	US-10-287-949A-12598	Sequence 12598, A	209	11.6	55.2	38	10	US-09-927-046-3569	Sequence 3569, Ap
c 136	12	57.1	38	17	US-10-287-949A-12629	Sequence 12629, A	210	11.6	55.2	38	10	US-09-927-046-3604	Sequence 3604, Ap
c 137	12	57.1	38	17	US-10-287-949A-12789	Sequence 12789, A	211	11.6	55.2	38	10	US-09-927-046-3684	Sequence 3684, Ap
c 138	12	57.1	38	17	US-10-669-841-7766	Sequence 7766, Ap	212	11.6	55.2	38	10	US-09-927-046-3836	Sequence 3836, Ap
c 139	12	57.1	50	15	US-10-173-730-7	Sequence 7, Appl	213	11.6	55.2	38	10	US-09-877-478-3891	Sequence 3891, Ap
c 140	12	57.1	50	16	US-10-062-188-193	Sequence 193, App	214	11.6	55.2	38	10	US-09-877-478-3891	Sequence 3891, Ap
c 141	11.8	56.2	15	9	US-09-504-231A-905	Sequence 905, App	215	11.6	55.2	38	10	US-09-848-754A-4612	Sequence 4612, Ap
c 142	11.8	56.2	15	9	US-09-740-553D-905	Sequence 905, App	216	11.6	55.2	38	10	US-09-848-754A-4622	Sequence 4622, Ap
c 143	11.8	56.2	17	10	US-09-740-332-1151	Sequence 1151, Ap	217	11.6	55.2	38	10	US-09-848-754A-4627	Sequence 4627, Ap
c 144	11.8	56.2	17	10	US-09-817-879-1151	Sequence 1151, Ap	218	11.6	55.2	38	10	US-09-848-754A-4630	Sequence 4630, Ap
c 145	11.8	56.2	17	17	US-10-663-841-3744	Sequence 3744, Ap	219	11.6	55.2	38	10	US-09-848-754A-4630	Sequence 4630, Ap
c 146	11.8	56.2	25	15	US-10-098-263B-9435	Sequence 9435, Ap	220	11.6	55.2	38	10	US-09-848-754A-4632	Sequence 4632, Ap
c 147	11.8	56.2	25	15	US-10-098-263B-20460	Sequence 20460, A	221	11.6	55.2	38	10	US-09-848-754A-5112	Sequence 5112, Ap
c 148	11.8	56.2	25	15	US-10-098-263B-28862	Sequence 28862, A	222	11.6	55.2	38	10	US-09-848-754A-5174	Sequence 5174, Ap
c 149	11.8	56.2	25	15	US-10-098-263B-32872	Sequence 32872, A	223	11.6	55.2	38	10	US-09-848-754A-5281	Sequence 5281, Ap
c 150	11.8	56.2	25	15	US-10-098-263B-36930	Sequence 36930, A	224	11.6	55.2	38	10	US-09-848-754A-5395	Sequence 5395, Ap
c 151	11.8	56.2	25	15	US-10-098-263B-86994	Sequence 86994, A	225	11.6	55.2	38	10	US-09-848-754A-5435	Sequence 5435, Ap
c 152	11.8	56.2	25	15	US-10-098-263B-98332	Sequence 98332, A	226	11.6	55.2	38	10	US-09-848-754A-5519	Sequence 5519, Ap
c 153	11.8	56.2	38	10	US-09-877-478-2972	Sequence 2972, Ap	227	11.6	55.2	38	10	US-09-930-423-2065	Sequence 2065, Ap
c 154	11.8	56.2	38	16	US-10-342-902-2972	Sequence 2972, Ap	228	11.6	55.2	38	10	US-09-930-423-2091	Sequence 2091, Ap
c 155	11.8	56.2	38	17	US-10-669-841-7863	Sequence 7863, Ap	229	11.6	55.2	38	10	US-09-930-423-2097	Sequence 2097, Ap
c 156	11.6	55.2	20	15	US-10-244-367-20	Sequence 20, Appl	230	11.6	55.2	38	10	US-09-930-423-2102	Sequence 2102, Ap
c 157	11.6	55.2	20	15	US-10-098-263B-787	Sequence 787, App	231	11.6	55.2	38	10	US-09-930-423-2106	Sequence 2106, Ap
c 158	11.6	55.2	25	15	US-10-098-263B-788	Sequence 788, App	231	11.6	55.2	38	10	US-09-930-423-2106	Sequence 2106, Ap

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233	11.6	55.2	38	10	US-09-930-423-2199	Sequence 2199, Ap	306	11.6	55.2	38	17	US-10-712-672-3326	Sequence 3326, Ap
234	11.6	55.2	38	10	US-09-930-423-2248	Sequence 2248, Ap	307	11.6	55.2	38	17	US-10-712-672-3370	Sequence 3370, Ap
235	11.6	55.2	38	10	US-09-930-423-2574	Sequence 2574, Ap	308	11.6	55.2	38	17	US-10-712-672-3401	Sequence 3401, Ap
236	11.6	55.2	38	10	US-09-930-423-2595	Sequence 2595, Ap	309	11.6	55.2	38	17	US-10-712-672-3412	Sequence 3412, Ap
237	11.6	55.2	38	10	US-09-827-395A-1245	Sequence 1245, Ap	310	11.6	55.2	38	17	US-10-712-672-3434	Sequence 3434, Ap
238	11.6	55.2	38	10	US-09-827-395A-1307	Sequence 1307, Ap	311	11.6	55.2	38	17	US-10-712-672-3494	Sequence 3494, Ap
239	11.6	55.2	38	10	US-09-827-395A-1337	Sequence 1337, Ap	312	11.6	55.2	38	17	US-10-712-672-3559	Sequence 3559, Ap
240	11.6	55.2	38	10	US-09-827-395A-1379	Sequence 1379, Ap	313	11.6	55.2	38	17	US-10-712-672-3661	Sequence 3666, Ap
241	11.6	55.2	38	10	US-09-827-395A-1404	Sequence 1404, Ap	314	11.6	55.2	38	17	US-10-712-672-3701	Sequence 3701, Ap
242	11.6	55.2	38	10	US-09-827-395A-1411	Sequence 1411, Ap	315	11.6	55.2	38	17	US-10-712-672-3708	Sequence 3708, Ap
243	11.6	55.2	38	10	US-09-827-395A-1465	Sequence 1465, Ap	316	11.6	55.2	38	17	US-10-712-672-3729	Sequence 3729, Ap
244	11.6	55.2	38	10	US-09-792-818-1284	Sequence 1284, Ap	317	11.6	55.2	38	17	US-10-712-672-3761	Sequence 3761, Ap
245	11.6	55.2	38	10	US-09-792-818-1359	Sequence 1359, Ap	318	11.6	55.2	38	17	US-10-712-672-4076	Sequence 4076, Ap
246	11.6	55.2	38	10	US-09-745-237A-2065	Sequence 2065, Ap	319	11.6	55.2	38	17	US-10-669-841-8341	Sequence 8341, Ap
247	11.6	55.2	38	10	US-09-745-237A-2091	Sequence 2091, Ap	320	11.6	55.2	38	17	US-10-669-841-8455	Sequence 8455, Ap
248	11.6	55.2	38	10	US-09-745-237A-2097	Sequence 2097, Ap	321	11.6	55.2	38	17	US-10-669-841-8460	Sequence 8460, Ap
249	11.6	55.2	38	10	US-09-745-237A-2102	Sequence 2102, Ap	322	11.6	55.2	38	17	US-10-669-841-8495	Sequence 8495, Ap
250	11.6	55.2	38	10	US-09-745-237A-2106	Sequence 2106, Ap	323	11.6	55.2	38	17	US-10-669-841-8575	Sequence 8575, Ap
251	11.6	55.2	38	10	US-09-745-237A-2119	Sequence 2119, Ap	324	11.6	55.2	38	17	US-10-669-841-8575	Sequence 8575, Ap
252	11.6	55.2	38	10	US-09-745-237A-2199	Sequence 2199, Ap	325	11.6	55.2	38	17	US-10-669-841-8782	Sequence 8782, Ap
253	11.6	55.2	38	10	US-09-745-237A-2248	Sequence 2248, Ap	326	11.6	55.2	39	13	US-10-072-152-26	Sequence 26, Appl
254	11.6	55.2	38	10	US-09-745-237A-2574	Sequence 2574, Ap	327	11.6	55.2	39	15	US-10-277-471A-11	Sequence 11, Appl
255	11.6	55.2	38	10	US-09-745-237A-2595	Sequence 2595, Ap	328	11.6	55.2	39	15	US-10-339-674-633	Sequence 633, Appl
256	11.6	55.2	38	15	US-10-156-306-2222	Sequence 2222, Ap	329	11.6	55.2	39	15	US-10-339-674-633	Sequence 2615, Ap
257	11.6	55.2	38	15	US-10-156-306-5439	Sequence 5439, Ap	330	11.6	55.2	39	16	US-10-655-433-26	Sequence 26, Appl
258	11.6	55.2	38	15	US-10-156-306-5442	Sequence 5442, Ap	331	11.4	54.3	15	9	US-09-504-231A-904	Sequence 904, Appl
259	11.6	55.2	38	15	US-10-156-306-5538	Sequence 5538, Ap	332	11.4	54.3	15	9	US-09-274-553D-904	Sequence 904, Appl
260	11.6	55.2	38	15	US-10-156-306-5615	Sequence 5615, Ap	333	11.4	54.3	19	9	US-09-969-373-4574	Sequence 4574, Ap
261	11.6	55.2	38	15	US-10-156-306-5717	Sequence 5717, Ap	334	11.4	54.3	22	15	US-10-296-995-93	Sequence 93, Appl
262	11.6	55.2	38	15	US-10-157-580A-88	Sequence 88, Appl	335	11.4	54.3	23	15	US-10-214-932-14	Sequence 14, Appl
263	11.6	55.2	38	15	US-10-230-006-863	Sequence 863, Appl	336	11.4	54.3	23	16	US-10-474-290-6	Sequence 6, Appl
264	11.6	55.2	38	15	US-10-230-006-873	Sequence 873, Appl	337	11.4	54.3	24	10	US-09-940-185-2381	Sequence 2381, Ap
265	11.6	55.2	38	15	US-10-230-006-887	Sequence 887, Appl	338	11.4	54.3	25	14	US-10-215-112-3435	Sequence 3435, Ap
266	11.6	55.2	38	15	US-10-230-006-896	Sequence 896, Appl	339	11.4	54.3	25	14	US-10-215-112-5874	Sequence 5874, Ap
267	11.6	55.2	38	15	US-10-230-006-930	Sequence 930, Appl	340	11.4	54.3	25	14	US-10-215-112-10677	Sequence 10677, A
268	11.6	55.2	38	15	US-10-230-006-970	Sequence 970, Appl	341	11.4	54.3	25	15	US-10-098-2638-34732	Sequence 34732, A
269	11.6	55.2	38	15	US-10-230-006-1002	Sequence 1002, Ap	342	11.4	54.3	25	15	US-10-098-2638-56624	Sequence 56624, A
270	11.6	55.2	38	15	US-10-230-006-1051	Sequence 1051, Ap	343	11.4	54.3	25	15	US-10-098-2638-69290	Sequence 69290, A
271	11.6	55.2	38	15	US-10-230-006-1058	Sequence 1058, Ap	344	11.4	54.3	25	15	US-10-098-2638-71594	Sequence 71594, A
272	11.6	55.2	38	15	US-10-230-006-1108	Sequence 1108, Ap	345	11.4	54.3	25	15	US-10-098-2638-71594	Sequence 89565, A
273	11.6	55.2	38	15	US-10-430-882-1245	Sequence 1245, Ap	346	11.4	54.3	25	15	US-10-098-2638-89566	Sequence 89566, A
274	11.6	55.2	38	15	US-10-430-882-1307	Sequence 1307, Ap	347	11.4	54.3	25	15	US-10-098-2638-104298	Sequence 104298, A
275	11.6	55.2	38	15	US-10-430-882-1337	Sequence 1337, Ap	348	11.4	54.3	25	15	US-10-098-2638-104438	Sequence 104438, A
276	11.6	55.2	38	15	US-10-430-882-1379	Sequence 1379, Ap	349	11.4	54.3	25	15	US-10-098-2638-110567	Sequence 110567, A
277	11.6	55.2	38	15	US-10-430-882-1404	Sequence 1404, Ap	350	11.4	54.3	25	15	US-10-098-2638-121446	Sequence 121446, A
278	11.6	55.2	38	15	US-10-430-882-1411	Sequence 1411, Ap	351	11.4	54.3	26	9	US-09-895-141-8	Sequence 8, Appl
279	11.6	55.2	38	15	US-10-430-882-1465	Sequence 1465, Ap	352	11.4	54.3	27	10	US-09-877-705A-11	Sequence 11, Appl
280	11.6	55.2	38	16	US-10-342-902-3450	Sequence 3450, Ap	353	11.4	54.3	27	10	US-09-877-705A-12	Sequence 12, Appl
281	11.6	55.2	38	16	US-10-342-902-3564	Sequence 3564, Ap	354	11.4	54.3	27	10	US-09-947-274-11	Sequence 11, Appl
282	11.6	55.2	38	16	US-10-342-902-3569	Sequence 3569, Ap	355	11.4	54.3	27	10	US-09-947-274-12	Sequence 12, Appl
283	11.6	55.2	38	16	US-10-342-902-3604	Sequence 3604, Ap	356	11.4	54.3	27	10	US-09-877-738A-11	Sequence 11, Appl
284	11.6	55.2	38	16	US-10-342-902-3684	Sequence 3684, Ap	357	11.4	54.3	27	10	US-09-877-738A-12	Sequence 12, Appl
285	11.6	55.2	38	16	US-10-342-902-3836	Sequence 3836, Ap	358	11.4	54.3	27	12	US-09-877-403A-11	Sequence 11, Appl
286	11.6	55.2	38	16	US-10-342-902-3891	Sequence 3891, Ap	359	11.4	54.3	27	12	US-09-877-403A-12	Sequence 12, Appl
287	11.6	55.2	38	16	US-10-138-674-13690	Sequence 13690, A	360	11.4	54.3	27	15	US-10-057-810-11	Sequence 11, Appl
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289	11.6	55.2	38	16	US-10-138-674-14432	Sequence 14432, A	362	11.4	54.3	27	15	US-10-057-828-11	Sequence 11, Appl
290	11.6	55.2	38	16	US-10-138-674-14657	Sequence 14657, A	363	11.4	54.3	27	15	US-10-057-828-12	Sequence 12, Appl
291	11.6	55.2	38	16	US-10-138-674-14673	Sequence 14673, A	364	11.4	54.3	27	17	US-10-779-595-11	Sequence 11, Appl
292	11.6	55.2	38	16	US-10-138-674-15466	Sequence 15466, A	365	11.4	54.3	27	17	US-10-779-595-12	Sequence 12, Appl
293	11.6	55.2	38	16	US-10-138-674-15727	Sequence 15727, A	366	11.4	54.3	28	14	US-10-066-007-31	Sequence 31, Appl
294	11.6	55.2	38	17	US-10-287-949A-13690	Sequence 13690, A	367	11.2	53.3	18	18	US-10-740-926-406	Sequence 406, Appl
295	11.6	55.2	38	17	US-10-287-949A-14351	Sequence 14351, A	368	11.2	53.3	18	18	US-10-740-926-436	Sequence 436, Appl
296	11.6	55.2	38	17	US-10-287-949A-14432	Sequence 14432, A	369	11.2	53.3	20	17	US-10-319-914-77	Sequence 77, Appl
297	11.6	55.2	38	17	US-10-287-949A-14657	Sequence 14657, A	370	11.2	53.3	20	17	US-10-319-914-155	Sequence 155, Appl
298	11.6	55.2	38	17	US-10-287-949A-14673	Sequence 14673, A	371	11.2	53.3	20	17	US-10-619-739-322	Sequence 322, Appl
299	11.6	55.2	38	17	US-10-287-949A-15466	Sequence 15466, A	372	11.2	53.3	25	14	US-10-215-112-308	Sequence 308, Appl
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301	11.6	55.2	38	17	US-10-712-672-3204	Sequence 3204, Ap	374	11.2	53.3	25	14	US-10-215-112-9916	Sequence 9916, Ap
302	11.6	55.2	38	17	US-10-712-672-3228	Sequence 3228, Ap	375	11.2	53.3	25	14	US-10-215-112-10028	Sequence 10028, A
303	11.6	55.2	38	17	US-10-712-672-3234	Sequence 3234, Ap	376	11.2	53.3	25	15	US-10-098-2638-1018	Sequence 1018, Ap
304	11.6	55.2	38	17	US-10-712-672-3242	Sequence 3242, Ap	377	11.2	53.3	25	15	US-10-098-2638-2080	Sequence 2080, Ap

c 524	11	52.4	25	15	US-10-098-263B-94252	Sequence 94252, A	c 597	11	52.4	37	10	US-09-848-754A-6078	Sequence 6078, Ap
525	11	52.4	25	15	US-10-098-263B-96360	Sequence 96360, A	c 598	11	52.4	37	10	US-09-848-754A-6272	Sequence 6272, Ap
526	11	52.4	25	15	US-10-098-263B-100534	Sequence 100534, A	c 599	11	52.4	37	10	US-09-827-395A-1813	Sequence 1813, Ap
c 527	11	52.4	25	15	US-10-098-263B-112398	Sequence 112398, A	c 600	11	52.4	37	15	US-10-156-306-2614	Sequence 2614, Ap
528	11	52.4	28	16	US-10-312-273-525	Sequence 525, App	c 601	11	52.4	37	15	US-10-156-306-6035	Sequence 6035, Ap
529	11	52.4	32	9	US-09-929-901-15	Sequence 15, Appl	c 602	11	52.4	37	15	US-10-156-306-6240	Sequence 6240, Ap
530	11	52.4	33	9	US-09-504-231A-3131	Sequence 3131, Ap	c 603	11	52.4	37	15	US-10-230-006-1551	Sequence 1551, Ap
531	11	52.4	33	9	US-09-274-553D-3131	Sequence 3131, Ap	c 604	11	52.4	37	15	US-10-230-006-1563	Sequence 1563, Ap
532	11	52.4	35	9	US-09-864-785-3828	Sequence 3828, Ap	c 605	11	52.4	37	15	US-10-230-006-1606	Sequence 1606, Ap
533	11	52.4	35	9	US-09-864-785-3830	Sequence 3830, Ap	c 606	11	52.4	37	15	US-10-430-882-1813	Sequence 1813, Ap
534	11	52.4	36	9	US-09-504-231A-1645	Sequence 1645, Ap	607	11	52.4	37	16	US-10-342-902-6277	Sequence 6277, Ap
535	11	52.4	36	9	US-09-504-231A-1682	Sequence 1682, Ap	608	11	52.4	37	16	US-10-342-902-6373	Sequence 6373, Ap
536	11	52.4	36	9	US-09-504-231A-1808	Sequence 1808, Ap	c 609	11	52.4	37	16	US-10-138-674-18727	Sequence 18727, A
537	11	52.4	36	9	US-09-504-231A-1894	Sequence 1894, Ap	c 610	11	52.4	37	16	US-10-138-674-18872	Sequence 18872, A
538	11	52.4	36	9	US-09-504-231A-1980	Sequence 1980, Ap	c 611	11	52.4	37	16	US-10-138-674-18891	Sequence 18891, A
539	11	52.4	36	9	US-09-504-231A-2001	Sequence 2001, Ap	c 612	11	52.4	37	16	US-10-138-674-20186	Sequence 20186, A
540	11	52.4	36	9	US-09-504-231A-2052	Sequence 2052, Ap	c 613	11	52.4	37	16	US-10-138-674-20624	Sequence 20624, A
541	11	52.4	36	9	US-09-504-231A-2101	Sequence 2101, Ap	c 614	11	52.4	37	16	US-10-138-674-20731	Sequence 20731, A
542	11	52.4	36	9	US-09-504-231A-2174	Sequence 2174, Ap	c 615	11	52.4	37	16	US-10-138-674-20743	Sequence 20743, A
543	11	52.4	36	9	US-09-504-231A-2184	Sequence 2184, Ap	c 616	11	52.4	37	16	US-10-138-674-20759	Sequence 20759, A
544	11	52.4	36	9	US-09-504-231A-2186	Sequence 2186, Ap	c 617	11	52.4	37	17	US-10-287-949A-18727	Sequence 18727, A
545	11	52.4	36	9	US-09-504-231A-2190	Sequence 2190, Ap	c 618	11	52.4	37	17	US-10-287-949A-18872	Sequence 18872, A
546	11	52.4	36	9	US-09-504-231A-2378	Sequence 2378, Ap	c 619	11	52.4	37	17	US-10-287-949A-18891	Sequence 18891, A
547	11	52.4	36	9	US-09-504-231A-2384	Sequence 2384, Ap	c 620	11	52.4	37	17	US-10-287-949A-20186	Sequence 20186, A
548	11	52.4	36	9	US-09-504-231A-2458	Sequence 2458, Ap	c 621	11	52.4	37	17	US-10-287-949A-20624	Sequence 20624, A
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550	11	52.4	36	9	US-09-504-231A-2513	Sequence 2513, Ap	c 623	11	52.4	37	17	US-10-287-949A-20743	Sequence 20743, A
551	11	52.4	36	9	US-09-504-231A-2618	Sequence 2618, Ap	c 624	11	52.4	37	17	US-10-287-949A-20759	Sequence 20759, A
552	11	52.4	36	9	US-09-274-553D-1645	Sequence 1645, Ap	625	11	52.4	37	17	US-10-669-841-10936	Sequence 10936, A
553	11	52.4	36	9	US-09-274-553D-1682	Sequence 1682, Ap	626	11	52.4	37	17	US-10-669-841-11032	Sequence 11032, A
554	11	52.4	36	9	US-09-274-553D-1808	Sequence 1808, Ap	c 627	11	52.4	38	9	US-09-874-547-75	Sequence 75, Appl
555	11	52.4	36	9	US-09-274-553D-1894	Sequence 1894, Ap	c 628	11	52.4	38	9	US-09-874-547-79	Sequence 79, Appl
556	11	52.4	36	9	US-09-274-553D-1980	Sequence 1980, Ap	c 629	11	52.4	38	9	US-09-874-547-84	Sequence 84, Appl
557	11	52.4	36	9	US-09-274-553D-2001	Sequence 2001, Ap	630	11	52.4	38	9	US-09-864-785-721	Sequence 721, App
558	11	52.4	36	9	US-09-274-553D-2052	Sequence 2052, Ap	631	11	52.4	38	9	US-09-864-785-771	Sequence 771, App
559	11	52.4	36	9	US-09-274-553D-2101	Sequence 2101, Ap	632	11	52.4	38	9	US-09-864-785-775	Sequence 775, App
560	11	52.4	36	9	US-09-274-553D-2174	Sequence 2174, Ap	633	11	52.4	38	9	US-09-864-785-787	Sequence 787, App
561	11	52.4	36	9	US-09-274-553D-2184	Sequence 2184, Ap	634	11	52.4	38	9	US-09-864-785-910	Sequence 910, App
562	11	52.4	36	9	US-09-274-553D-2186	Sequence 2186, Ap	635	11	52.4	38	9	US-09-864-785-932	Sequence 932, App
563	11	52.4	36	9	US-09-274-553D-2190	Sequence 2190, Ap	636	11	52.4	38	9	US-09-864-785-951	Sequence 951, App
564	11	52.4	36	9	US-09-274-553D-2378	Sequence 2378, Ap	637	11	52.4	38	9	US-09-864-785-990	Sequence 990, App
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c 572	11	52.4	36	10	US-09-825-805-1495	Sequence 1495, Ap	645	11	52.4	38	9	US-09-864-785-1151	Sequence 1151, Ap
573	11	52.4	36	16	US-10-420-194-565	Sequence 565, App	646	11	52.4	38	9	US-09-864-785-1196	Sequence 1196, Ap
574	11	52.4	36	16	US-10-420-194-573	Sequence 573, App	647	11	52.4	38	9	US-09-864-785-1198	Sequence 1198, Ap
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577	11	52.4	36	16	US-10-420-194-602	Sequence 602, App	650	11	52.4	38	9	US-09-864-785-1276	Sequence 1276, Ap
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c 586	11	52.4	37	9	US-09-864-785-1891	Sequence 1891, Ap	659	11	52.4	38	10	US-09-730-2898-2407	Sequence 2407, Ap
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589	11	52.4	37	9	US-09-864-785-3853	Sequence 3853, Ap	662	11	52.4	38	10	US-09-730-2898-2563	Sequence 2563, Ap
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c 592	11	52.4	37	10	US-09-927-046-3759	Sequence 3759, Ap	665	11	52.4	38	10	US-09-730-2898-2733	Sequence 2733, Ap
593	11	52.4	37	10	US-09-877-478-6277	Sequence 6277, Ap	666	11	52.4	38	10	US-09-780-533A-2684	Sequence 2684, Ap
594	11	52.4	37	10	US-09-877-478-6373	Sequence 6373, Ap	667	11	52.4	38	10	US-09-780-533A-2763	Sequence 2763, Ap
c 595	11	52.4	37	10	US-09-848-754A-5984	Sequence 5984, Ap	668	11	52.4	38	10	US-09-780-533A-2792	Sequence 2792, Ap
c 596	11	52.4	37	10	US-09-848-754A-6061	Sequence 6061, Ap	669	11	52.4	38	10	US-09-780-533A-2945	Sequence 2945, Ap

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672	11	52.4	38	10	US-09-780-533A-3474	Sequence 3474, Ap	745	11	52.4	38	10	US-09-877-478-3898	Sequence 3898, Ap
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711	11	52.4	38	10	US-09-927-046-3140	Sequence 3140, Ap	784	11	52.4	38	10	US-09-848-754A-5734	Sequence 5734, Ap
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720	11	52.4	38	10	US-09-877-478-3247	Sequence 3247, Ap	793	11	52.4	38	10	US-09-776-474-1734	Sequence 1734, Ap
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723	11	52.4	38	10	US-09-877-478-3300	Sequence 3300, Ap	796	11	52.4	38	10	US-09-930-423-1790	Sequence 1790, Ap
724	11	52.4	38	10	US-09-877-478-3331	Sequence 3331, Ap	797	11	52.4	38	10	US-09-930-423-1804	Sequence 1804, Ap
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727	11	52.4	38	10	US-09-877-478-3481	Sequence 3481, Ap	800	11	52.4	38	10	US-09-930-423-2083	Sequence 2083, Ap
728	11	52.4	38	10	US-09-877-478-3497	Sequence 3497, Ap	801	11	52.4	38	10	US-09-930-423-2138	Sequence 2138, Ap
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730	11	52.4	38	10	US-09-877-478-3530	Sequence 3530, Ap	803	11	52.4	38	10	US-09-930-423-2150	Sequence 2150, Ap
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732	11	52.4	38	10	US-09-877-478-3633	Sequence 3633, Ap	805	11	52.4	38	10	US-09-930-423-2163	Sequence 2163, Ap
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735	11	52.4	38	10	US-09-877-478-3680	Sequence 3680, Ap	808	11	52.4	38	10	US-09-930-423-2336	Sequence 2336, Ap
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737	11	52.4	38	10	US-09-877-478-3695	Sequence 3695, Ap	810	11	52.4	38	10	US-09-930-423-2366	Sequence 2366, Ap
738	11	52.4	38	10	US-09-877-478-3707	Sequence 3707, Ap	811	11	52.4	38	10	US-09-930-423-2369	Sequence 2369, Ap
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740	11	52.4	38	10	US-09-877-478-3816	Sequence 3816, Ap	813	11	52.4	38	10	US-09-930-423-2403	Sequence 2403, Ap
741	11	52.4	38	10	US-09-877-478-3840	Sequence 3840, Ap	814	11	52.4	38	10	US-09-930-423-2411	Sequence 2411, Ap
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824	11	52.4	38	10	US-09-930-423-2603	Sequence 2603, Ap	897	11	52.4	38	10	US-09-745-237A-2549	Sequence 2549, Ap
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835	11	52.4	38	10	US-09-780-164-1595	Sequence 1595, Ap	908	11	52.4	38	15	US-10-156-306-1013	Sequence 1013, Ap
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840	11	52.4	38	10	US-09-780-164-1679	Sequence 1679, Ap	913	11	52.4	38	15	US-10-156-306-2091	Sequence 2091, Ap
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863	11	52.4	38	10	US-09-792-818-1112	Sequence 1112, Ap	936	11	52.4	38	15	US-10-156-306-5533	Sequence 5533, Ap
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865	11	52.4	38	10	US-09-792-818-1163	Sequence 1163, Ap	938	11	52.4	38	15	US-10-156-306-5550	Sequence 5550, Ap
866	11	52.4	38	10	US-09-792-818-1184	Sequence 1184, Ap	939	11	52.4	38	15	US-10-156-306-5552	Sequence 5552, Ap
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997 11 52.4 38 16 US-10-342-902-3399 Sequence 3399, Ap
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ALIGNMENTS

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RESULT 1
US-10-087-631B-2/c
; Sequence 2, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exempl
; OTHER INFORMATION: principle
US-10-087-631B-2
Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 21 CGGTCATTAGACCGTACGCGA 1
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US-10-087-631B-17
; Sequence 17, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence to exemplify principl
US-10-087-631B-17
Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CGGTCATTAGACCGTACGCGA 21
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US-10-419-022-2/c
; Sequence 2, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exempl
; OTHER INFORMATION: principle
US-10-419-022-2
Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 21 CGGTCATTAGACCGTACGCGA 1
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US-10-419-022-17
; Sequence 17, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; OTHER INFORMATION: principle
US-10-419-022-17
Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence to exemplify princ
US-10-419-022-17

Query Match      100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGGTCATTAGACCGTACGCGA 21

RESULT 5
US-10-098-263B-56047
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SEQ ID NO 56047
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-56047

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Best Local Similarity 84.2%; Pred. No. 8.2e+02;
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RESULT 6
US-09-374-046A-218
; Sequence 218, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
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; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: biotinylated phosphoramidite residue
US-09-374-046A-218

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Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACGCGA 21
    |||||
Db 5 GGTCAATAGACAGTACTCCA 24

RESULT 7
US-10-616-263-218
; Sequence 218, Application US/10616263
; Publication No. US20040039276A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000103.5
; CURRENT APPLICATION NUMBER: US/10/616,263
; CURRENT FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: biotinylated phosphoramidite residue
US-10-616-263-218

Query Match      64.8%; Score 13.6; DB 16; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACGCGA 21
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RESULT 8
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Wed Nov 24 08:46:00 2004

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US-10-138-674-20182/c
; Sequence 20182, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20182
Query Match 64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCGTACGCG 18
RESULT 9
US-10-138-674-20479/c
; Sequence 20479, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20479
Query Match 64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCGTACGCG 18
RESULT 10
US-10-287-949A-20182/c
; Sequence 20182, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

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; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20182
Query Match 64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCGTACGCG 18
RESULT 11
US-10-287-949A-20479/c
; Sequence 20479, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20479
Query Match 64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCGTACGCG 18
RESULT 12
US-10-098-263B-9436/c
; Sequence 9436, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; APPLICANT: Human Microarray
; TITLE OF INVENTION: 3118.1
; FILE REFERENCE: US/10/098,263B
; CURRENT APPLICATION NUMBER: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759

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; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 9436
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-9436

Query Match 63.8%; Score 13.4; DB 15; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTAC 17
||| ||||| |||||
Db 18 GTCATTAGACTGTAC 4

RESULT 13
US-10-098-263B-88235
; Sequence 88235, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88235
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-88235

Query Match 62.9%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTAGCGGA 21
||| ||||| |||||
Db 7 TCAATAGACCTTAGCGGA 24

RESULT 14
US-10-098-263B-88853
; Sequence 88853, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88853
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-88853

Query Match 62.9%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTAGCGGA 21
||| ||||| |||||

Db 8 TCAATAGACCTTAGCGGA 25

RESULT 15
US-10-098-263B-71593/c
; Sequence 71593, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-71593

Query Match 61.9%; Score 13; DB 15; Length 25;
Best Local Similarity 76.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGGTCAATTAGACCGTAGCGGA 21
||| ||||| ||||| |||||
Db 21 CGGTGGGTAGTCCGTACGAGA 1

RESULT 16
US-10-098-263B-71008
; Sequence 71008, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-71008

Query Match 61.0%; Score 12.8; DB 15; Length 25;
Best Local Similarity 87.5%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTAGC 18
||| ||||| ||||| |||||
Db 5 GTCATGTGACCGTAGC 20

RESULT 17
US-10-098-263B-25744
; Sequence 25744, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

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NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 25744
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-098-263B-25744

Query Match 60.0%; Score 12.6; DB 15; Length 25;
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGC 19
 Db 7 CGTCCCTTAGACCGACGC 25

RESULT 18
 US-10-098-263B-56048
 Sequence 56048, Application US/10098263B
 Publication No. US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Mittman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 56048
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-098-263B-56048

Query Match 60.0%; Score 12.6; DB 15; Length 25;
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTACGCGA 21
 Db 6 GTCATTACACCGTGTGCA 24

RESULT 19
 US-10-098-263B-118819/c
 Sequence 118819, Application US/10098263B
 Publication No. US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Mittman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 118819
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-098-263B-118819

Query Match 60.0%; Score 12.6; DB 15; Length 25;
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGC 19
 Db 21 CTGTCATTGACCGCACAC 3

RESULT 20

US-10-098-263B-118820/c
 Sequence 118820, Application US/10098263B
 Publication No. US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Mittman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 118820
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-098-263B-118820

Query Match 60.0%; Score 12.6; DB 15; Length 25;
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGC 19
 Db 21 CTGTCATTGACCGCACAC 3

RESULT 21

US-09-864-785-3885/c
 Sequence 3885, Application US/09864785
 Patent No. US20020177568A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Draper, Ken
 APPLICANT: McSwiggen, Jim
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 FILE REFERENCE: 400/022 (MBH00-812-D)
 CURRENT APPLICATION NUMBER: US/09/864,785
 CURRENT FILING DATE: 2001-05-23
 NUMBER OF SEQ ID NOS: 3929
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3885
 LENGTH: 36
 TYPE: RNA
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
 NAME/KEY: misc feature
 LOCATION: (1)..(4)
 OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
 NAME/KEY: misc feature
 LOCATION: (1)..(16)
 OTHER INFORMATION: 2'-O-Methyl
 NAME/KEY: misc feature
 LOCATION: (18)..(23)
 OTHER INFORMATION: 2'-O-Methyl
 NAME/KEY: misc feature
 LOCATION: (25)..(26)
 OTHER INFORMATION: 2'-O-Methyl
 NAME/KEY: misc feature
 LOCATION: (28)..(35)
 OTHER INFORMATION: 2'-O-Methyl
 NAME/KEY: misc feature
 LOCATION: (17)..(17)
 OTHER INFORMATION: 2'-deoxy-2'-Amino
 NAME/KEY: misc feature
 LOCATION: (27)..(27)

OTHER INFORMATION: 2'-deoxy-2'-Amino
NAME/KEY: misc_feature
LOCATION: (36)..(36)
OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-864-785-3885

Query Match 60.0%; Score 12.6; DB 9; Length 36;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCATTAGCGTACGCG 20
Db 35 GGCCATTAGCCTCACTCG 17

RESULT 22
US-09-864-785-1812/c
Sequence 1812, Application US/09864785
Patent No. US20020177568A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Stinchcomb, Dan
APPLICANT: Draper, Ken
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
TITLE OF INVENTION: Levels of NP-Kappa B
FILE REFERENCE: 400/022 (MBH800-812-D)
CURRENT APPLICATION NUMBER: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1812
LENGTH: 37
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1812

Query Match 60.0%; Score 12.6; DB 9; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCATTAGCGTACGCG 20
Db 36 GGCCATTAGCCTCACTCG 18

RESULT 23
US-09-740-332-9583
Sequence 9583, Application US/09740332
Publication No. US20030125270A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9583
LENGTH: 37
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)..(37)
OTHER INFORMATION: n is an inverted deoxyabasic moiety
NAME/KEY: misc_feature
LOCATION: (30)..(30)
OTHER INFORMATION: n is inosine
NAME/KEY: misc_feature

LOCATION: (1)..(7)
OTHER INFORMATION: 2'-O-methyl derivative
NAME/KEY: misc_feature
LOCATION: (15)..(26)
OTHER INFORMATION: 2'-O-methyl derivative
NAME/KEY: misc_feature
LOCATION: (31)..(36)
OTHER INFORMATION: 2'-O-methyl derivative
US-09-740-332-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGCGTACGCGA 21
Db 15 GGCCGUUAGCCGAANGCGA 34

RESULT 24

US-09-817-879-9583
Sequence 9583, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBH800-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9583
LENGTH: 37
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)..(37)
OTHER INFORMATION: n is an inverted deoxyabasic moiety
NAME/KEY: misc_feature
LOCATION: (30)..(30)
OTHER INFORMATION: n is inosine
NAME/KEY: misc_feature
LOCATION: (1)..(7)
OTHER INFORMATION: 2'-O-methyl derivative
NAME/KEY: misc_feature
LOCATION: (15)..(26)
OTHER INFORMATION: 2'-O-methyl derivative
NAME/KEY: misc_feature
LOCATION: (31)..(36)
OTHER INFORMATION: 2'-O-methyl derivative
US-09-817-879-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGCGTACGCGA 21
Db 15 GGCCGUUAGCCGAANGCGA 34

RESULT 25

US-10-138-674-18225/c
Sequence 18225, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18225
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18225

Query Match 60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCG 20
DB 36 GGTCTTTAGACCTCACTCG 18

RESULT 26
US-10-138-674-18462/c
; Sequence 18462, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18462
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18462

Query Match 60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCG 20
DB 36 GGTCTTTAGACCTCACTCG 18

RESULT 27
US-10-138-674-20525/c
; Sequence 20525, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20525
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20525

Query Match 60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCG 20
DB 36 GGTCTTTAGACCTCACTCG 18

RESULT 28
US-10-287-949A-18225/c
; Sequence 18225, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18225
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18225

Query Match 60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCG 20
DB 36 GGTCTTTAGACCTCACTCG 18

RESULT 29
US-10-287-949A-18462/c
; Sequence 18462, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18462
; LENGTH: 37
; TYPE: RNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18462

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy  2  GGTGATTAGACCTCACTCG 20
Db   36  GGTGATTAGACCTCACTCG 18

RESULT 30
US-10-287-949A-20525/c
; Sequence 20525, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20525
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20525

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy  2  GGTGATTAGACCTCACTCG 20
Db   36  GGTGATTAGACCTCACTCG 18

RESULT 31
US-10-669-841-16128
; Sequence 16128, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
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; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16128
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is inosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(7)
; OTHER INFORMATION: 2'-O-Methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(26)
; OTHER INFORMATION: 2'-O-Methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)..(36)
; OTHER INFORMATION: 2'-O-Methyl
; US-10-669-841-16128

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy  2  GGTGATTAGACCTCACTCG 21
Db   15  GGTGATTAGACCTCACTCG 34

RESULT 32
US-09-874-547-83/c
; Sequence 83, Application US/09874547
; Patent No. US20020058269A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020058269A1k, Steffen
; APPLICANT: Kassner, Paul D.
; APPLICANT: Zyomyx, Inc.
; TITLE OF INVENTION: Screening of Phage Displayed Peptides
; TITLE OF INVENTION: Without Clearing of the Cell Culture
; FILE REFERENCE: 020144-001110US
; CURRENT APPLICATION NUMBER: US/09/874,547
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,503
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 38
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers for ScFv and Fab library generation (Table
; OTHER INFORMATION: I) - MVR24
US-09-874-547-83

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTAGCGG 20
      |||||  |||  |||  |||
Db   30  GGTCAATCAATGTCGCG 12

RESULT 33
US-09-864-785-1169.
; Sequence 1169, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1169
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-864-785-1169

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTAGCGG 21
      |||  |||  |||  |||  |||
Db   16  GGCCGUUAGGCCGAANGCGA 35

RESULT 34
US-09-780-533A-3557
; Sequence 3557, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3557
; LENGTH: 38
; TYPE: RNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3557

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTAGCGG 21
      |||  |||  |||  |||  |||
Db   16  GGCCGUUAGGCCGAANGCGA 35

RESULT 35
US-09-780-533A-3581
; Sequence 3581, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3581
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3581

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTAGCGG 21
      |||  |||  |||  |||  |||
Db   16  GGCCGUUAGGCCGAANGCGA 35

RESULT 36
US-09-927-046-3026
; Sequence 3026, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3026
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3026

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GGTCAATTAGACCGTAGCGGA 21
Db      16  GGCCGUUAGGCCGAANGCGA 35

RESULT 37
US-09-927-046-3197
; Sequence 3197, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3197
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3197

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GGTCAATTAGACCGTAGCGGA 21
Db      16  GGCCGUUAGGCCGAANGCGA 35

RESULT 38
US-09-927-478-3468
; Sequence 3468, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
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; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3468
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3468

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GGTCAATTAGACCGTAGCGGA 21
Db      16  GGCCGUUAGGCCGAANGCGA 35

RESULT 39
US-09-877-478-3764
; Sequence 3764, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3764
; LENGTH: 38
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Wed Nov 24 08:46:00 2004

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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3764

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 GGTCAATTAGACCGTACGCGA 21
Db      16 GGCCGUUAGCGCGAANGCGA 35
      |||::||| ||| |||
      |||::||| ||| |||

RESULT 40
US-09-848-754A-5094
; Sequence 5094, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5094
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-848-754A-5094

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 GGTCAATTAGACCGTACGCGA 21
Db      16 GGCCGUUAGCGCGAANGCGA 35
      |||::||| ||| |||
      |||::||| ||| |||

Search completed: November 24, 2004, 03:43:10
Job time : 99.5719 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1006.82 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-17

Perfect score: 21
Sequence: 1 cggcttagacgcgcga 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gssi.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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c 2	12.2	58.1	50	1	AW004201
c 3	12	57.1	33	6	CF338319
c 4	11.6	55.2	36	5	BQ592384
c 5	11.6	55.2	43	8	BH903257
c 6	11.4	54.3	29	9	CL660557
c 7	11.4	54.3	39	9	CL293866
c 8	11.4	54.3	50	1	AU106620
c 9	11.4	54.3	50	1	AU106620
c 10	11.2	53.3	31	8	BH615074
c 11	11.2	53.3	43	9	CL303319
c 12	11.2	53.3	45	9	BX287629
c 13	11.2	53.3	45	9	BX650703
c 14	11.2	53.3	46	8	AZ583945
c 15	11.2	53.3	49	9	CG774856
c 16	11	52.4	42	9	AL754718
c 17	11	52.4	47	9	AL939959
c 18	11	52.4	48	8	BH895527
c 19	10.8	51.4	32	4	B1223057
c 20	10.8	51.4	36	8	BH810122
c 21	10.8	51.4	36	8	BH810143
c 22	10.8	51.4	36	9	CF360542
c 23	10.8	51.4	44	9	CL524591
c 24	10.8	51.4	45	9	AG192385

C 98 9.8 46.7 37 1 AA765049
C 99 9.8 46.7 38 1 AJ803928
C 100 9.8 46.7 39 8 BZ289706 SALK 0231
C 101 9.8 46.7 39 8 CC053623 SALK 0458
C 102 9.8 46.7 40 5 BX564806 BX564806
C 103 9.8 46.7 40 8 BZ287846 SALK 0212
C 104 9.8 46.7 40 9 AL759372 Arabidops
C 105 9.8 46.7 41 8 BH863752 SALK 0944
C 106 9.8 46.7 41 8 BH863753 SALK 0944
C 107 9.8 46.7 41 8 BH864990 SALK 0972
C 108 9.8 46.7 42 6 CD530457 06G12 Ara
C 109 9.8 46.7 43 1 AI196640 u153d01.y
C 110 9.8 46.7 44 9 TA130E32Q
C 111 9.8 46.7 44 9 CL528344 ASV25C07.
C 112 9.8 46.7 45 8 BZ384047 SALK 1349
C 113 9.8 46.7 45 9 CL002876 02S0169-0
C 114 9.8 46.7 46 1 AA736376 zg77a12.s
C 115 9.8 46.7 46 8 BZ770587 SALK 1435
C 116 9.8 46.7 46 8 CC027411 3591_1_5
C 117 9.8 46.7 47 9 AL758197 Arabidops
C 118 9.8 46.7 48 1 AI313698 EST010 Mo
C 119 9.8 46.7 49 1 AI359268 qy27c06.x
C 120 9.8 46.7 49 1 AA124225 mp98d08.r
C 121 9.8 46.7 49 1 AV833344 AV833344
C 122 9.8 46.7 49 6 CC0961 HUMGS00331
C 123 9.8 46.7 49 9 CR402941 Arabidops
C 124 9.8 46.7 49 9 CR402942 Arabidops
C 125 9.8 46.7 50 1 AU104155 AU104155
C 126 9.8 46.7 50 1 AU105980 AU105980
C 127 9.8 46.7 50 1 AU106625 AU106625
C 128 9.8 46.7 50 9 BX945487 Arabidops
C 129 9.6 45.7 24 4 BM397712 5009-0-35
C 130 9.6 45.7 25 8 CC458426 SALK 1187
C 131 9.6 45.7 27 9 TA143H1LP
C 132 9.6 45.7 30 8 BH449994 SALK 0706
C 133 9.6 45.7 31 1 AU258240 AU258240
C 134 9.6 45.7 31 7 D18722 MUSGS01784
C 135 9.6 45.7 31 8 BH810158 SALK 0414
C 136 9.6 45.7 34 9 TA124F07P
C 137 9.6 45.7 35 2 BE275280
C 138 9.6 45.7 38 8 BH613959 SALK 0352
C 139 9.6 45.7 40 4 BJ060137 BJ060137
C 140 9.6 45.7 40 8 BH911408 SALK 0684
C 141 9.6 45.7 40 9 TA71C08Q AL457678 T. brucei
C 142 9.6 45.7 41 7 CN755514 ID0AA16A
C 143 9.6 45.7 41 8 BH908133 SALK 0458
C 144 9.6 45.7 41 8 CNS07FPE AL608756 Anopheles
C 145 9.6 45.7 42 9 AL763403 Arabidops
C 146 9.6 45.7 43 9 AG217405 Drosophila
C 147 9.6 45.7 44 8 BH172536 SALK 0058
C 148 9.6 45.7 44 8 BH214294 SALK 0105
C 149 9.6 45.7 44 8 BH252344 SALK 0131
C 150 9.6 45.7 44 8 BH612495 SALK 0328
C 151 9.6 45.7 44 8 BH635702 1008007C1
C 152 9.6 45.7 44 8 BH752299 SALK 0140
C 153 9.6 45.7 44 8 DR102GGS AL979618 Danio rer
C 154 9.6 45.7 45 8 CC023725 3591_1_36
C 155 9.6 45.7 46 7 CN758478 ID0AA22B
C 156 9.6 45.7 46 8 BH610910 SALK 0182
C 157 9.6 45.7 46 9 AB081994 Drosophila
C 158 9.6 45.7 47 9 CL523386 SANS7D03 F
C 159 9.6 45.7 48 4 BG253356 602362952
C 160 9.6 45.7 48 8 BH251093 SALK 0109
C 161 9.6 45.7 48 8 BH611118 SALK 0299
C 162 9.6 45.7 48 9 TA194C12Q
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C 184 9.4 44.8 37 9 DR68G5T Danio rer
C 185 9.4 44.8 37 9 TA3SD05P T. brucei
C 186 9.4 44.8 37 9 CC797773 SALK 1453
C 187 9.4 44.8 38 5 BX559481 BX559481
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DR68G5T Danio rer
TA3SD05P T. brucei
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245	9.2	43.8	27	8	AZ2810485	AZ2810485	1M0076H05	C 318	9.2	43.8	50	1	AU108048	AU108048
C 246	9.2	43.8	28	8	AZ441205	AZ441205	1M0232B10	C 319	9.2	43.8	50	5	BX722422	BX722422
247	9.2	43.8	29	1	AJ674160	AJ674160	AJ674160	C 320	9.2	43.8	50	7	CR4377050	CR4377050
248	9.2	43.8	29	1	AJ594026	AJ594026	Arabidops	C 321	9.2	43.8	50	9	BX977848	Forward s
249	9.2	43.8	29	9	AG198112	AG198112	Pan trogl	C 322	9.2	43.8	50	9	CR209280	Forward s
C 250	9.2	43.8	30	7	CF543220	CF543220	S014680-0	C 323	9.2	43.8	50	9	CLS19142	SA66G09 F
C 251	9.2	43.8	30	8	AZ431038	AZ431038	1M0215I15	C 324	9.2	43.8	50	8	AZ592202	1M0402L19
C 252	9.2	43.8	30	8	BZ762449	BZ762449	SALK 1047	C 325	9.2	43.8	50	9	TA390C02P	T. brucei
C 253	9.2	43.8	30	9	CG714388	CG714388	1119036D1	C 326	9.2	43.8	50	8	AZ818662	2M0088Q14
C 254	9.2	43.8	32	8	AZ765095	AZ765095	1M0561A22	C 327	9.2	43.8	50	23	AZ818662	2M0088Q14
C 255	9.2	43.8	32	8	DNE545578	DNE545578		C 328	9.2	43.8	50	23	AZ818662	2M0088Q14
C 256	9.2	43.8	34	1	AI125992	AI125992	QC46d12.x	C 329	9.2	43.8	50	24	AZ818662	2M0088Q14
C 257	9.2	43.8	34	8	BH907363	BH907363	SALK 0397	C 330	9.2	43.8	50	25	AZ818662	2M0088Q14
C 258	9.2	43.8	34	8	BZ288240	BZ288240	SALK 0216	C 331	9.2	43.8	50	25	AZ818662	2M0088Q14
C 259	9.2	43.8	35	8	AZ820699	AZ820699	2M0093L02	C 332	9.2	43.8	50	25	AZ818662	2M0088Q14
C 260	9.2	43.8	35	9	TA103A09Q	TA103A09Q		C 333	9.2	43.8	50	27	AZ818662	2M0088Q14
C 261	9.2	43.8	37	9	DR10838	DR10838	Danio rer	C 334	9.2	43.8	50	27	AZ818662	2M0088Q14
C 262	9.2	43.8	38	1	AU260238	AU260238	AU260238	C 335	9.2	43.8	50	27	AZ818662	2M0088Q14
C 263	9.2	43.8	38	8	AZ659279	AZ659279	1M0536L02	C 336	9.2	43.8	50	27	AZ818662	2M0088Q14
C 264	9.2	43.8	39	8	BH809708	BH809708	SALK 0050	C 337	9.2	43.8	50	28	AZ818662	2M0088Q14
C 265	9.2	43.8	39	8	BH908228	BH908228	SALK 0465	C 338	9.2	43.8	50	28	AZ818662	2M0088Q14
C 266	9.2	43.8	40	8	BZ589975	BZ589975	3590_1_73	C 339	9.2	43.8	50	28	AZ818662	2M0088Q14
C 267	9.2	43.8	40	9	CLS23373	CLS23373	DAL2H04 F	C 340	9.2	43.8	50	29	AZ818662	2M0088Q14
C 268	9.2	43.8	41	1	AZ253540	AZ253540	SNMFCAL43	C 341	9.2	43.8	50	31	AZ818662	2M0088Q14
C 269	9.2	43.8	41	8	AZ274470	AZ274470	2M0003P13	C 342	9.2	43.8	50	31	AZ818662	2M0088Q14
C 270	9.2	43.8	41	8	BZ765629	BZ765629	SALK 1319	C 343	9.2	43.8	50	31	AZ818662	2M0088Q14
C 271	9.2	43.8	41	9	TA151G10Q	TA151G10Q		C 344	9.2	43.8	50	31	AZ818662	2M0088Q14
C 272	9.2	43.8	42	8	AZ666806	AZ666806	1M0549N10	C 345	9.2	43.8	50	31	AZ818662	2M0088Q14
C 273	9.2	43.8	43	1	AA815634	AA815634	vt03d02.r	C 346	9.2	43.8	50	31	AZ818662	2M0088Q14
C 274	9.2	43.8	43	1	AA921653	AA921653	vy22d03.r	C 347	9.2	43.8	50	32	AZ818662	2M0088Q14
C 275	9.2	43.8	44	8	AZ646714	AZ646714	1M0512D21	C 348	9.2	43.8	50	32	AZ818662	2M0088Q14
C 276	9.2	43.8	44	8	TA372A04P	TA372A04P		C 349	9.2	43.8	50	32	AZ818662	2M0088Q14
C 277	9.2	43.8	45	9	CG892752	CG892752	0150617-0	C 350	9.2	43.8	50	32	AZ818662	2M0088Q14
C 278	9.2	43.8	46	1	AI884160	AI884160	fc74e12.x	C 351	9.2	43.8	50	32	AZ818662	2M0088Q14
C 279	9.2	43.8	46	1	AA625631	AA625631	ad10d01.s	C 352	9.2	43.8	50	33	AZ818662	2M0088Q14
C 280	9.2	43.8	46	9	AJ591587	AJ591587	Arabidops	C 353	9.2	43.8	50	33	AZ818662	2M0088Q14
C 281	9.2	43.8	46	9	CR360032	CR360032	Arabidops	C 354	9.2	43.8	50	33	AZ818662	2M0088Q14
C 282	9.2	43.8	47	4	B1089840	B1089840	602855085	C 355	9.2	43.8	50	33	AZ818662	2M0088Q14
C 283	9.2	43.8	47	4	AQ026076	AQ026076	1(2)k1420	C 356	9.2	43.8	50	35	AZ818662	2M0088Q14
C 284	9.2	43.8	47	8	BH813914	BH813914	SALK 0654	C 357	9.2	43.8	50	35	AZ818662	2M0088Q14
C 285	9.2	43.8	47	8	BH846892	BH846892		C 358	9.2	43.8	50	35	AZ818662	2M0088Q14
C 286	9.2	43.8	47	9	DNE545407	DNE545407		C 359	9.2	43.8	50	35	AZ818662	2M0088Q14
C 287	9.2	43.8	47	9	AG197950	AG197950	Pan trogl	C 360	9.2	43.8	50	35	AZ818662	2M0088Q14
C 288	9.2	43.8	48	4	BJ083470	BJ083470		C 361	9.2	43.8	50	35	AZ818662	2M0088Q14
C 289	9.2	43.8	48	9	CR358002	CR358002	Arabidops	C 362	9.2	43.8	50	35	AZ818662	2M0088Q14
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C 291	9.2	43.8	49	4	BG292262	BG292262	602386710	C 364	9.2	43.8	50	35	AZ818662	2M0088Q14
C 292	9.2	43.8	49	4	BI760726	BI760726	603044726	C 365	9.2	43.8	50	36	AZ818662	2M0088Q14
C 293	9.2	43.8	49	8	CC325828	CC325828	RRG292.Ba	C 366	9.2	43.8	50	36	AZ818662	2M0088Q14
C 294	9.2	43.8	49	9	CG779221	CG779221	1123032D0	C 367	9.2	43.8	50	36	AZ818662	2M0088Q14
C 295	9.2	43.8	49	9	AG190566	AG190566	Pan trogl	C 368	9.2	43.8	50	36	AZ818662	2M0088Q14
C 296	9.2	43.8	50	1	AI920149	AI920149	1679.Pine	C 369	9.2	43.8	50	36	AZ818662	2M0088Q14
C 297	9.2	43.8	50	1	AU102923	AU102923		C 370	9.2	43.8	50	37	AZ818662	2M0088Q14
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C 303	9.2	43.8	50	1	AU102937	AU102937		C 376	9.2	43.8	50	37	AZ818662	2M0088Q14
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BH752619 SALK_0189
BH908840 SALK_0507
AL757126 Arabidops
CG714300 1119081D0
CG724480 1119081D0
AZ815371 2M0083M04

C 536	9	42.9	45	8	BH168809	BH168809	SALK_0002	C 609	9	42.9	48	8	BH172074	BH172074	SALK_0052
C 537	9	42.9	45	8	BH169016	BH169016	SALK_0004	C 610	9	42.9	48	8	BH172483	BH172483	SALK_0057
C 538	9	42.9	45	8	BH169715	BH169715	SALK_0017	C 611	9	42.9	48	8	BH173104	BH173104	SALK_0013
C 539	9	42.9	45	8	BH170991	BH170991	SALK_0036	C 612	9	42.9	48	8	BH211911	BH211911	SALK_0068
C 540	9	42.9	45	8	BH171160	BH171160	SALK_0038	C 613	9	42.9	48	8	BH212124	BH212124	SALK_0071
C 541	9	42.9	45	8	BH172480	BH172480	SALK_0057	C 614	9	42.9	48	8	BH212192	BH212192	SALK_0072
C 542	9	42.9	45	8	BH251855	BH251855	SALK_0057	C 615	9	42.9	48	8	BH212362	BH212362	SALK_0074
C 543	9	42.9	45	8	BH252041	BH252041	SALK_0122	C 616	9	42.9	48	8	BH213362	BH213362	SALK_0091
C 544	9	42.9	45	8	BH252624	BH252624	SALK_0136	C 617	9	42.9	48	8	BH213445	BH213445	SALK_0092
C 545	9	42.9	45	8	BH253683	BH253683	SALK_0152	C 618	9	42.9	48	8	BH213559	BH213559	SALK_0093
C 546	9	42.9	45	8	BH610643	BH610643	SALK_0177	C 619	9	42.9	48	8	BH214012	BH214012	SALK_0100
C 547	9	42.9	45	8	BH613489	BH613489	SALK_0343	C 620	9	42.9	48	8	BH214058	BH214058	SALK_0101
C 548	9	42.9	45	8	BH617238	BH617238	SALK_0361	C 621	9	42.9	48	8	BH251827	BH251827	SALK_0121
C 549	9	42.9	45	8	BH617343	BH617343	SALK_0363	C 622	9	42.9	48	8	BH252179	BH252179	SALK_0128
C 550	9	42.9	45	8	BH617375	BH617375	SALK_0364	C 623	9	42.9	48	8	BH252272	BH252272	SALK_0130
C 551	9	42.9	45	8	BH617528	BH617528	SALK_0372	C 624	9	42.9	48	8	BH253038	BH253038	SALK_0143
C 552	9	42.9	45	8	BH618005	BH618005	SALK_0383	C 625	9	42.9	48	8	BH253184	BH253184	SALK_0145
C 553	9	42.9	45	8	BH618006	BH618006	SALK_0383	C 626	9	42.9	48	8	BH253291	BH253291	SALK_0147
C 554	9	42.9	45	8	BH618252	BH618252	SALK_0387	C 627	9	42.9	48	8	BH253306	BH253306	SALK_0147
C 555	9	42.9	45	8	BH619123	BH619123	SALK_0402	C 628	9	42.9	48	8	BH253358	BH253358	SALK_0148
C 556	9	42.9	45	8	BH749090	BH749090	SALK_0472	C 629	9	42.9	48	8	BH253833	BH253833	SALK_0155
C 557	9	42.9	45	8	BH790393	BH790393	SALK_0569	C 630	9	42.9	48	8	BH254186	BH254186	SALK_0161
C 558	9	42.9	46	1	A1735034	A1735034	as68H04.x	C 631	9	42.9	48	8	BH254463	BH254463	SALK_0165
C 559	9	42.9	46	1	A3399336	A3399336	zt49c12.x	C 632	9	42.9	48	8	BH254917	BH254917	SALK_0174
C 560	9	42.9	46	7	H55294	H55294	CHR220233.C	C 633	9	42.9	48	8	BH610731	BH610731	SALK_0179
C 561	9	42.9	46	8	BH168816	BH168816	SALK_0002	C 634	9	42.9	48	8	BH610835	BH610835	SALK_0181
C 562	9	42.9	46	8	BH169680	BH169680	SALK_0017	C 635	9	42.9	48	8	BH610916	BH610916	SALK_0182
C 563	9	42.9	46	8	BH212329	BH212329	SALK_0074	C 636	9	42.9	48	8	BH611306	BH611306	SALK_0306
C 564	9	42.9	46	8	BH212348	BH212348	SALK_0061	C 637	9	42.9	48	8	BH611439	BH611439	SALK_0309
C 565	9	42.9	46	8	BH213521	BH213521	SALK_0093	C 638	9	42.9	48	8	BH611499	BH611499	SALK_0310
C 566	9	42.9	46	8	BH252530	BH252530	SALK_0135	C 639	9	42.9	48	8	BH611861	BH611861	SALK_0318
C 567	9	42.9	46	8	BH611610	BH611610	SALK_0312	C 640	9	42.9	48	8	BH612357	BH612357	SALK_0325
C 568	9	42.9	46	8	BH618888	BH618888	SALK_0399	C 641	9	42.9	48	8	BH613342	BH613342	SALK_0341
C 569	9	42.9	46	8	BH641999	BH641999	1008052B0	C 642	9	42.9	48	8	BH614164	BH614164	SALK_0355
C 570	9	42.9	46	8	BH747763	BH747763	SALK_0340	C 643	9	42.9	48	8	BH617377	BH617377	SALK_0364
C 571	9	42.9	46	8	BH751055	BH751055	SALK_0487	C 644	9	42.9	48	8	BH617696	BH617696	SALK_0374
C 572	9	42.9	46	8	BH910540	BH910540	SALK_0601	C 645	9	42.9	48	8	BH633587	BH633587	SALK_0428
C 573	9	42.9	46	9	CC887473	CC887473	SALK_1502	C 646	9	42.9	48	8	BH748267	BH748267	SALK_0450
C 574	9	42.9	46	9	CG782542	CG782542	1123050H0	C 647	9	42.9	48	8	BH748292	BH748292	SALK_0451
C 575	9	42.9	47	8	AZ623246	AZ623246	1M0460C17	C 648	9	42.9	48	8	BH748882	BH748882	SALK_0469
C 576	9	42.9	47	8	AZ779546	AZ779546	2M0016C09	C 649	9	42.9	48	8	BH749772	BH749772	SALK_0302
C 577	9	42.9	47	8	BH169602	BH169602	SALK_0016	C 650	9	42.9	48	8	BH749892	BH749892	SALK_0303
C 578	9	42.9	47	8	BH172194	BH172194	SALK_0053	C 651	9	42.9	48	8	BH750103	BH750103	SALK_0347
C 579	9	42.9	47	8	BH172688	BH172688	SALK_0060	C 652	9	42.9	48	8	BH751416	BH751416	SALK_0501
C 580	9	42.9	47	8	BH213222	BH213222	SALK_0089	C 653	9	42.9	48	8	BH753224	BH753224	SALK_0199
C 581	9	42.9	47	8	BH213678	BH213678	SALK_0095	C 654	9	42.9	48	8	BH753678	BH753678	SALK_0294
C 582	9	42.9	47	8	BH214187	BH214187	SALK_0103	C 655	9	42.9	48	8	BH902361	BH902361	SALK_0917
C 583	9	42.9	47	8	BH252265	BH252265	SALK_0130	C 656	9	42.9	48	8	BZ382688	BZ382688	SALK_1186
C 584	9	42.9	47	8	BH252797	BH252797	SALK_0138	C 657	9	42.9	48	9	BX286631	BX286631	ArabiDops
C 585	9	42.9	47	8	BH253337	BH253337	SALK_0147	C 658	9	42.9	49	1	AA706582	AA706582	ah27b06.s
C 586	9	42.9	47	8	BH253852	BH253852	SALK_0155	C 659	9	42.9	49	1	AA726836	AA726836	vu94g12.r
C 587	9	42.9	47	8	BH611281	BH611281	SALK_0306	C 660	9	42.9	49	1	A1558595	A1558595	fb68a10.y
C 588	9	42.9	47	8	BH611531	BH611531	SALK_0310	C 661	9	42.9	49	1	A1584385	A1584385	fb92h12.x
C 589	9	42.9	47	8	BH612570	BH612570	SALK_0329	C 662	9	42.9	49	1	A1883392	A1883392	fc63c06.y
C 590	9	42.9	47	8	BH617563	BH617563	SALK_0372	C 663	9	42.9	49	1	AU013938	AU013938	AU013938
C 591	9	42.9	47	8	BH618704	BH618704	SALK_0395	C 664	9	42.9	49	5	BQ587334	BQ587334	E012340w-
C 592	9	42.9	47	8	BH747945	BH747945	SALK_0397	C 665	9	42.9	49	5	BQ587752	BQ587752	E012340w-
C 593	9	42.9	47	8	BH748581	BH748581	SALK_0461	C 666	9	42.9	49	7	X98140	X98140	MMEST49.Mou
C 594	9	42.9	47	8	BH752651	BH752651	SALK_0189	C 667	9	42.9	49	8	BH168986	BH168986	SALK_0004
C 595	9	42.9	47	8	BH753401	BH753401	SALK_0287	C 668	9	42.9	49	8	BH169475	BH169475	SALK_0014
C 596	9	42.9	47	8	BH851673	BH851673	SALK_0733	C 669	9	42.9	49	8	BH170166	BH170166	SALK_0024
C 597	9	42.9	47	9	AL946412	AL946412	ArabiDops	C 670	9	42.9	49	8	BH170234	BH170234	SALK_0025
C 598	9	42.9	47	9	CG174468	CG174468	1119036H0	C 671	9	42.9	49	8	BH172398	BH172398	SALK_0056
C 599	9	42.9	48	1	AV967257	AV967257	AV967257	C 672	9	42.9	49	8	BH212186	BH212186	SALK_0072
C 600	9	42.9	48	8	BH169127	BH169127	SALK_0006	C 673	9	42.9	49	8	BH212189	BH212189	SALK_0072
C 601	9	42.9	48	8	BH169913	BH169913	SALK_0020	C 674	9	42.9	49	8	BH213269	BH213269	SALK_0089
C 602	9	42.9	48	8	BH170421	BH170421	SALK_0028	C 675	9	42.9	49	8	BH251862	BH251862	SALK_0122
C 603	9	42.9	48	8	BH170455	BH170455	SALK_0029	C 676	9	42.9	49	8	BH252868	BH252868	SALK_0139
C 604	9	42.9	48	8	BH170532	BH170532	SALK_0030	C 677	9	42.9	49	8	BH253161	BH253161	SALK_0145
C 605	9	42.9	48	8	BH170799	BH170799	SALK_0033	C 678	9	42.9	49	8	BH253743	BH253743	SALK_0153
C 606	9	42.9	48	8	BH171310	BH171310	SALK_0040	C 679	9	42.9	49	8	BH253938	BH253938	SALK_0157
C 607	9	42.9	48	8	BH171340	BH171340	SALK_0041	C 680	9	42.9	49	8	BH614128	BH614128	SALK_0355
C 608	9	42.9	48	8	BH171719	BH171719	SALK_0047	C 681	9	42.9	49	8	BH748794	BH748794	SALK_0467

C 682	9	42.9	49	8	BH752698	SALK_0192	8.8	41.9	31	9	AG194290	Pan trogl
C 683	9	42.9	49	8	BH753750	SALK_0295	8.8	41.9	32	8	AZ485865	IM0313H02
C 684	9	42.9	49	9	AJ596083	Arabidops	8.8	41.9	32	8	AZ583239	IM0378K08
C 685	9	42.9	49	9	CNS0789C	Anopheles	8.8	41.9	32	8	BZ381666	SALK_1170
C 686	9	42.9	49	9	CR400023	Arabidops	8.8	41.9	32	8	BZ383892	SALK_1347
C 687	9	42.9	50	1	AL802196	AL802196	8.8	41.9	32	9	EX656781	Arabidops
C 688	9	42.9	50	1	AL802196	AL802196	8.8	41.9	32	9	CR359094	Arabidops
C 689	9	42.9	50	1	AU102484	AU102484	8.8	41.9	32	9	AJ545221	Drosophila
C 690	9	42.9	50	1	AU104254	AU104254	8.8	41.9	32	9	AV834380	AV834380
C 691	9	42.9	50	1	AU105296	AU105296	8.8	41.9	32	9	BI656215	603283594
C 692	9	42.9	50	1	AU107262	AU107262	8.8	41.9	32	9	DM545321	DM545321
C 693	9	42.9	50	1	AU107263	AU107263	8.8	41.9	32	9	AV834380	AV834380
C 694	9	42.9	50	1	AU107510	AU107510	8.8	41.9	32	9	BI656215	603283594
C 695	9	42.9	50	1	AU107860	AU107860	8.8	41.9	32	9	Y89682	Y89682
C 696	9	42.9	50	1	AU107868	AU107868	8.8	41.9	32	9	AZ316728	IM0035A15
C 697	9	42.9	50	1	AU107968	AU107968	8.8	41.9	32	9	BZ380694	SALK_1155
C 698	9	42.9	50	8	AZ308799	AZ308799	8.8	41.9	32	9	BZ382892	SALK_1190
C 699	9	42.9	50	8	BH211702	SALK_0065	8.8	41.9	32	9	CC049737	01S0506-0
C 700	9	42.9	50	8	BH213709	SALK_0096	8.8	41.9	32	9	AJ599957	Arabidops
C 701	9	42.9	50	8	BH253148	SALK_0145	8.8	41.9	32	9	BZ377896	SALK_1063
C 702	9	42.9	50	8	BH611167	SALK_0299	8.8	41.9	32	9	BZ380603	SALK_1153
C 703	9	42.9	50	8	BH612727	SALK_0331	8.8	41.9	32	9	CG723116	1119074G1
C 704	9	42.9	50	8	BH617293	SALK_0362	8.8	41.9	32	9	AZ838159	2M0133C15
C 705	9	42.9	50	8	BH617418	SALK_0364	8.8	41.9	32	9	BH847051	SALK_0129
C 706	9	42.9	50	8	BH750106	SALK_0347	8.8	41.9	32	9	BH852456	SALK_0746
C 707	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ378301	SALK_1079
C 708	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380621	SALK_1154
C 709	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 710	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 711	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 712	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 713	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 714	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 715	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 716	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 717	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 718	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 719	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 720	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 721	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
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C 723	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 724	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 725	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 726	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 727	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 728	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 729	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 730	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 731	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 732	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 733	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 734	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 735	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 736	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 737	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 738	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 739	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 740	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 741	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 742	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 743	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 744	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 745	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 746	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 747	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 748	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 749	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
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C 751	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 752	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 753	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156
C 754	9	42.9	50	8	BH753469	SALK_0288	8.8	41.9	32	9	BZ380790	SALK_1156

C 828	8.8	41.9	37	8	BZ381631	BZ381631 SALK 1170	C 901	8.8	41.9	45	8	BH908303	BH908303 SALK 0471
C 829	8.8	41.9	37	8	BZ381688	BZ381688 SALK 1171	902	8.8	41.9	45	8	CC178546	CC178546 NPX482 Ba
C 830	8.8	41.9	37	8	BZ381722	BZ381722 SALK 1171	903	8.8	41.9	45	8	AL764750	AL764750 Arabidops
C 831	8.8	41.9	37	8	BZ381723	BZ381723 SALK 1171	C 904	8.8	41.9	46	1	AV834157	AV834157 AV834157
C 832	8.8	41.9	37	8	BZ381736	BZ381736 SALK 1171	C 905	8.8	41.9	46	1	AA616469	AA616469 vtn66d10.r
C 833	8.8	41.9	37	8	BZ381575	BZ381575 SALK 1341	C 906	8.8	41.9	46	8	BH861568	BH861568 SALK 0818
C 834	8.8	41.9	37	8	BZ383596	BZ383596 SALK 1341	C 907	8.8	41.9	46	8	BZ287326	BZ287326 SALK 0206
C 835	8.8	41.9	37	8	BZ383623	BZ383623 SALK 1341	C 908	8.8	41.9	46	8	BZ383801	BZ383801 SALK 1345
C 836	8.8	41.9	37	8	BZ383627	BZ383627 SALK 1341	C 909	8.8	41.9	46	9	AJ622642	AJ622642 Drosophil
C 837	8.8	41.9	37	8	BZ383631	BZ383631 SALK 1342	C 910	8.8	41.9	46	9	AJ758842	AJ758842 Arabidops
C 838	8.8	41.9	37	8	BZ383632	BZ383632 SALK 1342	C 911	8.8	41.9	47	6	CF329526	CF329526 NACL-04-
C 839	8.8	41.9	37	8	BZ383659	BZ383659 SALK 1342	C 912	8.8	41.9	47	6	AZ856490	AZ856490 ZM0160K22
C 840	8.8	41.9	37	8	BZ383661	BZ383661 SALK 1342	C 913	8.8	41.9	47	8	CC039002	CC039002 3591_1_99
C 841	8.8	41.9	37	8	BZ383666	BZ383666 SALK 1342	C 914	8.8	41.9	48	1	AI749566	AI749566 at30f01.x
C 842	8.8	41.9	37	8	BZ383686	BZ383686 SALK 1342	915	8.8	41.9	48	7	D19123	D19123 MUGSG01337
C 843	8.8	41.9	37	8	BZ383862	BZ383862 SALK 1346	C 916	8.8	41.9	48	8	AZ458771	AZ458771 1M0263H10
C 844	8.8	41.9	37	8	BZ383914	BZ383914 SALK 1347	C 917	8.8	41.9	48	8	AZ503560	AZ503560 1M0343E21
C 845	8.8	41.9	37	8	BZ766033	BZ766033 SALK 1365	918	8.8	41.9	48	8	CC179090	CC179090 SALK_0582
C 846	8.8	41.9	38	8	BH857421	BH857421 SALK 0748	919	8.8	41.9	48	9	EX122790	EX122790 Danilo rer
C 847	8.8	41.9	38	8	BZ380646	BZ380646 SALK 1154	C 920	8.8	41.9	48	9	CG778060	CG778060 1123025E0
848	8.8	41.9	38	8	BZ768853	BZ768853 SALK 1408	921	8.8	41.9	48	9	CG918667	CG918667 01S0556-0
849	8.8	41.9	38	9	AL942413	AL942413 Arabidops	922	8.8	41.9	48	9	CL528747	CL528747 ASV7F07.f
C 850	8.8	41.9	38	9	BX287148	BX287148 Arabidops	C 923	8.8	41.9	49	1	AA657082	AA657082 v823c09.r
C 851	8.8	41.9	38	9	AG217395	AG217395 Drosophil	924	8.8	41.9	49	1	AA948394	AA948394 on52b09.s
C 852	8.8	41.9	39	8	AZ595333	AZ595333 1M0407F23	C 925	8.8	41.9	49	1	AI004508	AI004508 ot66g10.s
853	8.8	41.9	39	8	AZ773859	AZ773859 ZM0001110	926	8.8	41.9	49	1	AI359268	AI359268 qy27C06.x
854	8.8	41.9	39	9	AG261161	AG261161 Lotus cor	C 927	8.8	41.9	49	1	AI444171	AI444171 fb43b07.y
C 855	8.8	41.9	40	1	AI219362	AI219362 qg14e08.x	928	8.8	41.9	49	1	AI638467	AI638467 tt07d10.x
856	8.8	41.9	40	1	AI433170	AI433170 ti46a06.x	C 929	8.8	41.9	49	4	BI525053	BI525053 602925110
857	8.8	41.9	40	6	CF305521	CF305521 CLD1--01-	C 930	8.8	41.9	49	6	CB337845	CB337845 laa29h07.
C 858	8.8	41.9	40	8	AZ772376	AZ772376 1M0583011	931	8.8	41.9	49	6	CD681046	CD681046 tab67e02.
C 859	8.8	41.9	40	8	BZ385044	BZ385044 SALK 1363	C 932	8.8	41.9	49	8	AZ405394	AZ405394 1M0174N07
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861	8.8	41.9	40	9	BX893447	BX893447 Arabidops	C 934	8.8	41.9	49	8	BZ383782	BZ383782 SALK_1344
C 862	8.8	41.9	40	9	AG189131	AG189131 Pan trogl	935	8.8	41.9	49	8	CC045158	CC045158 3591_1_17
C 863	8.8	41.9	41	1	AU266348	AU266348 AUX266348	C 936	8.8	41.9	49	8	CC060297	CC060297 EY04028-5
C 864	8.8	41.9	41	7	CO732377	CO732377 LLL01b01	937	8.8	41.9	49	8	CG718294	CG718294 Arabidops
C 865	8.8	41.9	41	7	H89001	H89001 Yw26b07.r1	938	8.8	41.9	49	9	AJ599619	AJ599619 Arabidops
C 866	8.8	41.9	41	7	TI7567	TI7567 mps v288 Th	C 939	8.8	41.9	49	9	CG722873	CG722873 1119073G1
C 867	8.8	41.9	41	9	AJ600758	AJ600758 Arabidops	C 940	8.8	41.9	49	9	CL213029	CL213029 G030H04 G
868	8.8	41.9	41	9	AL756926	AL756926 Arabidops	941	8.8	41.9	50	1	AA116917	AA116917 mq25g06.r
869	8.8	41.9	41	9	DNE547050	DNE547050 Drosophil	942	8.8	41.9	50	1	AU102357	AU102357 AU102357
870	8.8	41.9	41	9	CC799936	CC799936 01S0783-0	943	8.8	41.9	50	1	AU102880	AU102880 AU102880
C 871	8.8	41.9	41	9	CC884734	CC884734 SALK 1350	C 944	8.8	41.9	50	1	AU102957	AU102957 AU102957
C 872	8.8	41.9	41	9	AB081895	AB081895 Drosophil	C 945	8.8	41.9	50	1	AU103632	AU103632 AU103632
873	8.8	41.9	42	7	H07866	H07866 Y186b08.s1	C 946	8.8	41.9	50	1	AU103633	AU103633 AU103633
C 874	8.8	41.9	42	8	BH000535	BH000535 2M0288B05	C 947	8.8	41.9	50	1	AU103997	AU103997 AU103997
875	8.8	41.9	42	8	BH799740	BH799740 1008109H1	C 948	8.8	41.9	50	1	AU104135	AU104135 AU104135
C 876	8.8	41.9	42	9	AL763435	AL763435 Arabidops	C 949	8.8	41.9	50	1	AU104175	AU104175 AU104175
C 877	8.8	41.9	42	9	DNE545209	AJ545209 Drosophil	C 950	8.8	41.9	50	1	AU104448	AU104448 AU104448
878	8.8	41.9	43	1	AA948203	AA948203 op99h09.s	C 951	8.8	41.9	50	1	AU104885	AU104885 AU104885
879	8.8	41.9	43	1	AA976713	AA976713 qg06d06.s	C 952	8.8	41.9	50	1	AU104953	AU104953 AU104953
C 880	8.8	41.9	43	1	AA976713	AA976713 qg06d06.s	C 953	8.8	41.9	50	1	AU105325	AU105325 AU105325
C 881	8.8	41.9	43	1	AI115342	AI115342 uh84a06.r	C 954	8.8	41.9	50	1	AU105434	AU105434 AU105434
C 882	8.8	41.9	43	1	AJ666206	AJ666206 AJ666206	C 955	8.8	41.9	50	1	AU105452	AU105452 AU105452
C 883	8.8	41.9	43	4	BI333375	BI333375 602996772	C 956	8.8	41.9	50	1	AU105954	AU105954 AU105954
C 884	8.8	41.9	43	5	BX551512	BX551512 BX551512	C 957	8.8	41.9	50	1	AU106291	AU106291 AU106291
C 885	8.8	41.9	43	5	CF321300	CF321300 HD--12-I0	C 958	8.8	41.9	50	1	AU107257	AU107257 AU107257
886	8.8	41.9	43	7	W38487	W38487 zb19b07.r1	959	8.8	41.9	50	1	AU107258	AU107258 AU107258
C 887	8.8	41.9	43	8	BH643347	BH643347 1008057B0	960	8.8	41.9	50	1	AU107260	AU107260 AU107260
888	8.8	41.9	43	8	BX892893	BX892893 Arabidops	961	8.8	41.9	50	1	AU107261	AU107261 AU107261
889	8.8	41.9	44	6	CF315888	CF315888 HD--04-P1	962	8.8	41.9	50	1	AU107612	AU107612 AU107612
C 890	8.8	41.9	44	7	TI7569	TI7569 mps v3 The	C 963	8.8	41.9	50	1	AU107636	AU107636 AU107636
891	8.8	41.9	44	8	BH905113	BH905113 SALK 1056	964	8.8	41.9	50	1	AU107648	AU107648 AU107648
C 892	8.8	41.9	44	8	BZ384007	BZ384007 SALK 1349	C 965	8.8	41.9	50	1	AU107652	AU107652 AU107652
C 893	8.8	41.9	44	8	BZ384717	BZ384717 SALK 1359	C 966	8.8	41.9	50	1	AU107653	AU107653 AU107653
C 894	8.8	41.9	44	8	CC455081	CC455081 SALK 0476	C 967	8.8	41.9	50	1	AU107654	AU107654 AU107654
C 895	8.8	41.9	44	9	CC795527	CC795527 SALK 0814	C 968	8.8	41.9	50	1	AU107892	AU107892 AU107892
896	8.8	41.9	45	8	AZ345886	AZ345886 1M0080P17	C 969	8.8	41.9	50	1	AU108020	AU108020 AU108020
C 897	8.8	41.9	45	8	AZ605963	AZ605963 1M0427A12	C 970	8.8	41.9	50	1	AU108057	AU108057 AU108057
C 898	8.8	41.9	45	8	BH638406	BH638406 1008022D0	971	8.8	41.9	50	1	AV836264	AV836264 AV836264
C 899	8.8	41.9	45	8	BH759240	BH759240 KG00542-3	972	8.8	41.9	50	1	BE732496	BE732496 601567696
C 900	8.8	41.9	45	8	BH789424	BH789424 SALK_0293	973	8.8	41.9	50	2		

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c 974      8.8  41.9  50  2  BE978663
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c 976      8.8  41.9  50  7  CK984500
c 977      8.8  41.9  50  8  A2446391
c 978      8.8  41.9  50  8  BZ664163
c 979      8.8  41.9  50  8  CC325469
c 980      8.8  41.9  50  9  BX659110
c 981      8.8  41.9  50  9  CR105452
c 982      8.8  41.9  50  9  CR397867
c 983      8.8  41.9  50  9  CT300F12Q
c 984      8.8  41.9  50  9  CT794988
c 985      8.6  41.0  20  1  AF683142
c 986      8.6  41.0  20  6  CF337542
c 987      8.6  41.0  20  8  AZ989202
c 988      8.6  41.0  20  9  AG201749
c 989      8.6  41.0  21  7  CO785256
c 990      8.6  41.0  21  8  AZ352290
c 991      8.6  41.0  22  1  AA991491
c 992      8.6  41.0  22  8  AZ824852
c 993      8.6  41.0  23  9  TA184F06Q
c 994      8.6  41.0  23  9  TA270E01Q
c 995      8.6  41.0  24  4  BM396768
c 996      8.6  41.0  24  9  AJ587571
c 997      8.6  41.0  25  6  CA850879
c 998      8.6  41.0  25  8  AZ591086
c 999      8.6  41.0  25  8  AZ806433
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ALIGNMENTS

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RESULT 1
TA199C08P/c
LOCUS      TA199C08P      32 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 199c08, forward sequence,
            genomic survey sequence.
ACCESSION  AL475986
VERSION    AL475986.1  GI:11842726
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 32)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
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                /db_xref="taxon:5691"
                /clone="199c08"
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FEATURES

source

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Query Match      58.1%; Score 12.2; DB 1; Length 50;
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4  TCATTAGACCGTACGCG 20
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DB      31  TCAATATACCGGACGCG 47
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RESULT 3
CF338319/c
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Query Match      60.0%; Score 12.6; DB 9; Length 32;
Best Local Similarity 78.9%; Pred. No. 3.3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2  GGTCAATTAGACCGTACGCG 20
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DB      25  GGTCAATTAGAAAGCAGCG 7
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RESULT 2
AW004201
LOCUS      AW004201      50 bp      mRNA      linear      EST 08-SEP-1999
DEFINITION 701550260 A. thaliana, Columbia Col-0, inflorescence-2 Arabidopsis
            thaliana cDNA clone 701550260, mRNA sequence.
ACCESSION  AW004201
VERSION    AW004201.1  GI:5851230
KEYWORDS   EST.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 50)
AUTHORS   Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
            Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzozka,P.,
            Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,
            Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,
            Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
            Nobrega,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and
            Hanson,D.
TITLE      Arabidopsis thaliana Gene Expression MicroArray
JOURNAL    Unpublished (1999)
COMMENT    Contact: David Smoller, Ph.D.
            Genome Systems, Inc., a wholly owned subsidiary of Incyte
            Pharmaceuticals, Inc.
            4633 World Parkway Circle, St. Louis, MO 63134, USA
            Tel: 877-577-2733
            Fax: 314-427-3324
            Email: service@genomesystems.com.
            Location/Qualifiers
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                /db_xref="taxon:3702"
                /clone="701550260"
                /tissue type="inflorescence"
                /dev stage="4 - 7 weeks"
                /clone lib="A. thaliana, Columbia Col-0, inflorescence-2"
                /note="Vector: pSPORT, Site 1: NotI; Site 2: SalI; cDNA
            library was derived from untreated inflorescence tissue
            from Arabidopsis thaliana, Columbia Col-0, at 4 - 7
            weeks. Plants were grown in 1:1:1 peat
            moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C
            under constant light, and watered with fertilizer. cDNA
            synthesis was initiated using a NotI-oligo(dT) primer.
            Double-stranded cDNA was blunted, ligated to SalI
            adaptors, digested with NotI, size-selected, and cloned
            into the NotI and SalI sites of the pSPORT vector."
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FEATURES

source

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Query Match      58.1%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4  TCATTAGACCGTACGCG 20
        |||||
DB      31  TCAATATACCGGACGCG 47
        |||||

RESULT 3
CF338319/c
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LOCUS CF338319 33 bp mRNA linear EST 18-AUG-2003
 DEFINITION RCL1--01-F04.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oriza sativa (japonica cultivar-group) cDNA clone RCL1--01-F04,
 mRNA sequence.
 ACCESSION CF338319
 VERSION CF338319.1 GI:33825024
 KEYWORDS EST.
 SOURCE Oriza sativa (japonica cultivar-group)
 ORGANISM Oriza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
 FEATURES
 source Location/Qualifiers
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 /organism="Oriza sativa (japonica cultivar-group)"
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 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
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 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"
 ORIGIN
 Query Match 57.1%; Score 12; DB 6; Length 33;
 Best Local Similarity 75.0%; Pred. No. 7.3e+04;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 GGTATTAGACCGTACGCGA 21
 ||| ||||| ||| ||
 Db 27 GGTATTAGACACTACTTGA 8
 RESULT 4
 BQ592384/c
 LOCUS BQ592384 36 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012691-024-020-N04-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
 cDNA clone 024-020-N04 5-PRIME, mRNA sequence.
 ACCESSION BQ592384
 VERSION BQ592384.1 GI:26121967
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189

12472698
 CONTACT: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 36 Std Error: 0.00
 Plate: 20 row: N column: 04
 Seq primer: SP6; CATACGATTGAGTGCACACTATAG.
 FEATURES
 source Location/Qualifiers
 1. .36
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:190371"
 /db_xref="taxon:161934"
 /clone="024-020-N04"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-developing root"
 /note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
 cDNA library from sugar beet, library provided by XMS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
 orientation:
 SP6-Sall-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"
 ORIGIN
 Query Match 55.2%; Score 11.6; DB 5; Length 36;
 Best Local Similarity 77.8%; Pred. No. 1.2e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 3 GTCATTAGACCGTACGCG 20
 ||| ||||| ||| |||
 Db 22 GTATAAATCGTACGCG 5
 RESULT 5
 BH903257/c
 LOCUS BH903257 43 bp DNA linear GSS 04-SEP-2002
 DEFINITION SALK_102332.18.30.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_102332.18.30.x, genomic
 survey sequence.
 ACCESSION BH903257
 VERSION BH903257.1 GI:22714417
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 REFERENCE 1 (bases 1 to 43)
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrin, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmerman, J. and Ecker, J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

Class: TDNA tagged.
Location/Qualifiers
1. .43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK 102332.19.30.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html."

ORIGIN

Query Match 55.2%; Score 11.6; DB 8; Length 43;
Best Local Similarity 77.8%; Pred. No. 1.2e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTTCATTAGACCGTACGC 19
|||||
Db 30 GGTATACAGACCAACGC 13

RESULT 6
CL660557/c 29 bp DNA linear GSS 09-JUL-2004
LOCUS
DEFINITION
PRI0137b H04 - PRI0137b.B21 (29) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an Acedb database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: 17
Class: fosmid ends.
Location/Qualifiers
1. .29
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 54.3%; Score 11.4; DB 9; Length 29;
Best Local Similarity 92.3%; Pred. No. 1.6e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGT 15
|||||
Db 28 GTCATTAGATCGT 16

RESULT 7
CL293866 39 bp DNA linear GSS 12-FEB-2004
LOCUS
DEFINITION
02S0349-08A1-E04 UniformMu MUTAIL Library Zea mays genomic clone
02S0349-08A1-E04, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 39)
Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
Sequence tagged transposon insertions from the UniformMu maize population
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
02S0349-08, Primer set: A
Class: transposon insertion site.
Location/Qualifiers
1. .39
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="02S0349-08A1-E04"
/clone_lib="UniformMu MUTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric intercalated PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 54.3%; Score 11.4; DB 9; Length 39;
Best Local Similarity 71.4%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACCGCA 21
|||||
Db 14 CGGGGATTATACCGGAGTGA 34

RESULT 8
AU106620 50 bp mRNA linear EST 28-JAN-2004
LOCUS
DEFINITION
AU106620 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT06186, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale

REFERENCE 1 (bases 1 to 43)
 AUTHORS Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
 TITLE A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
 MEDLINE 22810117
 PUBMED 12904583
 COMMENT On Jun 30, 2004 this sequence version replaced gi:42744159.
 Contact: GGTC
 German Genetrap Consortium (GGTC)
 Email: info@genetrap.de
 pribeageo gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
 'http://genetrap.gsf.de/project/web/new/database/result_clone.html?clone_id=W130C02'. ES cell line harboring insertion mutation of target gene is available at:
 'http://genetrap.gsf.de/project/web/new/order_clones/howtoorder.htm
 1' Inhouse Sequence Identifier: 08816
 Class: Gene Trap.

FEATURES

source
 1..43
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 Sv"
 /db_xref="taxon:10090"
 /clone="W130C02"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /cell_line="ES cells 129S2 (formerly 129/SvPas)"
 /clone_lib="GGTC Gene Trap Library GV03C04"
 /note="Vector: pTribetageo"

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 43;
 Best Local Similarity 72.2%; Pred. No. 2.1e+05;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CGGTTCATTAGACCGTACG 18
 ||||| ||||| |||||
 Db 21 CGGTTTTTANNACGTACG 38

RESULT 12
 BX287629/c
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-403C11-017864,
 DEFINITION genomic survey sequence.
 ACCESSION BX287629.1 GI:28886625
 VERSION BX287629.1
 KEYWORDS GSS.
 ORGANISM Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)
 MEDLINE 22755823
 PUBMED 12874060
 2
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 JOURNAL 23117147
 MEDLINE

PUBMED

14756321

REFERENCE

3
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weissshaar, B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 JOURNAL 14682050
 PUBMED

REFERENCE

4 (bases 1 to 45)
 Rosso, M.G., Li, Y., Strizhov, N. and Weissshaar, B.
 Direct Submission
 Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 It indicates an insertion within the locus defined by BAC clone T12C14. Details on the protocols used for generation of the sequences are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..45
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-403C11-017864"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 45;
 Best Local Similarity 81.2%; Pred. No. 2.1e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 6 ATTAGACCGTACGCGA 21
 ||||| ||||| |||||
 Db 38 AGTAGACGTACCGCA 23

RESULT 13

BX650703/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL
MEDLINE
PUBMED

REFERENCE

AUTHORS

Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and

Weisshaar,B.

High-throughput generation of sequence indexes from T-DNA

mutagenized Arabidopsis thaliana lines

Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL

PUBMED

REFERENCE

AUTHORS

JOURNAL

TITLE

COMMENT

4 (bases 1 to 45)

Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At3g53580.

Details on the protocols used for generation of the sequence are

described in References 1-3. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. .45

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clones="GK-55IH04-022301"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector PAC161 (GenBank accession number: AJ537514). The

lines contain one or more T-DNA insertions. The DNA

fragment(s) resulting from the PCR were directly sequenced

to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed."

Query Match 53.3%; Score 11.2; DB 9; Length 45;

Best Local Similarity 81.2%; Pred. No. 2.1e+05;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATTAGACCGTACGCG 20

Db 28 CATTAGACACTATGCG 13

RESULT 14

AZ583945/c

LOCUS

DEFINITION

IM0388107F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0388107 F, genomic UUC1M sequence.

ACCESSION

AZ583945

VERSION

AZ583945.1 GI:11704336

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 46)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0388 row: I column: 07

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 46.

Location/Qualifiers

1. .46

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUC1M0388107"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 53.3%; Score 11.2; DB 8; Length 46;

Best Local Similarity 81.2%; Pred. No. 2.1e+05;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGGTCAATTAGACCGTA 16

Db 19 CTGTCATTAGTCCCTA 4

RESULT 15

CG774856

LOCUS

DEFINITION

1123021C02.1EL_xl 1123 - RescueMu.Grid L Zea mays genomic, genomic

survey sequence.

ACCESSION

CG774856

VERSION

CG774856.1 GI:38031309

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1. (bases 1 to 49)

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1123021. row: 16
Class: transposon-tagged.
Location/Qualifiers
1. 49
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES
source
1. 42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 52.4%; Score 11; DB 9; Length 42;
Best Local Similarity 73.7%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TCATTAGACCGTACGC 19
|||||
Db 21 TTATTCGACCATACGC 36

RESULT 16
AL754718/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-055D02-012479,
genomic survey sequence.
ACCESSION
AL754718.1 GI:21487216
KEYWORDS
GSS.
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE
22755829
PUBMED
12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
PUBMED
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BioTechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 42)
Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At1g78560.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. 42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 52.4%; Score 11; DB 9; Length 42;
Best Local Similarity 73.7%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 GTCATTAGACCGTACGCCA 21
|||||
Db 29 GTCATTAGATAGCATCGA 11

RESULT 17
AL939959/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-243C02-014389,
genomic survey sequence.
ACCESSION
AL939959
VERSION
AL939959.1 GI:24396408
KEYWORDS
GSS.
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE
22755829
PUBMED
12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
PUBMED
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

FEATURES
source

Location/Qualifiers

1. .45
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-068014.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 51.4%; Score 10.8; DB 9; Length 45;
Best Local Similarity 85.7%; Pred. No. 3.6e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTAGACCGTACGG 20
DB 15 TTATACCGTATGCG 2

RESULT 25

AU102564
LOCUS BZ358744
DEFINITION AU102564 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP07440, mRNA sequence.

ACCESSION AU102564
VERSION AU102564
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Rata.H., Ota.T., Isegai.T., Tanaka.T., Morishita.S., Okubo.K.,
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072
FUEMED 11375929

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and
Sugano.S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP07440"
/clone_lib="Sugano Homo sapiens cDNA library"

QY 4 TCATTAGACCGTAC 17
DB 2 TCATTAGACCGTGC 15

Query Match 51.4%; Score 10.8; DB 1; Length 50;
Best Local Similarity 85.7%; Pred. No. 3.6e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTAC 17
DB 2 TCATTAGACCGTGC 15

RESULT 26

BZ358744/c

LOCUS BZ358744

DEFINITION BZ358744 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

HEP07440, mRNA sequence.

ACCESSION AU102564

VERSION AU102564

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Rata.H., Ota.T., Isegai.T., Tanaka.T., Morishita.S., Okubo.K.,
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072
FUEMED 11375929

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and
Sugano.S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP07440"
/clone_lib="Sugano Homo sapiens cDNA library"

QY 4 TCATTAGACCGTAC 17
DB 2 TCATTAGACCGTGC 15

Query Match 51.4%; Score 10.8; DB 1; Length 50;
Best Local Similarity 85.7%; Pred. No. 3.6e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTAC 17
DB 2 TCATTAGACCGTGC 15

RESULT 26

BZ358744/c

LOCUS BZ358744

DEFINITION BZ358744 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

HEP07440, mRNA sequence.

ACCESSION AU102564

VERSION AU102564

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Rata.H., Ota.T., Isegai.T., Tanaka.T., Morishita.S., Okubo.K.,
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

FEATURES
source

survey sequence.

BZ358744
VERSION BZ358744.1 GI:24951173
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

Arabidopsis Genome

COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu

This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES

Location/Qualifiers

1. 32
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="Col-0"
/clone="SALK_133243.27.05.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

QY 2 GGTCTATTAGACCGTACG 18
DB 28 GCTCATGTGTCGTCGACG 12

Query Match 50.5%; Score 10.6; DB 8; Length 32;
Best Local Similarity 76.5%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCTATTAGACCGTACG 18
DB 28 GCTCATGTGTCGTCGACG 12

RESULT 27

AZ492641

LOCUS AZ492641

DEFINITION AZ492641

ACCESSION AZ492641

VERSION AZ492641

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 38)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

QY 2 GGTCTATTAGACCGTACG 18
DB 28 GCTCATGTGTCGTCGACG 12

Query Match 50.5%; Score 10.6; DB 8; Length 32;
Best Local Similarity 76.5%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCTATTAGACCGTACG 18
DB 28 GCTCATGTGTCGTCGACG 12

RESULT 27

AZ492641

LOCUS AZ492641

DEFINITION AZ492641

ACCESSION AZ492641

VERSION AZ492641

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 38)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

QY 2 GGTCTATTAGACCGTACG 18
DB 28 GCTCATGTGTCGTCGACG 12

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0326 row: D column: 24
Seq primer: CACACAGGAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 38.

FEATURES
source
1...38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUC1M0326D24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector AF129072-1, a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 50.5%; Score 10.6; DB 8; Length 38;
Best Local Similarity 76.5%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCATTAGACCTAGCGG 20
|||||
Db 18 TCATTAGATGACGGG 34

RESULT 28
DME545378/c
LOCUS 39 bp DNA linear GSS 24-FEB-2003
DEFINITION Drosophila melanogaster flanking sequence of RS P element insertion P[RS]5-SZ-3505, clone library P[RS5], genomic survey sequence.
ACCESSION AJ545378
VERSION AJ545378.1 GI:28553187
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS Ryder, E.J., Ashburner, M., Bagunya, J.J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P., Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A., Reuter, G., Roote, J., Sridonya, J., Wang, S., Webster, J. and Russell, S.
TITLE Mapping of RS P element insertions in *Drosophila melanogaster* for the DrosDel second generation deficiency kit

JOURNAL
REFERENCE 2 (bases 1 to 39)
AUTHORS Ryder, E.J.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-2003) Ryder E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
COMMENT The insertion point of the P element is before base 1 of the sequence. Further information about this P element insertion line can be found at <http://www.flyseq.org.uk> and <http://www.drosdel.org.uk>.

FEATURES
Location/Qualifiers
1...39
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="3L"
/clone="P[RS5]5-SZ-3505"
/clone_lib="P[RS5]"
/note="read=5' end"
1...39
misc_feature
/note="P element insertion in the 5' to 3' orientation"

ORIGIN
Query Match 50.5%; Score 10.6; DB 9; Length 39;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCATTAGACCTAGCGG 20
|||||
Db 18 TCATTAAACATTACGTG 2

RESULT 29
BH213213/c
LOCUS 43 bp DNA linear GSS 24-OCT-2001
DEFINITION SALK_008917 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_008917, genomic survey sequence.
ACCESSION BH213213
VERSION BH213213.1 GI:16394927
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 43)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1...43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clones="SALK_008917"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

```

ORIGIN
Query Match          50.5%; Score 10.6; DB 8; Length 43;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTACGCG 20
|||||
Db 41 TCATTATAGGCACGCG 25
|||||

RESULT 30
AA441847
LOCUS
DEFINITION
zw62c04.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:774630 5' similar to TR:G558458 G558458 ACIDIC 82 KDA
PROTEIN. i, mRNA sequence.
ACCESSION
AA441847
VERSION
AA441847.1 GI:2153731
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
JOURNAL
COMMENT
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:774630"
/dev_stage="8-9 weeks"
/lab_host="PH10B"
/clone_lib="Soares total_fetus_Nb2HF8_9w"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(GT) primer [5'
TGTTCACCATCTAGATGGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Facima Bonaldo."

ORIGIN
Query Match          50.5%; Score 10.6; DB 1; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTATTAGCGGTAC 17
|||||

```

```

Db 27 CGTCATTACACCTGAC 43

RESULT 31
AZ769367/c
LOCUS
DEFINITION
1M0569021R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0569021 R, genomic survey sequence.
ACCESSION
AZ769367
VERSION
AZ769367.1 GI:12889428
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0569 row: 0 column: 21
Seq primer: CACACAGGAAACAGCTATGACC
CLASS: plasmid ends
High quality sequence stop: 46.
FEATURES
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0569021"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match          50.5%; Score 10.6; DB 8; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CATTAGACCGTACGCGA 21
|||||

```


Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
Hillier, L., Clark, N., Dubuc, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1530
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 1530 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3841573"
/db_xref="taxon:9606"
/clone="IMAGE:179377"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55y"
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TTTTACCATCTGAGTGGACGCCGCTTTTATTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Ronaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

Query Match 50.5%; Score 10.6; DB 7; Length 49;
Best Local Similarity 65.0%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGTCTATTAGACCGTAGCGCA 21
|||||
Db 10 GNTCATTGGCTGTGCNCA 29
|||||
ORIGIN
Query Match 50.5%; Score 10.6; DB 7; Length 49;
Best Local Similarity 65.0%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGTCTATTAGACCGTAGCGCA 21
|||||
Db 10 GNTCATTGGCTGTGCNCA 29
|||||
RESULT 35
AW004243
LOCUS
DEFINITION
AW004243
701552628 A. thaliana, Columbia Col-0, root-2 Arabidopsis thaliana cDNA clone 701552628, mRNA sequence.
ACCESSION
AW004243

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
Hillier, L., Clark, N., Dubuc, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1530
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 1530 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3841573"
/db_xref="taxon:9606"
/clone="IMAGE:179377"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55y"
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TTTTACCATCTGAGTGGACGCCGCTTTTATTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Ronaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

Query Match 50.5%; Score 10.6; DB 7; Length 49;
Best Local Similarity 65.0%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGTCTATTAGACCGTAGCGCA 21
|||||
Db 10 GNTCATTGGCTGTGCNCA 29
|||||
ORIGIN
Query Match 50.5%; Score 10.6; DB 7; Length 49;
Best Local Similarity 65.0%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGTCTATTAGACCGTAGCGCA 21
|||||
Db 10 GNTCATTGGCTGTGCNCA 29
|||||
RESULT 35
AW004243
LOCUS
DEFINITION
AW004243
701552628 A. thaliana, Columbia Col-0, root-2 Arabidopsis thaliana cDNA clone 701552628, mRNA sequence.
ACCESSION
AW004243

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
Hillier, L., Clark, N., Dubuc, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1530
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 1530 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3841573"
/db_xref="taxon:9606"
/clone="IMAGE:179377"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55y"
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TTTTACCATCTGAGTGGACGCCGCTTTTATTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Ronaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

Query Match 50.5%; Score 10.6; DB 7; Length 49;
Best Local Similarity 65.0%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGTCTATTAGACCGTAGCGCA 21
|||||
Db 10 GNTCATTGGCTGTGCNCA 29
|||||
ORIGIN
Query Match 50.5%; Score 10.6; DB 7; Length 49;
Best Local Similarity 65.0%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGTCTATTAGACCGTAGCGCA 21
|||||
Db 10 GNTCATTGGCTGTGCNCA 29
|||||
RESULT 35
AW004243
LOCUS
DEFINITION
AW004243
701552628 A. thaliana, Columbia Col-0, root-2 Arabidopsis thaliana cDNA clone 701552628, mRNA sequence.
ACCESSION
AW004243

AW004243.1 GI:5951272
EST.
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 25)
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastyur, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobrega, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
Arabidopsis thaliana Gene Expression Microarray
Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
Location/Qualifiers
1..25
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="701552628"
/tissue_type="root"
/dev_stage="4 - 7 weeks"
/clone_lib="A. thaliana, Columbia Col-0, root-2"
/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; cDNA library was derived from untreated root tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adapters, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."

Query Match 49.5%; Score 10.4; DB 1; Length 25;
Best Local Similarity 70.0%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CGGTCTATTAGACCGTAGCGG 20
|||||
Db 3 CGGAAACACACCGGACGCG 22
|||||
RESULT 36
AZ317845/c
LOCUS
DEFINITION
1M0036K16R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0036K16 R, genomic survey sequence.
ACCESSION
AZ317845
VERSION
AZ317845.1 GI:10367047
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
1. .37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1301547"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IGD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGTGGAGCGCGCTCATTTTTTTTTTTT-3',
1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 49.5%; Score 10.4; DB 1; Length 37;
Best Local Similarity 70.0%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

1 CGGTCTATTAGACCGTACGCG 20

Db

14 CGCTGCATGACCGTACGCG 33

RESULT 39

BZ377768/c

LOCUS

DEFINITION BZ377768 37 bp DNA linear GSS 26-NOV-2002
SALK 106163.28.55.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_106163.28.55.n, genomic survey sequence.

ACCESSION

BZ377768

VERSION

BZ377768.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 37)

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckergalk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of AT2g25610.

Class: TDNA tagged.

Location/Qualifiers

source

1. .37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_106163.28.55.n"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 37;

Best Local Similarity 91.7%; Pred. No. 6.1e+05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

4 TCATTAGACCGT 15

Db

24 TCATTAGACCGT 13

RESULT 40

BZ383634/c

LOCUS

DEFINITION BZ383634 37 bp DNA linear GSS 26-NOV-2002
SALK_134205.28.00.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_134205.28.00.n, genomic survey sequence.

ACCESSION

BZ383634

VERSION

BZ383634.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 37)

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckergalk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 5' end of

AT2g25610.

Class: TDNA tagged.

Location/Qualifiers

source

1. .37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_134205.28.00.n"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 37;
 Best Local Similarity 91.7%; Pred. NO. 6.1e+05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGT 15
 |||||
 Db 24 TCATTAGACCGT 13

Search completed: November 23, 2004, 22:25:16
 Job time : 1007.82 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 504.21 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-7
Perfect score: 28
Sequence: 1 gaaagccattatcaggcaggtaccacaa 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	6	AR054576 Sequence
2	28	100.0	28	6	AR094138 Sequence
3	28	100.0	28	6	BD181368 A method
4	28	100.0	28	6	AX147022 Sequence
5	28	100.0	28	6	AX523948 Sequence
6	28	100.0	28	6	AX524846 Sequence
c 7	28	100.0	47	6	AR204716 Sequence
c 8	28	100.0	47	6	AX284180 Sequence
9	27	96.4	27	6	AR054577 Sequence
10	27	96.4	27	6	AR411541 Sequence
11	27	96.4	27	6	BD000267 Oligonucle
c 12	27	96.4	29	6	BD183052 Nucleic a
13	25	89.3	40	6	E17189 Partial seq
14	24	85.7	28	6	AR094974 Sequence
15	24	85.7	33	6	AR004397 Sequence
16	24	85.7	33	6	AR064936 Sequence
17	24	85.7	33	6	AR097189 Sequence
18	24	85.7	33	6	AR130687 Sequence
19	24	85.7	33	6	AR172036 Sequence

93	19	67.9	32	6	BD141965	BD141965 Gene dete	c 166	15	53.6	15	6	I57476	I57476 Sequence 13
94	18.8	67.1	40	6	BD185270	BD185270 Method fo	c 167	15	53.6	15	6	I57477	I57477 Sequence 14
95	18.4	65.7	26	6	AR011614	AR011614 Sequence	c 168	15	53.6	16	6	AR285646	AR285646 Sequence
96	18.2	65.0	32	6	BD141963	BD141963 Gene dete	c 169	15	53.6	16	6	AR397637	AR397637 Sequence
97	18	64.3	25	6	AR250673	AR250673 Sequence	170	15	53.6	18	6	AR11531	AR11531 Sequence
98	18	64.3	28	6	AR094973	AR094973 Sequence	171	15	53.6	18	6	AR144108	AR144108 Sequence
99	18	64.3	28	6	AR094996	AR094996 Sequence	172	15	53.6	18	6	AR199465	AR199465 Sequence
100	18	64.3	28	6	AR094997	AR094997 Sequence	173	15	53.6	18	6	AR200936	AR200936 Sequence
101	18	64.3	45	6	BD185818	BD185818 A stabili	174	15	53.6	18	6	AR488698	AR488698 Sequence
102	17.4	62.1	34	6	BD177932	BD177932 A method	175	15	53.6	18	6	AR488922	AR488922 Sequence
103	17.4	62.1	34	6	BD177934	BD177934 Sequence	176	15	53.6	18	6	AX419687	AX419687 Sequence
104	17.4	62.1	34	6	AR351580	AR351580 Sequence	177	15	53.6	18	6	BD084949	BD084949 Target-de
105	17.4	62.1	34	6	AR351582	AR351582 Sequence	178	15	53.6	19	6	BD084951	BD084951 Sequence
106	17.4	62.1	34	6	AR351584	AR351584 Sequence	179	15	53.6	19	6	AR165153	AR165153 Sequence
107	17.4	62.1	34	6	AR351586	AR351586 Sequence	180	15	53.6	19	6	E08191	E08191 Primer. 9/1
108	17.4	62.1	34	6	AR351588	AR351588 Sequence	181	15	53.6	19	6	E50436	E50436 Method for
109	17.4	62.1	34	6	AR351590	AR351590 Sequence	182	15	53.6	19	6	AR272180	AR272180 Sequence
110	17.4	62.1	34	6	AR351592	AR351592 Sequence	183	15	53.6	19	6	AR338422	AR338422 Sequence
111	17.4	62.1	34	6	AR351594	AR351594 Sequence	184	15	53.6	19	6	AR353617	AR353617 Sequence
112	17.4	62.1	34	6	AR351596	AR351596 Sequence	185	15	53.6	19	6	BD004753	BD004753 Method fo
113	17.4	62.1	34	6	AR351598	AR351598 Sequence	186	15	53.6	19	6	BD069501	BD069501 Nucleic a
114	17.4	62.1	34	6	AR351600	AR351600 Sequence	187	15	53.6	19	6	BD083973	BD083973 Nucleic a
115	17.4	62.1	34	6	AR351602	AR351602 Sequence	188	15	53.6	19	6	E08279	E08279 PCR primer
116	17.4	62.1	34	6	AR351604	AR351604 Sequence	189	15	53.6	19	6	E11704	E11704 PCR primer
117	17.4	62.1	34	6	AR351606	AR351606 Sequence	190	15	53.6	20	6	E11711	E11711 PCR primer
118	17.4	62.1	34	6	AR351608	AR351608 Sequence	191	15	53.6	20	6	E15665	E15665 PCR primer.
119	17.4	62.1	34	6	AR351610	AR351610 Sequence	192	15	53.6	20	6	E17190	E17190 A reverse p
120	17.4	62.1	34	6	AR351612	AR351612 Sequence	193	15	53.6	20	6	AR222518	AR222518 Sequence
121	17.4	62.1	34	6	AR351614	AR351614 Sequence	194	15	53.6	20	6	E07366	E07366 PCR primer
122	17.4	62.1	34	6	AR351616	AR351616 Sequence	195	15	53.6	20	6	AR400913	AR400913 Sequence
123	17.4	62.1	34	6	AR351618	AR351618 Sequence	196	15	53.6	20	6	AR400922	AR400922 Sequence
124	17.4	62.1	34	6	AR351620	AR351620 Sequence	197	15	53.6	20	6	AR411543	AR411543 Sequence
125	17.4	62.1	34	6	AR351622	AR351622 Sequence	198	15	53.6	20	6	BD000247	BD000247 Oligonuc
126	17.4	62.1	34	6	AR351624	AR351624 Sequence	199	15	53.6	20	6	BD000256	BD000256 Oligonuc
127	16.8	60.0	21	6	AR351626	AR351626 Sequence	200	15	53.6	20	6	BD000269	BD000269 Oligonuc
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130	16.8	60.0	21	6	AR351632	AR351632 Sequence	203	15	53.6	20	6	E07372	E07372 PCR primer
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132	16.4	58.6	33	6	AR351636	AR351636 Sequence	205	15	53.6	20	6	AX003972	AX003972 Sequence
133	16.4	58.6	33	6	AR351638	AR351638 Sequence	206	15	53.6	20	6	AX021592	AX021592 Sequence
134	16.4	58.6	33	6	AR351640	AR351640 Sequence	207	15	53.6	20	6	AX021648	AX021648 Sequence
135	16.4	58.6	33	6	AR351642	AR351642 Sequence	208	15	53.6	20	6	BD138688	BD138688 Specific
136	16.4	58.6	33	6	AR351644	AR351644 Sequence	209	15	53.6	20	6	AR090031	AR090031 Sequence
137	16.4	58.6	33	6	AR351646	AR351646 Sequence	210	15	53.6	20	6	AR197066	AR197066 Sequence
138	16.4	58.6	33	6	AR351648	AR351648 Sequence	211	15	53.6	20	6	AR259220	AR259220 Sequence
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140	16.4	58.6	33	6	AR351652	AR351652 Sequence	213	15	53.6	20	6	AX1652	AX1652 Synthetic P
141	16.4	58.6	33	6	AR351654	AR351654 Sequence	214	15	53.6	20	6	AX4417	AX4417 Sequence 32
142	15.8	56.4	18	6	AR351656	AR351656 Sequence	215	15	53.6	20	6	CO829941	CO829941 Sequence
143	15.8	56.4	18	6	AR351658	AR351658 Sequence	216	15	53.6	20	6	AR279896	AR279896 Sequence
144	15.8	56.4	18	6	AR351660	AR351660 Sequence	217	15	53.6	20	6	AX427316	AX427316 Sequence
145	15.8	56.4	18	6	AR351662	AR351662 Sequence	218	15	53.6	20	6	BD082518	BD082518 A method
146	15.8	56.4	18	6	AR351664	AR351664 Sequence	219	15	53.6	20	6	AX003975	AX003975 Sequence
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148	15.8	56.4	18	6	AR351668	AR351668 Sequence	221	15	53.6	20	6	AX021597	AX021597 Sequence
149	15.8	56.4	18	6	AR351670	AR351670 Sequence	222	15	53.6	20	6	AX021601	AX021601 Sequence
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151	15.8	56.4	18	6	AR351674	AR351674 Sequence	224	15	53.6	20	6	AX021657	AX021657 Sequence
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171	15.8	56.4	18	6	AR351714	AR351714 Sequence	244	15	53.6	20	6	AX003966	AX003966 Sequence
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173	15.8	56.4	18	6	AR351718	AR351718 Sequence	246	15	53.6	20	6	AX021645	AX021645 Sequence
174	15.8	56.4	18	6	AR351720	AR351720 Sequence	247	15	53.6	20	6	BD138685	BD138685 Specific
175	15.8	56.4	18	6	AR351722	AR351722 Sequence	248	15	53.6	20	6	AX021647	AX021647 Sequence
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177	15.8	56.4	18	6	AR351726	AR351726 Sequence	250	15	53.6	20	6	AX021651	AX021651 Sequence
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181	15.8	56.4	18	6	AR351734	AR351734 Sequence	254	15	53.6	20	6	BD138699	BD138699 Specific
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183	15.8	56.4	18	6	AR351738	AR351738 Sequence	256	15	53.6	20	6	AX021589	AX021589 Sequence
184	15.8	56.4	18	6	AR351740	AR351740 Sequence	257	15	53.6	20	6	AX021645	AX021645 Sequence
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186	15.8	56.4	18	6	AR351744	AR351744 Sequence	259	15	53.6	20	6	AX021647	AX021647 Sequence
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c 241	14	50.0	30	6	AR071738	Sequence	314	12.8	45.7	26	6	BD073565	Novel Pic
c 242	14	50.0	41	6	AX514331	Sequence	c 315	12.8	45.7	26	6	BD073567	Novel Pic
c 243	14	50.0	41	6	AX519898	Sequence	316	12.8	45.7	29	6	BD259030	Regulation
c 244	14	50.0	43	6	AX697252	Sequence	317	12.8	45.7	31	6	AR217198	Sequence
c 245	14	50.0	44	6	AX397949	Sequence	318	12.8	45.7	31	6	AR217204	Sequence
c 246	14	50.0	44	6	AX397961	Sequence	319	12.8	45.7	31	6	AX088379	Sequence
247	14	50.0	46	6	BD175036	Method fo	320	12.8	45.7	31	6	AX088385	Sequence
248	14	50.0	46	6	BD102536	Method fo	c 321	12.8	45.7	47	6	AR291109	Sequence
249	14	50.0	50	6	CQ003036	Sequence	322	12.8	45.7	47	6	AX612137	Sequence
c 250	14	50.0	50	6	CQ008879	Sequence	323	12.8	45.7	48	6	CQ654228	Sequence
c 251	14	50.0	50	6	AX397948	Sequence	c 324	12.8	45.7	50	6	CQ007050	Sequence
c 252	14	50.0	50	6	AX397960	Sequence	325	12.8	45.7	50	6	AR218541	Sequence
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c 254	13.8	49.3	40	6	BD185267	Method fo	327	12.8	45.7	50	6	AX657047	Sequence
255	13.6	48.6	20	6	AX3564	Sequence 2	328	12.8	45.7	50	6	AX657048	Sequence
256	13.6	48.6	21	6	AR129461	Sequence	329	12.8	45.7	50	6	AX657049	Sequence
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258	13.6	48.6	39	6	AX769755	Sequence	331	12.6	45.0	19	6	CQ779508	Sequence
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260	13.6	48.6	48	6	AI8448	AR4448 oligonucleo	333	12.6	45.0	24	6	AR304628	Sequence
261	13.6	48.6	50	6	AX156818	Sequence	c 334	12.6	45.0	24	6	AX447057	Sequence
262	13.6	48.6	50	6	AX156820	Sequence	c 335	12.6	45.0	25	6	AX447057	Sequence
c 263	13.4	47.9	30	6	BD133378	Method fo	c 336	12.6	45.0	25	6	AX078473	Sequence
c 264	13.4	47.9	40	6	AX538429	Sequence	337	12.6	45.0	30	6	AX084173	Sequence
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c 272	13.2	47.1	25	6	AX196917	Sequence	345	12.6	45.0	38	6	AR333324	Sequence
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275	13.2	47.1	29	6	BD200428	BD200428 Method an	c 348	12.6	45.0	39	6	AX108742	Sequence
276	13.2	47.1	29	6	AR200602	Sequence	c 349	12.6	45.0	40	6	AI3294	Sequence
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c 279	13.2	47.1	30	6	AX084172	Sequence	c 352	12.6	45.0	41	6	A20761	Promoterreg
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c 282	13.2	47.1	37	6	AX183784	Sequence	355	12.6	45.0	41	6	AX519394	Sequence
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c 284	13.2	47.1	42	6	AX694662	Sequence	357	12.6	45.0	42	6	MMH2RNA	X60855 M.musculus
285	13.2	47.1	43	6	AR079783	Sequence	358	12.6	45.0	49	6	CQ654308	Sequence
286	13.2	47.1	43	6	AR081313	Sequence	359	12.6	45.0	50	6	CQ004215	Sequence
287	13.2	47.1	43	6	AR170673	Sequence	c 360	12.6	45.0	50	6	CQ008709	Sequence
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c 289	13.2	47.1	48	6	BD022525	BD022525 Multi-fun	c 362	12.4	44.3	18	6	AR048544	Sequence
290	13	46.4	19	6	E06600	E06600 PCR primer	c 363	12.4	44.3	18	6	AR051905	Sequence
291	13	46.4	19	6	BD004751	BD004751 Method fo	c 364	12.4	44.3	18	6	AR075933	Sequence
292	13	46.4	20	6	E06778	E06778 Primer to d	c 365	12.4	44.3	24	6	AR048537	Sequence
c 293	13	46.4	24	6	AR011821	AR011821 Sequence	c 366	12.4	44.3	24	6	AR075926	Sequence
c 294	13	46.4	24	6	I77144	I77144 Sequence 16	367	12.4	44.3	25	6	AX609288	Sequence
c 295	13	46.4	31	6	AX248123	AX248123 Sequence	368	12.4	44.3	26	6	A31651	Synthetic P
296	13	46.4	31	6	AX248843	Sequence	369	12.4	44.3	30	6	AR3158	Sequence 8
c 297	13	46.4	31	14	SV4EV14A	K01538 SV40 varian	370	12.4	44.3	30	6	AR207271	Sequence
298	13	46.4	35	6	BD186553	Gene tran	371	12.4	44.3	32	6	AR065300	Sequence
299	13	46.4	35	6	BD092072	Vector fo	c 372	12.4	44.3	32	6	AR065301	Sequence
300	13	46.4	36	6	BD209503	Enzymatic	c 373	12.4	44.3	38	6	AR329804	Sequence
301	13	46.4	38	6	AR332574	Sequence	c 374	12.4	44.3	38	6	AR331552	Sequence
c 302	13	46.4	38	6	AR333916	Sequence	c 375	12.4	44.3	38	6	AR334273	Sequence
c 303	13	46.4	40	6	AX514976	Sequence	c 376	12.4	44.3	38	6	AX219528	Sequence
c 304	13	46.4	40	6	AX517322	Sequence	c 377	12.4	44.3	38	6	AX273695	Sequence
305	13	46.4	42	9	S68042	S68042 hemoglobin	c 378	12.4	44.3	38	6	AX273729	Sequence
306	13	46.4	45	6	AR157675	Sequence	c 379	12.4	44.3	39	6	AR009887	Sequence
c 307	13	46.4	45	6	AR157676	Sequence	380	12.4	44.3	41	6	AX710963	Sequence
308	12.8	45.7	17	6	AX727750	Sequence	381	12.4	44.3	41	6	BD001104	Method an
c 309	12.8	45.7	18	6	AR437453	Sequence	382	12.4	44.3	41	6	BD001533	Method an
310	12.8	45.7	21	6	BD142103	A method	383	12.4	44.3	45	6	AR168078	Sequence
311	12.8	45.7	21	6	BD142139	A method	384	12.4	44.3	45	6	AR204849	Sequence

385	12.4	44.3	45	10	MM3AR5RNA	X60903 M.musculus	458	12	42.9	33	6	AX280443	Sequence
c 386	12.4	44.3	46	5	OMY517921	AJ517921 Oncorhynch	c 459	12	42.9	34	6	AX384900	Sequence
387	12.4	44.3	46	6	AX040127	Sequence	460	12	42.9	36	6	AR001578	Sequence
388	12.4	44.3	47	6	AR289042	Sequence	461	12	42.9	37	6	AR211686	Sequence
c 389	12.4	44.3	47	6	AR292084	Sequence	462	12	42.9	38	6	AR332085	Sequence
c 390	12.2	43.6	18	6	AR076783	Sequence	463	12	42.9	38	6	AX218427	Sequence
c 391	12.2	43.6	20	6	AR226034	Sequence	464	12	42.9	38	6	AX218653	Sequence
c 392	12.2	43.6	22	6	AR073920	Sequence	465	12	42.9	38	6	AX219590	Sequence
c 393	12.2	43.6	22	6	AR176064	Sequence	466	12	42.9	38	6	AX222811	Sequence
c 394	12.2	43.6	25	6	AX110464	Sequence	467	12	42.9	38	6	AX219590	Sequence
c 395	12.2	43.6	25	6	AX110487	Sequence	c 468	12	42.9	39	6	AX299895	Sequence
c 396	12.2	43.6	28	6	E05106	E05106 PCR primer	c 469	12	42.9	39	6	AX611632	Sequence
c 397	12.2	43.6	29	6	AX17131	AX17131 Oligonucleo	c 470	12	42.9	40	6	E32724	Small tripl
c 398	12.2	43.6	29	6	AR027515	Sequence	c 471	12	42.9	40	6	AX000280	Sequence
c 399	12.2	43.6	32	6	AX17130	AX17130 Oligonucleo	c 472	12	42.9	40	6	AX538428	Sequence
c 400	12.2	43.6	32	6	AR027514	Sequence	c 473	12	42.9	41	6	AX514947	Sequence
c 401	12.2	43.6	34	6	IO4231	IO4231 Sequence 3	c 474	12	42.9	41	6	AX514948	Sequence
c 402	12.2	43.6	36	6	AR078502	Sequence	c 475	12	42.9	41	6	AX515169	Sequence
c 403	12.2	43.6	36	6	AX030041	Sequence	c 476	12	42.9	41	6	AX517295	Sequence
c 404	12.2	43.6	36	6	AX030042	Sequence	c 477	12	42.9	41	6	AX517296	Sequence
c 405	12.2	43.6	38	6	A05043	A05043 Oligonucleo	c 478	12	42.9	41	6	AX517961	Sequence
c 406	12.2	43.6	38	6	A05057	A05057 NOR-361 oli	c 479	12	42.9	42	6	BD205021	Gene enco
c 407	12.2	43.6	38	6	A08153	A08153 Oligonucleo	c 480	12	42.9	42	6	BD205022	Gene enco
c 408	12.2	43.6	38	6	A13254	A13254 oligonucleo	c 481	12	42.9	42	6	AX014772	Sequence
c 409	12.2	43.6	38	6	A29677	A29677 NOR-361 oli	c 482	12	42.9	42	6	AX014773	Sequence
c 410	12.2	43.6	38	6	AR045842	Sequence	c 483	12	42.9	45	3	DROCOPCIS	
c 411	12.2	43.6	38	6	I33204	I33204 Sequence 27	c 484	12	42.9	47	6	AR288546	Sequence
c 412	12.2	43.6	38	6	I40183	I40183 Sequence 27	c 485	12	42.9	49	6	CQ828092	Sequence
c 413	12.2	43.6	38	6	I40415	I40415 Sequence 27	c 486	12	42.9	49	6	BD141204	Fungal ce
c 414	12.2	43.6	38	6	I52894	I52894 Sequence 63	c 487	12	42.9	50	6	AR252548	Sequence
c 415	12.2	43.6	39	6	A05042	A05042 Oligonucleo	c 488	12	42.9	50	6	AX403364	Sequence
c 416	12.2	43.6	39	6	A05056	A05056 NOR-360 oli	c 489	12	42.9	50	6	HUMUR1	
c 417	12.2	43.6	39	6	A08152	A08152 Oligonucleo	c 490	11.8	42.1	17	6	AX724658	Sequence
c 418	12.2	43.6	39	6	A13253	A13253 oligonucleo	c 491	11.8	42.1	18	6	A59327	Sequence
c 419	12.2	43.6	39	6	A29676	A29676 NOR-360 oli	c 492	11.8	42.1	18	6	AX838076	Sequence
c 420	12.2	43.6	39	6	I33203	I33203 Sequence 26	c 493	11.8	42.1	18	6	AX838302	Sequence
c 421	12.2	43.6	39	6	I40182	I40182 Sequence 26	c 494	11.8	42.1	20	6	AR165946	Sequence
c 422	12.2	43.6	39	6	I40414	I40414 Sequence 26	c 495	11.8	42.1	20	6	BD013359	Sequence
c 423	12.2	43.6	39	6	AX769757	Sequence	c 496	11.8	42.1	21	6	AX095891	Sequence
c 424	12.2	43.6	39	6	AX538442	Sequence	c 497	11.8	42.1	21	6	AX146004	Sequence
c 425	12.2	43.6	41	6	AR109150	Sequence	c 498	11.8	42.1	21	6	AX404938	Sequence
c 426	12.2	43.6	41	6	BD217553	Glucosamyl	c 499	11.8	42.1	22	6	AR404961	Sequence
c 427	12.2	43.6	41	6	AR198433	Sequence	c 500	11.8	42.1	22	6	AX441284	Sequence
c 428	12.2	43.6	41	6	AR200805	Sequence	c 501	11.8	42.1	22	6	AX441307	Sequence
c 429	12.2	43.6	42	6	AR031539	Sequence	c 502	11.8	42.1	22	6	BD161566	Base sequ
c 430	12.2	43.6	43	6	AX059013	Sequence	c 503	11.8	42.1	22	6	BD171607	Method fo
c 431	12.2	43.6	48	6	AX426331	Sequence	c 504	11.8	42.1	23	6	AX663305	Sequence
c 432	12.2	43.6	48	9	HSBOMB	X72102 H.sapiens (c 505	11.8	42.1	23	10	MMU459714	Mus muscu
c 433	12.2	43.6	49	6	CQ654493	CQ654493 Sequence	c 506	11.8	42.1	24	6	CQ816789	Sequence
c 434	12.2	43.6	50	6	BD274559	BD274559 Differ	c 507	11.8	42.1	24	6	AX447216	Sequence
c 435	12.2	43.6	50	6	CQ002459	Sequence	c 508	11.8	42.1	24	6	BD143469	Human Lhx
c 436	12.2	43.6	50	6	AX073412	Sequence	c 509	11.8	42.1	25	6	AR474227	Sequence
c 437	12	42.9	18	6	AX645652	AX645652 Sequence 3	c 510	11.8	42.1	25	6	AX043261	Sequence
c 438	12	42.9	20	6	AS2658	AS2658 Sequence 3	c 511	11.8	42.1	25	6	AX055920	Sequence
c 439	12	42.9	20	6	AR666820	Sequence	c 512	11.8	42.1	25	6	AR825359	Sequence
c 440	12	42.9	20	6	AX295758	Sequence	c 513	11.8	42.1	26	6	AR240247	Sequence
c 441	12	42.9	21	6	AX459913	AX459913 Sequence	c 514	11.8	42.1	27	6	AR066363	Sequence
c 442	12	42.9	22	6	E07368	E07368 PCR primer	c 515	11.8	42.1	27	6	AX317744	Sequence
c 443	12	42.9	22	6	AX802837	Sequence	c 516	11.8	42.1	28	6	AR096214	Sequence
c 444	12	42.9	24	6	AX291125	AX291125 Sequence	c 517	11.8	42.1	28	6	CQ787532	Sequence
c 445	12	42.9	24	6	AX445781	AX445781 Sequence	c 518	11.8	42.1	28	6	I33133	Sequence 3
c 446	12	42.9	25	6	AR487008	Sequence	c 519	11.8	42.1	28	6	AR626207	Sequence
c 447	12	42.9	25	6	AX149583	Sequence	c 520	11.8	42.1	28	6	AX224559	Sequence
c 448	12	42.9	25	6	AX197036	AX197036 Sequence	c 521	11.8	42.1	28	6	AX814770	Sequence
c 449	12	42.9	27	6	AR109741	Sequence	c 522	11.8	42.1	28	6	AX825677	Sequence
c 450	12	42.9	28	6	AX203856	AX203856 Sequence	c 523	11.8	42.1	28	6	BD080283	Sequence
c 451	12	42.9	29	6	AR432056	Sequence	c 524	11.8	42.1	30	6	A97525	Sequence
c 452	12	42.9	29	6	BD091724	Novel deo	c 525	11.8	42.1	30	6	AR125877	Sequence
c 453	12	42.9	30	6	BD196555	Prostatic	c 526	11.8	42.1	30	6	I24244	Sequence 31
c 454	12	42.9	30	6	AR308682	Sequence	c 527	11.8	42.1	30	6	AX428173	Sequence
c 455	12	42.9	30	6	AX665232	Sequence	c 528	11.8	42.1	30	6	AX791290	Sequence
c 456	12	42.9	31	6	AX248570	Sequence	c 529	11.8	42.1	31	6	AR195890	Sequence
c 457	12	42.9	31	6	AR275363	Sequence	c 530	11.8	42.1	31	6	AX248470	Sequence

531	11.8	42.1	31	6	AX249351	Sequence	AX249351	Sequence	604	11.6	41.4	21	6	BD074379	Method of
c 532	11.8	42.1	31	6	AX249453	Sequence	AX249453	Sequence	605	11.6	41.4	22	6	E13354	Primer, 4/1
c 533	11.8	42.1	32	6	AR053463	Sequence	AR053463	Sequence	c 606	11.6	41.4	22	12	AB069597	Synthetic
c 534	11.8	42.1	32	6	AR091088	Sequence	AR091088	Sequence	c 607	11.6	41.4	23	6	BD143681	Method of
c 535	11.8	42.1	32	6	BD206156	Human ant	BD206156	Human ant	c 608	11.6	41.4	24	6	AR438465	Sequence
c 536	11.8	42.1	32	6	BD206159	Human ant	BD206159	Human ant	c 609	11.6	41.4	24	6	AX447115	Sequence
c 537	11.8	42.1	32	6	BD206160	Human ant	BD206160	Human ant	c 610	11.6	41.4	24	6	AX447313	Sequence
c 538	11.8	42.1	32	6	AR198123	Sequence	AR198123	Sequence	c 611	11.6	41.4	25	6	AR106305	Sequence
c 539	11.8	42.1	32	6	AR260277	Sequence	AR260277	Sequence	c 612	11.6	41.4	25	6	AR126275	Sequence
c 540	11.8	42.1	33	6	AR078514	Sequence	AR078514	Sequence	c 613	11.6	41.4	25	6	AR136171	Sequence
c 541	11.8	42.1	34	6	BD185265	Method fo	BD185265	Method fo	c 614	11.6	41.4	25	6	BD230368	Total gen
c 542	11.8	42.1	35	6	AR0751490	Sequence	AR0751490	Sequence	c 615	11.6	41.4	25	6	AX475954	Sequence
c 543	11.8	42.1	36	6	AR077856	Sequence	AR077856	Sequence	c 616	11.6	41.4	25	6	AX475955	Sequence
c 544	11.8	42.1	36	6	I73341	Sequence 5	I73341	Sequence 5	c 617	11.6	41.4	25	6	AX475956	Sequence
c 545	11.8	42.1	36	6	I82500	Sequence 5	I82500	Sequence 5	c 618	11.6	41.4	25	6	AX475957	Sequence
c 546	11.8	42.1	36	6	AR287820	Sequence 5	AR287820	Sequence 5	c 619	11.6	41.4	25	6	AX475958	Sequence
c 547	11.8	42.1	39	6	A59196	Sequence	A59196	Sequence	c 620	11.6	41.4	25	6	AX475959	Sequence
c 548	11.8	42.1	39	6	AR149879	Sequence	AR149879	Sequence	c 621	11.6	41.4	25	6	AX475960	Sequence
c 549	11.8	42.1	39	6	AR0404972	Sequence	AR0404972	Sequence	c 622	11.6	41.4	25	6	AX475961	Sequence
c 550	11.8	42.1	39	6	AX441318	Sequence	AX441318	Sequence	c 623	11.6	41.4	26	6	AX512394	Sequence
c 551	11.8	42.1	39	6	BD171619	Method fo	BD171619	Method fo	c 624	11.6	41.4	27	6	AR143800	Sequence
c 552	11.8	42.1	40	6	E13039	Genomic RNA	E13039	Genomic RNA	c 625	11.6	41.4	27	6	AR185076	Sequence
c 553	11.8	42.1	40	6	AX538405	Sequence	AX538405	Sequence	c 626	11.6	41.4	28	6	AR064482	Sequence
c 554	11.8	42.1	41	6	AX059990	Sequence	AX059990	Sequence	c 627	11.6	41.4	28	6	AR143244	Sequence
c 555	11.8	42.1	41	6	AX514591	Sequence	AX514591	Sequence	c 628	11.6	41.4	28	6	AR300637	Sequence
c 556	11.8	42.1	41	6	AX514969	Sequence	AX514969	Sequence	c 629	11.6	41.4	28	6	AR448670	Sequence
c 557	11.8	42.1	41	6	AX515447	Sequence	AX515447	Sequence	c 630	11.6	41.4	28	6	AX473148	Sequence
c 558	11.8	42.1	41	6	AX516321	Sequence	AX516321	Sequence	c 631	11.6	41.4	28	6	BD085787	Alpha-amy
c 559	11.8	42.1	41	6	AX517315	Sequence	AX517315	Sequence	c 632	11.6	41.4	29	6	BD190754	Secreted
c 560	11.8	42.1	41	6	AX520201	Sequence	AX520201	Sequence	c 633	11.6	41.4	29	6	BD200040	Method an
c 561	11.8	42.1	41	6	AX520351	Sequence	AX520351	Sequence	c 634	11.6	41.4	29	6	BD252278	Regulat
c 562	11.8	42.1	41	6	AX520533	Sequence	AX520533	Sequence	c 635	11.6	41.4	29	6	BD271406	Molecular
c 563	11.8	42.1	41	6	AX520995	Sequence	AX520995	Sequence	c 636	11.6	41.4	29	6	AX049247	Sequence
c 564	11.8	42.1	41	6	AX838902	Sequence	AX838902	Sequence	c 637	11.6	41.4	29	6	AX049852	Sequence
c 565	11.8	42.1	42	6	AR306673	Sequence	AR306673	Sequence	c 638	11.6	41.4	29	6	AX050850	Sequence
c 566	11.8	42.1	42	6	AR340108	Sequence	AR340108	Sequence	c 639	11.6	41.4	29	6	AX095975	Sequence
c 567	11.8	42.1	42	6	AR412177	Sequence	AR412177	Sequence	c 640	11.6	41.4	29	6	AX329104	Sequence
c 568	11.8	42.1	43	9	HSLAS125A	Sequence	HSLAS125A	Sequence	c 641	11.6	41.4	29	6	AX511133	Sequence
c 569	11.8	42.1	45	6	AR242793	Sequence	AR242793	Sequence	c 642	11.6	41.4	29	6	AX05628	Sequence
c 570	11.8	42.1	45	10	NMTCRA25	Sequence	NMTCRA25	Sequence	c 643	11.6	41.4	30	6	AX1516	Sequence 9
c 571	11.8	42.1	47	6	AR289403	Sequence	AR289403	Sequence	c 644	11.6	41.4	30	6	AR145006	Sequence
c 572	11.8	42.1	47	6	AR290890	Sequence	AR290890	Sequence	c 645	11.6	41.4	30	6	BD184302	Method an
c 573	11.8	42.1	47	6	AR291603	Sequence	AR291603	Sequence	c 646	11.6	41.4	30	6	E59827	GMP synthas
c 574	11.8	42.1	47	6	AR292041	Sequence	AR292041	Sequence	c 647	11.6	41.4	30	6	AR359120	Sequence
c 575	11.8	42.1	49	6	BD233641	Neisseria	BD233641	Neisseria	c 648	11.6	41.4	30	6	AX742449	Sequence
c 576	11.8	42.1	49	6	AR476052	Sequence	AR476052	Sequence	c 649	11.6	41.4	30	6	AX791080	Sequence
c 577	11.8	42.1	50	6	CQ002433	Sequence	CQ002433	Sequence	c 650	11.6	41.4	30	6	AX799992	Sequence
c 578	11.8	42.1	50	6	CQ005423	Sequence	CQ005423	Sequence	c 651	11.6	41.4	31	6	BD185685	2,6-Pyrid
c 579	11.8	42.1	50	6	AR366381	Sequence	AR366381	Sequence	c 652	11.6	41.4	31	6	CQ800756	Sequence
c 580	11.8	42.1	50	6	AR435577	Sequence	AR435577	Sequence	c 653	11.6	41.4	31	6	AX248364	Sequence
c 581	11.8	42.1	50	6	AX157594	Sequence	AX157594	Sequence	c 654	11.6	41.4	31	6	AX248761	Sequence
c 582	11.8	42.1	50	6	AX199710	Sequence	AX199710	Sequence	c 655	11.6	41.4	32	6	AR066465	Sequence
c 583	11.8	42.1	50	6	AX199712	Sequence	AX199712	Sequence	c 656	11.6	41.4	32	6	AX375484	Sequence
c 584	11.8	42.1	50	6	AX199713	Sequence	AX199713	Sequence	c 657	11.6	41.4	32	6	AX805691	Sequence
c 585	11.8	42.1	50	6	AX899629	Sequence	AX899629	Sequence	c 658	11.6	41.4	33	6	AR152566	Sequence
c 586	11.8	42.1	50	6	AX951977	Sequence	AX951977	Sequence	c 659	11.6	41.4	33	6	I86635	Sequence 14
c 587	11.8	42.1	50	6	AX952571	Sequence	AX952571	Sequence	c 660	11.6	41.4	33	6	AX280457	Sequence
c 588	11.8	42.1	50	6	BD035162	Sequence	BD035162	Sequence	c 661	11.6	41.4	34	6	AX009755	Sequence
c 589	11.6	41.4	19	6	BD230626	Total gen	BD230626	Total gen	c 662	11.6	41.4	35	6	E13948	PCR primer
c 590	11.6	41.4	19	6	CQ768777	Sequence	CQ768777	Sequence	c 663	11.6	41.4	35	11	C75896	Homo sapien
c 591	11.6	41.4	19	6	CQ778373	Sequence	CQ778373	Sequence	c 664	11.6	41.4	36	6	A08048	Oligonucleo
c 592	11.6	41.4	20	6	AR085544	Sequence	AR085544	Sequence	c 665	11.6	41.4	36	6	A14247	REP sequenc
c 593	11.6	41.4	20	6	AR104211	Sequence	AR104211	Sequence	c 666	11.6	41.4	36	6	A19271	oligonucleo
c 594	11.6	41.4	20	6	AR216064	Sequence	AR216064	Sequence	c 667	11.6	41.4	36	6	AR033997	Sequence
c 595	11.6	41.4	20	6	AR272072	Sequence	AR272072	Sequence	c 668	11.6	41.4	36	6	AR124006	Sequence
c 596	11.6	41.4	20	6	AR293463	Sequence	AR293463	Sequence	c 669	11.6	41.4	36	6	AR236453	Sequence
c 597	11.6	41.4	20	6	BD226216	Sequence	BD226216	Sequence	c 670	11.6	41.4	36	6	AR349977	Sequence
c 598	11.6	41.4	20	6	BD086295	G protein	BD086295	G protein	c 671	11.6	41.4	36	6	AR408657	Sequence
c 599	11.6	41.4	21	4	DOGSP3001	L15646 Dog (Clone)	DOGSP3001	L15646 Dog (Clone)	c 672	11.6	41.4	36	6	BD102119	Method of
c 600	11.6	41.4	21	6	BD230834	Total gen	BD230834	Total gen	c 673	11.6	41.4	36	6	BD105763	Ciliary n
c 601	11.6	41.4	21	6	BD235619	Gene, 7/2	BD235619	Gene, 7/2	c 674	11.6	41.4	37	6	CQ759419	Sequence
c 602	11.6	41.4	21	6	E64450	Peptide hav	E64450	Peptide hav	c 675	11.6	41.4	38	6	AR125937	Sequence
c 603	11.6	41.4	21	6	AX000318	Sequence	AX000318	Sequence	c 676	11.6	41.4	38	6	BD263783	Adeno-ass

C 677	11.6	41.4	38	6	I24304	I24304 Sequence 91	C 750	11.6	41.4	42	6	AR198296	AR198296 Sequence
C 678	11.6	41.4	38	6	I49650	I49650 Sequence 2	C 751	11.6	41.4	42	6	AX469989	AX469989 Sequence
C 679	11.6	41.4	38	6	I56644	I56644 Sequence 2	C 752	11.6	41.4	42	9	S81405	S81405 T cell anti
C 680	11.6	41.4	38	6	AR236456	AR236456 Sequence	C 753	11.6	41.4	43	6	AR070510	AR070510 Sequence
C 681	11.6	41.4	38	6	AR236459	AR236459 Sequence	C 754	11.6	41.4	43	6	AR070526	AR070526 Sequence
C 682	11.6	41.4	38	6	AR236463	AR236463 Sequence	C 755	11.6	41.4	43	6	AR070530	AR070530 Sequence
C 683	11.6	41.4	38	6	AR236465	AR236465 Sequence	C 756	11.6	41.4	43	6	AR070534	AR070534 Sequence
C 684	11.6	41.4	38	6	AR236468	AR236468 Sequence	C 757	11.6	41.4	43	6	BD260002	BD260002 Polynucle
C 685	11.6	41.4	38	6	AX048269	AX048269 Sequence	C 758	11.6	41.4	43	6	AX045488	AX045488 Sequence
C 686	11.6	41.4	38	6	AX580618	AX580618 Sequence	C 759	11.6	41.4	44	6	AX483447	AX483447 Sequence
C 687	11.6	41.4	38	6	AX581172	AX581172 Sequence	C 760	11.6	41.4	44	6	AR051584	AR051584 Sequence
C 688	11.6	41.4	38	6	AX581172	AX581172 Sequence	C 761	11.6	41.4	44	6	AR088305	AR088305 Sequence
C 689	11.6	41.4	39	6	A26290	A26290 Subtilisin	C 762	11.6	41.4	44	6	AR112413	AR112413 Sequence
C 690	11.6	41.4	39	6	A26922	A26922 Oligonucleo	C 763	11.6	41.4	44	6	AR140204	AR140204 Sequence
C 691	11.6	41.4	39	6	AR0222568	AR0222568 Sequence	C 764	11.6	41.4	44	6	CO179278	CO179278 Sequence
C 692	11.6	41.4	39	6	AR037583	AR037583 Sequence	C 765	11.6	41.4	44	6	CO822734	CO822734 Sequence
C 693	11.6	41.4	39	6	AR083834	AR083834 Sequence	C 766	11.6	41.4	44	6	AR198563	AR198563 Sequence
C 694	11.6	41.4	39	6	AR138230	AR138230 Sequence	C 767	11.6	41.4	44	6	AR280488	AR280488 Sequence
C 695	11.6	41.4	39	6	AR140195	AR140195 Sequence	C 768	11.6	41.4	44	6	BD008442	BD008442 Fibroblas
C 696	11.6	41.4	39	6	AR140300	AR140300 Sequence	C 769	11.6	41.4	45	6	AR028569	AR028569 Sequence
C 697	11.6	41.4	39	6	AR150850	AR150850 Sequence	C 770	11.6	41.4	45	6	AR083215	AR083215 Sequence
C 698	11.6	41.4	39	6	AR173274	AR173274 Sequence	C 771	11.6	41.4	45	6	AR146461	AR146461 Sequence
C 699	11.6	41.4	39	6	AR178041	AR178041 Sequence	C 772	11.6	41.4	45	6	AR146531	AR146531 Sequence
C 700	11.6	41.4	39	6	I43379	I43379 Sequence 8	C 773	11.6	41.4	47	6	CO816919	CO816919 Sequence
C 701	11.6	41.4	39	6	I65730	I65730 Sequence 90	C 774	11.6	41.4	47	6	AR290076	AR290076 Sequence
C 702	11.6	41.4	39	6	I67962	I67962 Sequence 90	C 775	11.6	41.4	47	6	AR012090	AR012090 Sequence
C 703	11.6	41.4	39	6	I67962	I67962 Sequence 88	C 776	11.6	41.4	48	6	AR014529	AR014529 Sequence
C 704	11.6	41.4	39	6	I90181	I90181 Sequence	C 777	11.6	41.4	48	6	AR146457	AR146457 Sequence
C 705	11.6	41.4	39	6	AR236457	AR236457 Sequence	C 778	11.6	41.4	48	6	CO654096	CO654096 Sequence
C 706	11.6	41.4	39	6	AR255791	AR255791 Sequence	C 779	11.6	41.4	48	6	AR306678	AR306678 Sequence
C 707	11.6	41.4	39	6	AR275353	AR275353 Sequence	C 780	11.6	41.4	48	6	AR306678	AR306678 Sequence
C 708	11.6	41.4	39	6	AR344740	AR344740 Sequence	C 781	11.6	41.4	48	6	AR340113	AR340113 Sequence
C 709	11.6	41.4	39	6	BD074819	BD074819 Homolog o	C 782	11.6	41.4	48	6	AX006263	AX006263 Sequence
C 710	11.6	41.4	40	6	BD087227	BD087227 Mammalian	C 783	11.6	41.4	48	6	BD073398	BD073398 Respirato
C 711	11.6	41.4	40	6	AR022573	AR022573 Sequence	C 784	11.6	41.4	48	9	HS224216	HS224216 Homo sapi
C 712	11.6	41.4	40	6	AR024250	AR024250 Sequence	C 785	11.6	41.4	49	6	AR146496	AR146496 Sequence
C 713	11.6	41.4	40	6	AR026918	AR026918 Sequence	C 786	11.6	41.4	49	6	AR170484	AR170484 Sequence
C 714	11.6	41.4	40	6	AR037588	AR037588 Sequence	C 787	11.6	41.4	50	6	AX16122	AX16122 Synthetic p
C 715	11.6	41.4	40	6	AR045103	AR045103 Sequence	C 788	11.6	41.4	50	6	AX8858	AX8858 Sequence 12
C 716	11.6	41.4	40	6	AR146464	AR146464 Sequence	C 789	11.6	41.4	50	6	A73047	A73047 Sequence 23
C 717	11.6	41.4	40	6	AR146513	AR146513 Sequence	C 790	11.6	41.4	50	6	A73139	A73139 Sequence 23
C 718	11.6	41.4	40	6	AR157712	AR157712 Sequence	C 791	11.6	41.4	50	6	AR013763	AR013763 Sequence
C 719	11.6	41.4	40	6	AR166574	AR166574 Sequence	C 792	11.6	41.4	50	6	AR103941	AR103941 Sequence
C 720	11.6	41.4	40	6	AR178046	AR178046 Sequence	C 793	11.6	41.4	50	6	AR103942	AR103942 Sequence
C 721	11.6	41.4	40	6	CO819845	CO819845 Sequence	C 794	11.6	41.4	50	6	AR126943	AR126943 Sequence
C 722	11.6	41.4	40	6	E05394	E05394 DNA sequence	C 795	11.6	41.4	50	6	AR126943	AR126943 Sequence
C 723	11.6	41.4	40	6	E11592	E11592 PCR primer.	C 796	11.6	41.4	50	6	AR174688	AR174688 Sequence
C 724	11.6	41.4	40	6	E43797	E43797 Chimeric an	C 797	11.6	41.4	50	6	CO003432	CO003432 Sequence
C 725	11.6	41.4	40	6	AR236455	AR236455 Sequence	C 798	11.6	41.4	50	6	CO005043	CO005043 Sequence
C 726	11.6	41.4	40	6	AR236458	AR236458 Sequence	C 799	11.6	41.4	50	6	CO005573	CO005573 Sequence
C 727	11.6	41.4	40	6	AR236462	AR236462 Sequence	C 800	11.6	41.4	50	6	CO005574	CO005574 Sequence
C 728	11.6	41.4	40	6	AR364170	AR364170 Sequence	C 801	11.6	41.4	50	6	CO006885	CO006885 Sequence
C 729	11.6	41.4	40	6	AR481962	AR481962 Sequence	C 802	11.6	41.4	50	6	CO008337	CO008337 Sequence
C 730	11.6	41.4	40	6	AX538404	AX538404 Sequence	C 803	11.6	41.4	50	6	CO008668	CO008668 Sequence
C 731	11.6	41.4	40	6	BD011327	BD011327 Chimeric	C 804	11.6	41.4	50	6	CO009029	CO009029 Sequence
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C 733	11.6	41.4	41	6	I95137	I95137 Sequence 10	C 806	11.6	41.4	50	6	I24539	I24539 Sequence 19
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C 747	11.6	41.4	42	6	AR176725	AR176725 Sequence	C 820	11.4	40.7	20	6	BD088591	BD088591 A method
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ALIGNMENTS

RESULT 1
AR054576 28 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 2 from patent US 5837442.
DEFINITION AR054576
ACCESSION AR054576
VERSION AR054576.1 GI:5980153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Tsang,S.Yen.
TITLE Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL Patent: US 5837442-A 2 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
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DB 1 GCAAGCACCTTATCAGGCAGTACCACAA 28

RESULT 2
AR094138 28 bp DNA linear PAT 08-SEP-2000
LOCUS Sequence 4 from patent US 6001611.
DEFINITION AR094138
ACCESSION AR094138
VERSION AR094138.1 GI:10020883
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Will,S.Gordon.
TITLE Modified nucleic acid amplification primers
JOURNAL Patent: US 6001611-A 4 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 28; DB 6; Length 28;
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCAAGCACCTTATCAGGCAGTACCACAA 28

RESULT 3
BD181368 28 bp DNA linear PAT 15-MAY-2003
LOCUS A method for determination of a nucleic acid using a control.
DEFINITION BD181368
ACCESSION BD181368
VERSION BD181368.1 GI:30792286
KEYWORDS JP 2002335981-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 28)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 7 26-NOV-2002;
COMMENT F HOFFMANN LA ROCHE AG
OS Artificial Sequence
PN JP 2002335981-A/7
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC CI2NI5/09,CI2Q1/68,G01N33/50,G01N33/53,G01N33/566,G01N33/58,
PC CI2NI5/00
CC Description of Artificial Sequence: ST778 HCV-specific Primer-
CC sequence
FH Key Location/Qualifiers
FT source 1..28
FT /organism='Artificial Sequence',
FT Location/Qualifiers
source 1..28
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Best Local Similarity 100.0%; Pred. No. 0.23; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCAAGCACCTTATCAGGCAGTACCACAA 28

RESULT 4
AX147022 28 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 16 from Patent WO0137291.
DEFINITION AX147022
ACCESSION AX147022
VERSION AX147022.1 GI:14346293
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences

REFERENCE 1
AUTHORS Weindel, K., Riedling, M. and Geiger, A.
TITLE Magnetic glass particles, method for their preparation and uses
JOURNAL thereof
Patent: WO 0137291-A 16 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
source 1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide (HCV reverse)"
modified_base 28
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RESULT 5
AX523948
LOCUS AX523948 28 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 7 from Patent EP1236804.
ACCESSION AX523948
VERSION AX523948.1 GI:25168879
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences

REFERENCE 1
AUTHORS Jaeger, S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: EP 1236804-A 7 04-SEP-2002;
Roche Diagnostics GmbH (DE); F. Hoffmann-La Roche AG (CH)
FEATURES Location/Qualifiers
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AX524846
LOCUS AX524846 28 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 7 from Patent EP1236805.
ACCESSION AX524846
VERSION AX524846.1 GI:25169940
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences

REFERENCE 1
AUTHORS Jaeger, S.

TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 7 04-SEP-2002;
Roche Diagnostics GmbH (DE); F. Hoffmann-La Roche AG (CH)
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCAAGCACCTTATCAGGAGTACCACAA 28

RESULT 7
AR204716/c
LOCUS AR204716 47 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6368801.
ACCESSION AR204716
VERSION AR204716.1 GI:21502113
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Faruqi, A. Fawad.
TITLE Detection and amplification of RNA using target-mediated ligation
of DNA by RNA ligase
JOURNAL Patent: US 6368801-A 1 09-APR-2002;
FEATURES Location/Qualifiers
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ORIGIN

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RESULT 8
AX284180/c
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DEFINITION Sequence 1 from Patent WO0179420.
ACCESSION AX284180
VERSION AX284180.1 GI:17044868
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Faruqi, A. F.
TITLE Detection and amplification of rna using target-mediated ligation
of dna by rna ligase
JOURNAL Patent: WO 0179420-A 1 25-OCT-2001;
MOLECULAR STAGING, INC. (US)
FEATURES Location/Qualifiers
source 1..47
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
LOCUS AR054577 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837442.
ACCESSION AR054577
VERSION AR054577.1 GI:5980154
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Tsang,S.Yen.
TITLE Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL Patent: US 5837442-A 3 17-NOV-1998;
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QY 1 GCAAGCACCTTATCAGGAGTACCACAA 27
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RESULT 10
LOCUS AR411541 27 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6638714.
ACCESSION AR411541
VERSION AR411541.1 GI:40163885
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Linnen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL Patent: US 6638714-A 5 28-OCT-2003;
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LOCUS BD000267 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof.
Accession BD000267.1 GI:18623346
Keywords JP 2000279200-A/5.
Source synthetic construct
Organism artificial sequences.
Reference 1 (bases 1 to 27)
Authors Linnen,J.M. and Gorman,K.M.
Title Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof
Journal Patent: JP 2000279200-A 5 10-OCT-2000;
Comment ORTHO CLINICAL DIAGNOSTICS INC
OS Artificial Sequence
PN JP 2000279200-A/5
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNEN,KEVIN M GORMAN
PC C12Q1/68,C12N15/09//(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
CC C12R1:92)
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LOCUS BD183052/c 29 bp DNA linear PAT 17-JUN-2003
DEFINITION Nucleic acids for grouping hepatitis C virus and method for group
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Accession BD183052.1 GI:31875252
Version BD183052
Keywords JP 2002345467-A/24.
Source synthetic construct
Organism artificial sequences.
Reference 1 (bases 1 to 29)
Authors Mukaide,M., Tsunoda,K. and Hikiji,K.
Title Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same
Journal Patent: JP 2002345467-A 24 03-DEC-2002;
SRL INC
OS Artificial Sequence
PN JP 2002345467-A/24
PD 03-DEC-2002
PF 17-APR-2001 JP 2001118810
PI MASAKAZU MUKAIDE,KOICHI TSUNODA,KAZUMASA HIKIJI PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC Nucleic Acid
Used as signal-amplifying probe which hybridizes CC
with a
CC region in HCV 5'-UTR region
FH Key Location/Qualifiers
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DEFINITION Sequence 51 from patent US 5747244.											
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VERSION AR004397.1 GI:3965276											
KEYWORDS											
SOURCE Unknown.											
ORGANISM Unclassified.											
REFERENCE 1 (bases 1 to 33)											
AUTHORS Sheridan,P., Chang,C.-A., Running,J. and Urdea,M.S.											
TITLE Nucleic acid probes immobilized on polystyrene surfaces											
JOURNAL Patent: US 5747244-A 51 05-MAY-1998;											
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DEFINITION Sequence 61 from patent US 5849481.											
ACCESSION AR064936											
VERSION AR064936.1 GI:5995152											
KEYWORDS											
SOURCE Unknown.											
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AUTHORS Urdea,M.S.; Horn,T.; Chang,C.-A.; Warner,B. and Fultz,T.J.											
TITLE Nucleic acid hybridization assays employing large comb-type branched polynucleotides											
JOURNAL Patent: US 5849481-A 61 15-DEC-1998;											
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TITLE
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Qy
1 GCAAGCACCCCTATCAGGCAGTACC 24
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Db
10 GCAAGCACCCCTATCAGGCAGTACC 33
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REFERENCE
AUTHORS
TITLE
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COMMENT
Qy
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Db
10 GCAAGCACCCCTATCAGGCAGTACC 33
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AUTHORS
TITLE
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ORGANISM
REFERENCE
AUTHORS
TITLE
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ORGANISM
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AUTHORS
TITLE
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AUTHORS
TITLE
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COMMENT
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AUTHORS
TITLE
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TITLE
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PF 10-MAY-2002 JP 2002134999
PR 08-MAY-1991 US 697326
PI michael s adair,tai-ann cha,bruce irvine,janice kolberg,eileen
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CC synthetic construct
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Db 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 22
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LOCUS HCV Genomic Sequences For Diagnostics And Therapeutics. 33 bp DNA linear PAT 17-JUL-2003
DEFINITION
ACCESSION BD189447
VERSION BD189447.1 GI:32999186
KEYWORDS JP 2003009893-A/127.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 33)
AUTHORS Adair,M.S.; Cha,T.; Beal,E.; Irvine,B. and Kolberg,J.
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics
JOURNAL Patent: JP 2003009893-A 127 14-JAN-2003;
Chiron Corporation
COMMENT OS Artificial Sequence
PN JP 2003009893-A/127
PD 14-JAN-2003
PF 10-MAY-2002 JP 2002135000
PR 08-MAY-1991 US 697326
PI michael s adair,tai-ann cha,eileen beal,bruce irvine,janice
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 23
I82872
LOCUS I82872 Sequence 51 from patent US 5712383. 33 bp DNA linear PAT 10-JUN-1998
DEFINITION
ACCESSION I82872
VERSION I82872.1 GI:3211169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan,P.; Chang,C.-A.; Running,J. and Urdea,M.S.
TITLE Process for immobilizing nucleic acid probes on polystyrene
surfaces
JOURNAL Patent: US 5712383-A 51 27-JAN-1998;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGCACCTATCAGGCAGTACC 24
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Db 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 24
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LOCUS AX250665 24 bp DNA linear PAT 06-OCT-2001
DEFINITION Sequence 61 from Patent WO0168921.
ACCESSION AX250665
VERSION AX250665.1 GI:15984409
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Koshinsky,H.; Zwick,M.S. and Mccue,K.F.
TITLE Compositions and methods for simultaneous detection of multiple
biological entities
JOURNAL Patent: WO 0168921-A 61 20-SEP-2001;
Investigen (US)
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Location/Qualifiers
/organism="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 GCAAGCACCTATCAGGCAGTACC 24

RESULT 25
AX202931
LOCUS AX202931 27 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 6 from Patent WO0152612.
ACCESSION AX202931
VERSION AX202931.1 GI:15392394
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Elaisari,A.; Mandrand,B.; Delair,T.; Spencer,D. and Arkis,A.
TITLE Method for isolating proteins or protein and nucleic acid
associations, or particle and protein complexes, reagent and uses
JOURNAL Patent: WO 0152612-A 6 26-JUL-2001;
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QY 1 GCAAGCACCTATCAGGCAGTAC 23
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DB 5 GCAAGCACCTATCAGGCAGTAC 27
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RESULT 26
LOCUS AX202933 27 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 8 from Patent WO0152612.
ACCESSION AX202933
VERSION AX202933.1 GI:15392396
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Elaissari, A., Mandrand, B., Delair, T., Spencer, D. and Arkis, A.
TITLE Method for isolating proteins or protein and nucleic acid
JOURNAL associations, or particle and protein complexes, reagent and uses
PATENT: WO 0152612-A 8 26-JUL-2001;
BIO MERIEUX (FR)
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Best Local Similarity 100.0%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTAC 23
    |||||
DB 5 GCAAGCACCTATCAGGCAGTAC 27
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RESULT 27
LOCUS AR411542 27 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6638714.
ACCESSION AR411542
VERSION AR411542.1 GI:40163886
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Linnen, J.M. and Gorman, K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL virus (HCV) and methods of use thereof
PATENT: US 6638714-A 6 28-OCT-2003;
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QY 1 GCAAGCACCTATCAGGCAGTAC 22
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Db 6 GCAAGCACCTATCAGGCAGTAC 27

RESULT 28
LOCUS AX282438/c 27 bp RNA linear PAT 02-NOV-2001
DEFINITION Sequence 10 from Patent WO0166721.
ACCESSION AX282438
VERSION AX282438.1 GI:16609569
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Usman, N., Mcswiggen, J.A., Zinnen, S., Seiwert, S., Haeberli, P.,
Chowrira, B. and Blatt, L.
TITLE Nucleic acid sensor molecules
JOURNAL Patent: WO 0166721-A 10 13-SEP-2001;
RIBOZYME PHARMACEUTICALS, INC. (US)
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    /note="Synthetic target signaling sequence"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e+02;
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QY 1 GCAAGCACCTATCAGGCAGTAC 22
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RESULT 29
LOCUS BD000268 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof.
ACCESSION BD000268
VERSION BD000268.1 GI:18623347
KEYWORDS JP 2000279200-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
AUTHORS Linnen, J.M. and Gorman, K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL virus (HCV) and methods of use thereof
PATENT: JP 2000279200-A 6 10-OCT-2000;
ORTHOClinical Diagnostics Inc
COMMENT OS Artificial Sequence
PN JP 2000279200-A/6
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNEN, KEVIN M GORMAN
PC C12Q1/68, C12N15/09, C12R1/92, C12N15/00, (C12N15/00,
CC C12R1:92)
CH
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Query Match      78.6%; Score 22; DB 6; Length 27;

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Best Local Similarity 100.0%; Pred. No. 1e+02;
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Qy 1 GCAAGCACCTATCAGGCAGTA 22
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Db 6 GCAAGCACCTATCAGGCAGTA 27
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RESULT 30
E58845
LOCUS E58845 46 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting ribonucleic acid.
ACCESSION E58845
VERSION JP 2000333699-A/1
KEYWORDS JP 2000333699-A/1
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Fujii,T., Goda,H., Tsuruoka,M. and Karube,M.
TITLE Method for detecting ribonucleic acid
JOURNAL Patent: JP 2000333699-A 1 05-DEC-2000;
COMMENT MASAO KARUBE MAKOTO TSURUOKA, TOWA KAGAKU KK
OS Artificial Sequence
FN JP 2000333699-A/1
PD 05-DEC-2000
PF 31-MAY-1999 JP 1999152109
PR
PI TAKAKI FUJII, HIROSHI GODA, MAKOTO TSURUOKA, MASAO KARUBE PC
C12Q1/68, C12N15/09, G01N21/64, G01N21/64, G01N33/50, G01N33/566, PC
G01N33/58,
PC C12N15/00
CC
FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 78.6%; Score 22; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
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Db 25 GCAAGCACCTATCAGGCAGTA 46
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RESULT 31
AR124661
LOCUS AR124661 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6172046.
ACCESSION AR124661
VERSION AR124661.1 GI:14110022
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Albrecht,J.K.
TITLE Combination therapy for eradicating detectable HCV-RNA in patients
having chronic Hepatitis C infection
JOURNAL Patent: US 6172046-A 4 09-JAN-2001;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR167000 21 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 17 from patent US 6284458.
ACCESSION AR167000
VERSION AR167000.1 GI:16243416
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
Nakatake,H., Hamada,F., Eto,T. and Furukawa,S.
TITLE Compositions and methods for treatment of hepatitis C
JOURNAL virus-associated diseases
FEATURES
source
Location/Qualifiers
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ORIGIN
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Db 1 CCCTATCAGGCAGTACCACAA 21
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RESULT 33
AR210655
LOCUS AR210655 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 17 from patent US 6391542.
ACCESSION AR210655
VERSION AR210655.1 GI:21513440
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
Nakatake,H., Hamada,F., Eto,T., Furukawa,S., Furasako,S.,
Bruice,T.W. and Lima,W.F.
TITLE Compositions and methods for treatment of Hepatitis C
JOURNAL virus-associated diseases
FEATURES
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Location/Qualifiers
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RESULT 34
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AR242414
LOCUS AR242414 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6472373.
ACCESSION AR242414
VERSION AR242414.1 GI:27288683
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Albrecht J.K.
TITLE Combination therapy for eradicating detectable HCV-RNA in antiviral treatment naive patients having chronic hepatitis C infection
JOURNAL Patent: US 6472373-A 4 29-OCT-2002;
FEATURES
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RESULT 35
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LOCUS AX540625 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 4 from Patent WO0232414.
ACCESSION AX540625
VERSION AX540625.1 GI:25273610
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Albrecht J.
TITLE Ribavirin-pegylated interferon alfa hcv combination therapy
JOURNAL Patent: WO 0232414-A 4 25-APR-2002;
Schering Corporation (US)
FEATURES
source Location/Qualifiers
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Db 1 CCCTATCAGGCGTACCACAA 21

RESULT 36
I73294
LOCUS I73294 23 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 25 from patent US 5686272.
ACCESSION I73294
VERSION I73294.1 GI:3009433
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Marshall, R.L., Carrino, J.J. and Sustacheck, J.C.

TITLE Amplification of RNA sequences using the ligase chain reaction
JOURNAL Patent: US 5686272-A 25 11-NOV-1997;
FEATURES
source Location/Qualifiers
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Db 3 GCAAGCACCCCTATCAGGCAGT 23

RESULT 37
A68286
LOCUS A68286 24 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 7 from Patent WO9746716.
ACCESSION A68286
VERSION A68286.1 GI:4759407
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Bosio, P., Strumia, C. and Clemenza, F.
TITLE METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS
JOURNAL Patent: WO 9746716-A 7 11-DEC-1997;
WARCO B V (NL)
COMMENT Other publication IT RM960404 19971209.
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 38
AR011642/c
LOCUS AR011642 24 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 51 from patent US 5763159.
ACCESSION AR011642
VERSION AR011642.1 GI:3969632
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Simmonds, P., Chan, S.-W. and Yap, P. Lee.
TITLE Hepatitis-C virus testing
JOURNAL Patent: US 5763159-A 51 09-JUN-1998;
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LOCUS AR054579 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5837442.

ACCESSION AR054579

VERSION AR054579.1 GI:5980156

KEYWORDS

SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Tsang, S.Yen.

TITLE Oligonucleotide primers for amplifying HCV nucleic acid

JOURNAL Patent: US 5837442-A 5 17-NOV-1998;

FEATURES Location/Qualifiers

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RESULT 40

LOCUS BD183045 24 bp DNA linear PAT 17-JUN-2003
DEFINITION Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same.

ACCESSION BD183045

VERSION BD183045.1 GI:31875245

KEYWORDS JP 2002345467-A/17.

SOURCE synthetic construct

ORGANISM artificial sequences.

1 (bases 1 to 24)

REFERENCE Mukaide, M., Tsunoda, K. and Hikiji, K.

AUTHORS Nucleic acids for grouping hepatitis C virus and method for group

TITLE ing hepatitis C virus using the same

JOURNAL Patent: JP 2002345467-A 17 03-DEC-2002;

SRL INC

COMMENT OS Artificial Sequence

PN JP 2002345467-A/17

PD 03-DEC-2002

PF 17-APR-2001 JP 2001118810

PI MASAKAZU MUKAIDE, KOICHI TSUNODA, KAZUMASA HIKIJI PC

C12N15/09, C12Q1/68, G01N33/53, G01N33/566, C12N15/00 CC Nucleic Acid

Used as Primer amplifying a region in 5'-UTR of CC

Hepatitis C

CC virus

FH Key

FT source

1..24

Location/Qualifiers

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FT

Location/Qualifiers

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ORIGIN

Query Match 75.0%; Score 21; DB 6; Length 24;

Best Local Similarity 100.0%; Pred.No. 2.9e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 28
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Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
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- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
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- 8: Geneseq2003as:*
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- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	28	100.0	29	6	AAD43740 HCV DNA a
7	27	96.4	27	3	AAT67195 Hepatitis
8	27	96.4	27	3	AAV74623 HCV-speci
9	27	96.4	29	10	ADC54073
10	25	89.3	40	2	AAV54436 Nucleotid
11	25	89.3	47	8	ABV81791 HCV 5' UT
12	24	85.7	28	2	AAT05222 Hepatitis
13	24	85.7	28	3	AAZ57757 Hepatitis
14	24	85.7	30	2	AAQ55728 Hepatitis
15	24	85.7	33	2	AAQ31158 Probe 127
16	24	85.7	33	2	AAQ46464 Hepatitis
17	24	85.7	33	2	AAV07838 HCV.33.9
18	24	85.7	33	2	AAV83066 Amplifier
19	23	82.1	23	10	ADF52816 Hepatitis
20	23	82.1	23	10	ADF52808 Hepatitis
21	23	82.1	23	10	ADF52814 Hepatitis

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c	23	82.1	23	10	ADF52815	Adf52815 Hepatitis
c	24	82.1	24	4	AAAD19057	Adf19057 Hepatitis
c	25	82.1	27	3	AAZ87367	Aaz87367 Hepatitis
c	26	82.1	27	4	AAH78439	Aah78439 PCR prime
c	27	82.1	27	4	AAH78441	Aah78441 PCR prime
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c	30	78.6	27	3	AAQ71839	Aaq71839 PCR prime
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c	32	78.6	27	4	ABK09262	Abk09262 Enzymatic
c	33	78.6	27	4	ABK09264	Abk09264 Enzymatic
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c	35	78.6	27	4	ABA02738	Aba02738 Nucleic a
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c	38	75.0	21	2	AAQ75034	Aaq75034 PCR prime
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c	40	75.0	21	2	AAZ25792	Aaz25792 Hepatitis
c	41	75.0	21	2	AAZ25838	Aaz25838 Downstrea
c	42	75.0	21	3	AAA65201	Aaa65201 Hepatitis
c	43	75.0	21	3	AAAC62980	Aaa62980 Downstrea
c	44	75.0	21	3	AAAC63602	Aac63602 PCR prime
c	45	75.0	21	6	ABN86274	Abn86274 HCV gene
c	46	75.0	21	6	ABK50242	Abk50242 Hepatitis
c	47	75.0	21	6	ABZ21803	Abz21803 PCR prime
c	48	75.0	21	9	ABX16145	Abx16145 HCV PCR p
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c	50	75.0	21	9	ADAL13858	Adal13858 Short int
c	51	75.0	21	9	ADAL13859	Adal13859 Short int
c	52	75.0	21	9	ADAL13866	Adal13866 Short int
c	53	75.0	21	9	ACD26347	Acd26347 Hepatitis
c	54	75.0	21	10	ADE76489	Ade76489 PCR prime
c	55	75.0	21	10	ADF52860	Adf52860 Hepatitis
c	56	75.0	21	10	ADF52862	Adf52862 Hepatitis
c	57	75.0	21	10	ADF52869	Adf52869 Hepatitis
c	58	75.0	21	10	ADF52861	Adf52861 Hepatitis
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c	65	75.0	23	10	ADF52819	Adf52819 Hepatitis
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c	67	75.0	24	2	AAQ37586	Aaq37586 HCV conse
c	68	75.0	24	2	AAQ79963	Aaq79963 Primer KY
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c	78	75.0	24	4	AAH25404	Aah25404 PCR prime
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c	82	75.0	24	10	ADC54066	Adc54066 HCV 5'UTR
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c	86	75.0	24	12	ADH79951	Adh79951 HCV RT-PC
c	87	75.0	24	12	ADH79951	Adh79951 HCV RT-PC
c	88	75.0	24	12	ADO05660	Ado05660 HCV DNA f
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100	21	75.0	48	10	ADD55639	Add55639 PCR prime	c	173	19	67.9	23	10	ADP52975	Adp52975 Hepatitis
101	20	71.4	21	4	ABA03376	Aba03376 Human Gen	c	174	19	67.9	23	10	ADP52820	Adp52820 Hepatitis
102	20	71.4	21	9	ADA13865	Ada13865 Short int	c	175	19	67.9	23	10	ADP52913	Adp52913 Hepatitis
103	20	71.4	21	9	ADA13810	Ada13810 Short int	c	176	19	67.9	23	10	ADP52918	Adp52918 Hepatitis
104	20	71.4	21	10	ADP52987	Adp52987 Hepatitis	c	177	19	67.9	23	10	ADP52971	Adp52971 Hepatitis
105	20	71.4	21	10	ADP52834	Adp52834 Hepatitis	c	178	19	67.9	23	10	ADP52976	Adp52976 Hepatitis
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108	20	71.4	22	4	AAH44938	Aah44938 HCV speci	c	181	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
109	20	71.4	22	4	AH44912	Aah44912 HCV speci	c	182	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
110	20	71.4	23	2	AAV60676	Aav60676 Primer #1	c	183	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
111	20	71.4	23	10	ADP52916	Adp52916 Hepatitis	c	184	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
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114	20	71.4	24	2	AAQ62946	Aaq62946 AS5 - bin	c	187	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
115	20	71.4	24	2	AAX81679	Aax81679 Antisense	c	188	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
116	20	71.4	24	3	AAA39647	Aaa39647 HCV 5' UT	c	189	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
117	20	71.4	39	2	ABS70884	Abs70884 Hepatitis	c	190	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
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123	19.4	69.3	21	10	ADP52930	Adp52930 Hepatitis	c	196	19	67.9	32	6	ABL50820	AbL50820 INT-2-D p
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249 17 60.7 30 10 ABZ76308 Abz76308 HCV RNA 5
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254 16 57.1 16 3 AAZ36221 Aaz36221 PCR prime
255 16 57.1 17 8 ACD56920 Acd56920 HCV DNazY
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267 15.4 55.0 22 5 AAC86010 Aac86010 Internal
268 15.4 55.0 24 2 AAQ44488 Aaq44488 HCV virus
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272 15 53.6 15 3 AAZ62403 Aaz62403 Substrate
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280 15 53.6 15 6 ABX01755 Abx01755 Hepatitis
281 15 53.6 15 6 ABX01825 Abx01825 Hepatitis
282 15 53.6 15 8 ACD66205 Acd66205 Anti-HCV
283 15 53.6 15 8 ACD66281 Acd66281 Anti-HCV
284 15 53.6 15 8 ACD65978 Acd65978 Anti-HCV
285 15 53.6 15 8 ACD65979 Acd65979 Anti-HCV
286 15 53.6 15 8 ACD66190 Acd66190 Anti-HCV
287 15 53.6 15 8 ACD66204 Acd66204 Anti-HCV
288 15 53.6 15 8 ACD66257 Acd66257 Anti-HCV
289 15 53.6 15 8 ACD66256 Acd66256 Anti-HCV
290 15 53.6 15 8 ACD66191 Acd66191 Anti-HCV
291 15 53.6 15 12 ADI87710 Adi87710 Anti-HCV
292 15 53.6 15 12 ADI87686 Adi87686 Anti-HCV
293 15 53.6 15 12 ADI87547 Adi87547 Anti-HCV
294 15 53.6 15 12 ADI87655 Adi87655 Anti-HCV
295 15 53.6 15 12 ADI87548 Adi87548 Anti-HCV
296 15 53.6 15 12 ADI87669 Adi87669 Anti-HCV
297 15 53.6 15 12 ADI87654 Adi87654 Anti-HCV
298 15 53.6 15 12 ADI87668 Adi87668 Anti-HCV
299 15 53.6 15 12 ADI87685 Adi87685 Anti-HCV
300 15 53.6 17 8 ACD65753 Acd65753 HCV minus
301 15 53.6 17 8 ACD65749 Acd65749 HCV minus
302 15 53.6 17 12 ADI87247 Adi87247 HCV DNazY
303 15 53.6 17 12 ADI87243 Adi87243 HCV DNazY
304 15 53.6 18 2 AAV70447 Aav70447 HCV target
305 15 53.6 18 6 ABL46057 Abl46057 Hepatitis
306 15 53.6 18 6 ACA61798 Aca61798 Sample pr
307 15 53.6 18 12 ADJ87103 Adj87103 Probe use
308 15 53.6 18 12 ADK82247 Adk82247 Hepatitis
309 15 53.6 19 2 AAQ203674 Aaq203674 HCV-Hc59
310 15 53.6 19 2 AAT03674 Aat03674 Hepatitis
311 15 53.6 19 2 AAT30241 Aat30241 Primer fo
312 15 53.6 19 2 AAV20733 Aav20733 Hepatitis
313 15 53.6 19 2 AAV22783 Aav22783 Antisense

314 15 53.6 19 2 AAZ07085 Aaz07085 Hepatitis
315 15 53.6 19 3 AAZ57172 Aaz57172 Single st
316 15 53.6 19 5 AAH23737 Aah23737 Oligonuc
317 15 53.6 19 6 ABK86853 Abk86853 Hepatitis
318 15 53.6 19 6 AAD51015 Aad51015 Hepatitis
319 15 53.6 19 8 AAD58330 Aad58330 HCV RNA a
320 15 53.6 19 10 ADF51449 Adf51449 Hepatitis
321 15 53.6 19 10 ADF52127 Adf52127 Hepatitis
322 15 53.6 19 10 ADF51431 Adf51431 Hepatitis
323 15 53.6 19 10 ADF52145 Adf52145 Hepatitis
324 15 53.6 20 2 AAQ89250 Aaq89250 Hepatitis
325 15 53.6 20 2 AAQ64073 Aaq64073 NANSHV co
326 15 53.6 20 2 AAQ75228 Aaq75228 Antisense
327 15 53.6 20 2 AAT01494 Aat01494 Hepatitis
328 15 53.6 20 2 AAT36372 Aat36372 5'UTR reg
329 15 53.6 20 2 AAV54437 Aav54437 Nucleotid
330 15 53.6 20 3 AAZ88591 Aaz88591 Hepatitis
331 15 53.6 21 2 AAV35209 Aav35209 Hepatitis
332 15 53.6 21 2 AAV41667 Aav41667 Nucleotid
333 15 53.6 21 2 AAX00298 Aax00298 PCR prime
334 15 53.6 22 2 AAQ67618 Aaq67618 Primer fo
335 15 53.6 25 3 AAA96561 Aaa96561 Reverse p
336 15 53.6 25 3 AAA96552 Aaa96552 Reverse p
337 15 53.6 25 3 AAA74625 Aaa74625 HCV-speci
338 15 53.6 25 9 ACH56987 Ach56987 DNA targe
339 15 53.6 30 6 ABK89627 Abk89627 Chimeric
340 15 53.6 30 6 ABK89628 Abk89628 Chimeric
341 15 53.6 30 8 ACD17034 Acd17034 Sample pr
342 14.8 52.9 21 10 ADF75351 Adf75351 Human RT-
343 14.8 52.9 22 2 AAQ67624 Aaq67624 Primer fo
344 14.6 52.1 25 9 ACI36544 Aci36544 Human mic
345 14.6 52.1 25 9 ACI36545 Aci36545 Human mic
346 14.6 52.1 30 6 ABK66063 Abk66063 Human gen
347 14.6 52.1 48 2 AAQ27825 Aaq27825 Thrombomo
348 14.6 52.1 50 10 ADD01487 Ad01487 Human adu
349 14.4 51.4 25 9 ACI65494 Aci65494 Human mic
350 14.4 51.4 25 12 ADP14075 Adp14075 Renal cel
351 14.4 51.4 30 2 AAQ06963 Aaq06963 Pestiviru
352 14.4 51.4 31 2 AAV71016 Aav71016 PCR prime
353 14.2 50.7 20 8 ACC42196 Acc42196 Human GAT
354 14.2 50.7 25 9 ACH52589 Ach52589 DNA targe
355 14.2 50.7 40 9 ACD32830 Acd32830 Synthetic
356 14.2 50.7 50 12 ADH08314 Adh08314 Probe for
357 14.2 50.7 50 12 ADH08315 Adh08315 Probe for
358 14 50.0 14 3 AAZ64683 Aaz64683 Substrate
359 14 50.0 14 6 ABX01520 Abx01520 Hepatitis
360 14 50.0 15 6 ABX01754 Abx01754 Hepatitis
361 14 50.0 17 8 ACD56921 Acd56921 HCV DNazY
362 14 50.0 17 8 ACD56916 Acd56916 HCV DNazY
363 14 50.0 17 12 ADI82816 Adi82816 HCV DNazY
364 14 50.0 18 2 AAV41664 Aav41664 Nucleotid
365 14 50.0 19 3 AAA38182 Aaa38182 Primer us
366 14 50.0 19 10 ADF52120 Adf52120 Hepatitis
367 14 50.0 19 10 ADF51424 Adf51424 Hepatitis
368 14 50.0 19 10 ADF51455 Adf51455 Hepatitis
369 14 50.0 20 2 AAD52151 Aad52151 Hepatitis
370 14 50.0 20 2 AAX58050 Aax58050 PCR prime
371 14 50.0 21 3 AAZ88380 Aaz88380 Oligonuc
372 14 50.0 21 10 ADF52990 Adf52990 Hepatitis
373 14 50.0 21 10 ADF52992 Adf52992 Hepatitis
374 14 50.0 21 10 ADF52981 Adf52981 Hepatitis
375 14 50.0 23 10 ADF52969 Adf52969 Hepatitis
376 14 50.0 23 10 ADF52920 Adf52920 Hepatitis
377 14 50.0 23 10 ADF52978 Adf52978 Hepatitis
378 14 50.0 23 12 ADJ34749 Adj34749 Mouse 2'-
379 14 50.0 25 12 ADP16996 Adp16996 Renal cel
380 14 50.0 26 2 AAQ06961 Aaq06961 Pestiviru
381 14 50.0 26 2 AAX22794 Aax22794 PCR prime
382 14 50.0 30 2 AAV53190 Aav53190 Plasmid p
383 14 50.0 30 2 AAV18340 Aav18340 Saccharom
384 14 50.0 30 2 AAX27164 Aax27164 PCR prime
385 14 50.0 30 2 AAX05337 Aax05337 S. cerevi

C 387	14	50.0	30	2	AAX76357	Aax76357 PCR prime	460	13.4	47.9	45	12	ADM90618	Adm90618 Human DNA
C 388	14	50.0	33	6	ABL50363	Abi50363 Human rib	461	13.4	47.9	48	12	ADM91036	Adm91036 Human DNA
C 389	14	50.0	38	11	ADL52289	Adl52289 Human NOG	C 462	13.2	47.1	20	2	AAX21954	Aax21954 Human B-r
C 390	14	50.0	38	11	ADL52289	Adl52289 Human NOG	C 463	13.2	47.1	20	2	AAX21953	Aax21953 Human B-r
C 391	14	50.0	43	3	AA37285	Aaa37285 Human PRO	C 464	13.2	47.1	20	6	AA44817	Aad44817 Human B-r
C 392	14	50.0	43	3	AA37285	Aaa37285 Human PRO	C 465	13.2	47.1	20	6	AA44818	Aad44818 Human B-r
C 393	14	50.0	43	3	AA37285	Aaa37285 Human PRO	C 466	13.2	47.1	20	10	ADF09811	Adf09811 Human b-r
C 394	14	50.0	43	9	ACD68468	Ac68468 Novel hum	C 467	13.2	47.1	20	10	ADF09812	Adf09812 Human b-r
C 395	14	50.0	43	9	ACH04570	Ach04570 Human sec	C 468	13.2	47.1	20	10	ADG31594	Adg31594 PCR prime
C 396	14	50.0	43	9	ACH04570	Ach04570 Human sec	C 469	13.2	47.1	20	10	ADG31594	Adg31594 PCR prime
C 397	14	50.0	43	10	ADD18189	Adc18189 Human PRO	C 470	13.2	47.1	20	10	ADG31594	Adg31594 PCR prime
C 398	14	50.0	43	10	ADD70835	Adg70835 Human sec	C 471	13.2	47.1	25	5	AAI61993	Aai61993 Soybean 2
C 399	14	50.0	43	10	ADD39912	Adg39912 Human sec	C 472	13.2	47.1	25	9	ACI79134	Act79134 Human mic
C 400	14	50.0	43	10	ADD70358	Adg70358 Human sec	C 473	13.2	47.1	25	9	ACK25695	Ack25695 Human mic
C 401	14	50.0	43	10	ADD38479	Adg38479 Human sec	C 474	13.2	47.1	25	9	AAZ61905	Aaz61905 Hammerhea
C 402	14	50.0	43	10	ADD39435	Adg39435 Human sec	C 475	13.2	47.1	29	2	AAT64949	Aat64949 Primer N1
C 403	14	50.0	43	10	ADD39958	Adg39958 Human sec	C 476	13.2	47.1	29	2	AAZ60228	Aaz60228 Integrin
C 404	14	50.0	43	10	ADD40389	Adg40389 Human sec	C 477	13.2	47.1	29	6	ABQ82432	Abq82432 Human NOV
C 405	14	50.0	43	10	ADBE50610	Adg50610 Human sec	C 478	13.2	47.1	29	12	ADH42764	Adh42764 Novel hum
C 406	14	50.0	43	10	ADBE50133	Adg50133 Human sec	C 479	13.2	47.1	30	2	AAT44313	Aat44313 Primer KT
C 407	14	50.0	43	10	ADBE21691	Adg21691 Human sec	C 480	13.2	47.1	30	4	AAF60291	Aaf60291 Human CD4
C 408	14	50.0	43	10	ADF30116	Adf30116 Human sec	C 481	13.2	47.1	31	3	AAA78746	Aaa78746 Human gen
C 409	14	50.0	43	10	ADF56009	Adf56009 Human sec	C 482	13.2	47.1	31	8	ACD43936	Acd43936 Human gen
C 410	14	50.0	43	12	ADH99513	Adh99513 Human sec	C 483	13.2	47.1	33	5	AAZ90797	Aaz90797 Probe no.
C 411	14	50.0	43	12	ADP26004	Adp26004 Human sec	C 484	13.2	47.1	33	5	AAZ90797	Aaz90797 Probe no.
C 412	14	50.0	43	12	ADP24903	Adp24903 Human sec	C 485	13.2	47.1	33	5	AAZ90797	Aaz90797 Probe no.
C 413	14	50.0	43	12	ADP24903	Adp24903 Human sec	C 486	13.2	47.1	37	4	AAH91211	Aah91211 Human inf
C 414	14	50.0	43	12	ADP24903	Adp24903 Human sec	C 487	13.2	47.1	38	2	AAZ03525	Aaz03525 Fragment
C 415	14	50.0	43	12	ADH04162	Adh04162 Human sec	C 488	13.2	47.1	40	10	ACA55312	Act55312 Human mod
C 416	14	50.0	43	12	ADH04162	Adh04162 Human sec	C 489	13.2	47.1	42	9	ADA01770	Ada01770 Mouse car
C 417	14	50.0	43	12	ADH04162	Adh04162 Human sec	C 490	13.2	47.1	42	10	ADB71509	Adb71509 Mouse car
C 418	14	50.0	43	12	ADH04162	Adh04162 Human sec	C 491	13.2	47.1	43	2	AAS050261	Aas050261 HIV env I
C 419	14	50.0	43	12	ADH04162	Adh04162 Human sec	C 492	13.2	47.1	43	2	AAS050261	Aas050261 HIV env I
C 420	14	50.0	43	12	ADH04162	Adh04162 Human sec	C 493	13.2	47.1	45	3	AAZ96599	Aaz96599 T cell an
C 421	14	50.0	43	12	ADH04162	Adh04162 Human sec	C 494	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 422	14	50.0	46	8	ABA01126	Abc01126 HCV prime	C 495	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 423	14	50.0	46	8	ACC79266	Acc79266 Hepatitis	C 496	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 424	14	50.0	50	4	AAZ28468	Aal28468 Human SNP	C 497	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 425	14	50.0	50	4	AAZ28468	Aal28468 Human SNP	C 498	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 426	13.8	49.3	29	10	ABZ823761	Abz823761 Toxicolog	C 499	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 427	13.8	49.3	30	3	AAA46681	Aaa46681 Primer P2	C 500	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 428	13.8	49.3	33	10	ADG75110	Adg75110 Human her	C 501	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 429	13.8	49.3	38	2	AAT81937	Aat81937 Human c-m	C 502	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 430	13.8	49.3	39	10	ADC46974	Adc46974 Synthesis	C 503	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 431	13.8	49.3	40	10	ADC56754	Adc56754 Self asse	C 504	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 432	13.8	49.3	41	6	AAZ50613	Aal50613 Human coa	C 505	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 433	13.8	49.3	50	6	ABZ03017	Abz03017 Human leu	C 506	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 434	13.6	48.6	20	2	AAT87852	Aat87852 Human HCV	C 507	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 435	13.6	48.6	21	2	AAV52651	Aav52651 Hepatocyt	C 508	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 436	13.6	48.6	21	6	AAZ46495	Aaz46495 Human HNP	C 509	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 437	13.6	48.6	24	12	ADK97032	Adk97032 Primer of	C 510	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 438	13.6	48.6	25	9	ACI41544	Act41544 Human mic	C 511	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 439	13.6	48.6	26	6	ABK49738	Abk49738 Human mal	C 512	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 440	13.6	48.6	36	12	ADJ66773	Adj66773 Flea and	C 513	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 441	13.6	48.6	36	12	ADJ66771	Adj66771 Flea and	C 514	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 442	13.6	48.6	38	11	ADL52491	Adl52491 Human NOG	C 515	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 443	13.6	48.6	39	10	ADC60949	Adc60949 NASBA pri	C 516	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 444	13.6	48.6	50	3	AAZ48336	Aaz48336 Primer sp	C 517	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 445	13.6	48.6	50	4	AAI73207	Aai73207 Human sil	C 518	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 446	13.6	48.6	50	4	AAI73205	Aai73205 Human sil	C 519	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 447	13.6	48.6	50	6	ABZ05043	Abz05043 Human leu	C 520	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 448	13.6	48.6	50	10	ADG33400	Adg33400 Human DNA	C 521	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 449	13.4	47.9	25	9	ACH59994	Ach59994 DNA targe	C 522	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 450	13.4	47.9	25	9	ACH59994	Ach59994 DNA targe	C 523	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 451	13.4	47.9	25	12	ADP14074	Adp14074 Renal cel	C 524	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 452	13.4	47.9	26	12	ADP6382	Adp6382 Mouse GST	C 525	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 453	13.4	47.9	30	6	ABL58540	Abi58540 Human CDI	C 526	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 454	13.4	47.9	30	10	ADE28575	Ade28575 Human CDI	C 527	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 455	13.4	47.9	33	6	AAK92924	Aak92924 PCR prime	C 528	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 456	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 529	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 457	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 530	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 458	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 531	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 459	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 532	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 460	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 533	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 461	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 534	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 462	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 535	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 463	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 536	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 464	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 537	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 465	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 538	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 466	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 539	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 467	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 540	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 468	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 541	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 469	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 542	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 470	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 543	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 471	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 544	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 472	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 545	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 473	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 546	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 474	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 547	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 475	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 548	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 476	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 549	13.2	47.1	48	2	AAV55492	Aav55492 Linker pr
C 477	13.4	47.9	33	6	ABQ83740	Abq83740 Human ald	C 550	13.					

C 533	13	46.4	25	9	AC124149	Human mic	606	12.8	45.7	50	10	AAD54783	Aad54783 Human cys
C 534	13	46.4	25	9	ACH59841	DNA targe	607	12.8	45.7	50	10	AAD54782	Aad54782 Human cys
C 535	13	46.4	25	9	ACH59964	DNA targe	608	12.8	45.7	50	10	AAD54784	Aad54784 Human cys
C 536	13	46.4	27	8	ACD17040	Sample pr	609	12.6	45.0	19	12	ADK40294	Adk40294 Human HNF
C 537	13	46.4	27	8	ACD17035	Sample pr	610	12.6	45.0	19	12	ADQ61659	Adq61659 Anti-TP73
C 538	13	46.4	27	8	ACD17028	Sample pr	611	12.6	45.0	20	12	ADQ61659	Adq61659 Anti-TP73
C 539	13	46.4	30	10	ADE95711	Human NOV	C 611	12.6	45.0	20	12	ADP11180	Adp11180 Set 1 rig
C 540	13	46.4	31	8	ACD43614	Human gen	C 612	12.6	45.0	22	12	ADJ51105	Adj51105 Human NOV
C 541	13	46.4	33	6	ABL50390	Human tra	C 613	12.6	45.0	24	2	AAT73251	Aat73251 Detection
C 542	13	46.4	33	6	ABL50390	Human tra	C 614	12.6	45.0	24	6	ABQ03505	Abq03505 Oligonucle
C 543	13	46.4	33	6	ABZ70157	Beta lact	C 615	12.6	45.0	25	5	AAQ60073	Aaq60073 Primer fo
C 544	13	46.4	35	2	AAT71246	Basic fib	C 616	12.6	45.0	25	9	ACI29642	Act29642 Human mic
C 545	13	46.4	35	10	ABX11696	Primer #2	C 617	12.6	45.0	25	9	ACI29643	Act29643 Human mic
C 546	13	46.4	36	2	AAT71249	Basic fib	C 618	12.6	45.0	25	9	ACH52715	Ach52715 DNA targe
C 547	13	46.4	37	3	AAZ64925	RPI motif	C 619	12.6	45.0	29	2	AAZ76034	Aaz76034 TK-(teto)
C 548	13	46.4	37	6	ACN27367	Ribozyne	C 620	12.6	45.0	30	4	AAF60292	Aaf60292 Human CD4
C 549	13	46.4	38	6	ACN27267	WNV minus	C 621	12.6	45.0	30	6	ABX67519	Abx67519 Novel Hel
C 550	13	46.4	38	6	ACN28766	WNV minus	C 622	12.6	45.0	31	2	AAV60718	Aav60718 Primer #1
C 551	13	46.4	38	6	ACN17677	Inozy	C 623	12.6	45.0	31	2	AAV60718	Aav60718 Primer #1
C 552	13	46.4	38	6	ACN15558	WNV Hamme	C 624	12.6	45.0	32	10	ADD25850	Add25850 Binding d
C 553	13	46.4	38	11	ADL52118	Human NOG	C 625	12.6	45.0	32	10	AAAL56958	Aal56958 Human hyp
C 554	13	46.4	39	8	ABZ68718	PCR prime	C 626	12.6	45.0	35	4	AAH25064	Aah25064 PCR prime
C 555	13	46.4	40	6	ABZ46736	Human ATP	C 627	12.6	45.0	35	10	ADG84263	Adg84263 Human TMD
C 556	13	46.4	40	6	ABZ46736	Human ATP	C 628	12.6	45.0	36	2	AAT70249	Aat70249 KPI(1-55)
C 557	13	46.4	41	5	AAH46151	DNA ligas	C 629	12.6	45.0	36	3	AAZ57501	Aaz57501 Kunitz pr
C 558	13	46.4	41	6	ABL50387	Human tra	C 630	12.6	45.0	36	4	AAH14285	Aah14285 Oligonucle
C 559	13	46.4	41	6	ABL50386	Human tra	C 631	12.6	45.0	38	4	AAQ51681	Aaq51681 Primer to
C 560	13	46.4	41	6	ABZ70159	Beta lact	C 632	12.6	45.0	38	4	AAH96521	Aah96521 Human Chk
C 561	13	46.4	41	6	AAH16266	DNA probe	C 633	12.6	45.0	38	4	ABK05063	Abk05063 Human NOG
C 562	13	46.4	41	6	AAH16266	DNA probe	C 634	12.6	45.0	38	6	ACN29302	Acn29302 WNV minus
C 563	13	46.4	45	2	AAH88771	SV40 olig	C 635	12.6	45.0	39	4	AAH20281	Aah20281 Gol9 link
C 564	13	46.4	45	2	AAH88771	SV40 olig	C 636	12.6	45.0	40	2	AAZ22072	Aaz22072 Probe ana
C 565	13	46.4	45	4	AAH46035	SV40 orig	C 637	12.6	45.0	41	6	ABZ46298	Abz46298 Human ald
C 566	13	46.4	45	4	AAH46036	SV40 orig	C 638	12.6	45.0	41	6	ABZ46298	Abz46298 Human ald
C 567	12.8	45.7	17	8	ACC68190	Murine ol	C 639	12.6	45.0	42	2	AAH62133	Aah62133 Granule b
C 568	12.8	45.7	18	2	AAZ90242	GRK4 alle	C 640	12.6	45.0	45	3	AAH53222	Aaah53222 Human Gp
C 569	12.8	45.7	19	2	AAZ90242	GRK4 alle	C 641	12.6	45.0	45	8	ABX12052	Abx12052 Human NPY
C 570	12.8	45.7	21	6	ABN80440	DNA-RNA h	C 642	12.6	45.0	45	10	ADE78398	Ade78398 DNA encod
C 571	12.8	45.7	21	6	ABN80440	DNA-RNA h	C 643	12.6	45.0	45	12	ADM88037	Adm88037 Gene expr
C 572	12.8	45.7	23	12	ADN30310	Recombina	C 644	12.6	45.0	49	2	AAT80501	Aat80501 Hepatoma
C 573	12.8	45.7	24	12	ADH51112	Human can	C 645	12.6	45.0	49	6	ABN71825	Abn71825 Streptoco
C 574	12.8	45.7	25	9	AC165495	Human mic	C 646	12.6	45.0	49	6	ABN71825	Abn71825 Streptoco
C 575	12.8	45.7	25	9	AC122729	Human mic	C 647	12.6	45.0	50	4	AAH134141	Aah134141 Human SNP
C 576	12.8	45.7	25	9	ACK27780	Human mic	C 648	12.6	45.0	50	6	AAAL50075	Aal50075 Mammalian
C 577	12.8	45.7	25	9	ACK27881	Human mic	C 649	12.6	45.0	50	6	ABZ01668	Abz01668 Human leu
C 578	12.8	45.7	25	9	ADA14319	Human Skp	C 650	12.6	45.0	50	6	ABZ03723	Abz03723 Human leu
C 579	12.8	45.7	26	2	AAH19708	Pichia pa	C 651	12.4	44.3	18	2	AAH61268	Aah61268 NAG tumou
C 580	12.8	45.7	26	2	AAH19710	Pichia pa	C 652	12.4	44.3	20	2	AAQ33541	Aaq33541 PCR Prime
C 581	12.8	45.7	29	3	AAF06832	Hammerhea	C 653	12.4	44.3	20	2	AAZ02404	Aaz02404 PCR prime
C 582	12.8	45.7	31	4	AAF75367	CHO cell	C 654	12.4	44.3	20	2	AAZ03873	Aaz03873 PCR prime
C 583	12.8	45.7	31	4	AAF75373	CHO cell	C 655	12.4	44.3	23	12	ADJ57664	Adj57664 Primer of
C 584	12.8	45.7	34	10	ABZ23645	N. gonorr	C 656	12.4	44.3	24	2	AAT61261	Aat61261 NAG tumou
C 585	12.8	45.7	35	10	ADG40192	Human ade	C 657	12.4	44.3	25	9	ACI01859	Act01859 Human mic
C 586	12.8	45.7	37	11	ADO70335	PCR prime	C 658	12.4	44.3	25	9	ACI01859	Act01859 Human mic
C 587	12.8	45.7	41	6	AAH43812	Human mus	C 659	12.4	44.3	25	9	ACI54871	Act54871 Human mic
C 588	12.8	45.7	41	6	AAH43812	Human mus	C 660	12.4	44.3	25	9	ACH55029	Ach55029 DNA targe
C 589	12.8	45.7	41	6	ABZ43745	Human alc	C 661	12.4	44.3	25	9	ACH64829	Ach64829 DNA targe
C 590	12.8	45.7	44	3	AAZ88571	PCR prime	C 662	12.4	44.3	26	2	AAQ06962	Aaq06962 Pestiviru
C 591	12.8	45.7	47	3	AAZ68497	Human nap	C 663	12.4	44.3	26	4	AAH21123	Aah21123 C. glutam
C 592	12.8	45.7	47	3	AAZ66430	Human map	C 664	12.4	44.3	26	4	AAH21123	Aah21123 C. glutam
C 593	12.8	45.7	47	12	ADL00308	Human eng	C 665	12.4	44.3	30	6	ABL56189	AbL56189 Hordeum v
C 594	12.8	45.7	48	6	ABN71745	Streptoco	C 666	12.4	44.3	31	2	AAV33959	Aav33959 Human lun
C 595	12.8	45.7	50	4	AAAL32482	Human SNP	C 667	12.4	44.3	31	2	AAH06378	Aah06378 Human bla
C 596	12.8	45.7	50	4	AAH45616	Human cys	C 668	12.4	44.3	31	4	AAI30161	Aai30161 Human sin
C 597	12.8	45.7	50	4	AAH45615	Human cys	C 669	12.4	44.3	32	2	AAQ80042	Aaq80042 5' flanki
C 598	12.8	45.7	50	4	AAH45615	Human cys	C 670	12.4	44.3	32	2	AAQ80043	Aaq80043 3' flanki
C 599	12.8	45.7	50	6	ADZ4216	Human cys	C 671	12.4	44.3	33	6	AAH89688	Aah89688 Oligonucle
C 600	12.8	45.7	50	6	ADZ4216	Human cys	C 672	12.4	44.3	33	6	ABL40686	AbL40686 Human tra
C 601	12.8	45.7	50	6	ABZ07945	Human leu	C 673	12.4	44.3	33	6	AAH18047	Aah18047 Human poi
C 602	12.8	45.7	50	6	ABZ07631	Human leu	C 674	12.4	44.3	35	12	ADL14012	Adl14012 Tg-ragH2
C 603	12.8	45.7	50	6	ABZ00435	Human leu	C 675	12.4	44.3	38	3	AAZ54983	Aaz54983 Neisseria
C 604	12.8	45.7	50	6	ABZ05984	Human leu	C 676	12.4	44.3	38	4	ABK04970	Abk04970 Human NOG
C 605	12.8	45.7	50	8	ACC00244	rapL gene	C 677	12.4	44.3	38	4	ABL47665	AbL47665 Human GRI
							C 678	12.4	44.3	38	4	ABL47631	AbL47631 Human GRI

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C 679	12.4	44.3	38	6	ACN26411	Acn26411 WNV minus	752	12.2	43.6	45	2	AAV99361	Aav99361 3' PCR pr
C 680	12.4	44.3	38	6	ACN29778	Acn29778 WNV minus	C 753	12.2	43.6	47	3	AAZ66791	Aaz66791 Human map
C 681	12.4	44.3	38	6	ACN17697	Acn17697 WNV Inozy	C 754	12.2	43.6	47	3	Az68983	Az68983 Human map
C 682	12.4	44.3	38	6	ACN29626	Acn29626 WNV minus	C 755	12.2	43.6	48	6	ABK22020	Abk22020 Human ERG
C 683	12.4	44.3	38	8	ACD50492	Adm50492 HBV hamme	756	12.2	43.6	48	11	ADL76321	Adl76321 Human PTG
C 684	12.4	44.3	38	11	ADM54985	Adm54985 NCH riboz	757	12.2	43.6	49	6	ABN72010	Abn72010 Streptoco
C 685	12.4	44.3	38	11	ADM54951	Adm54951 NCH riboz	758	12.2	43.6	50	2	AAQ76358	Aaq76358 Antisense
C 686	12.4	44.3	38	12	ADM60468	Adm60468 Hepatitis	C 759	12.2	43.6	50	2	AAQ76359	Aaq76359 Antisense
C 687	12.4	44.3	39	2	AAT51498	Aat51498 Fragment	C 760	12.2	43.6	50	2	AAQ76353	Aaq76353 Antisense
C 688	12.4	44.3	39	12	ADL64610	Adl64610 Human sin	C 761	12.2	43.6	50	4	AAQ763217	Aaq763217 Alpha-car
C 689	12.4	44.3	41	2	AAQ52872	Aac52872 Cytoegal	762	12.2	43.6	50	4	AAAL27891	Aal27891 Human SNP
C 690	12.4	44.3	41	2	AAV50304	Aav50304 Maize pol	C 763	12.2	43.6	50	6	ABZ05101	Abz05101 Human leu
C 691	12.4	44.3	41	6	ABZ46709	Abz46709 Human ATP	764	12.2	43.6	50	6	ABZ06100	Abz06100 Human leu
C 692	12.4	44.3	41	6	ABZ46710	Abz46710 Human ATP	C 765	12.2	43.6	50	10	ADG33517	Adg33517 Human DNA
C 693	12.4	44.3	41	6	ABZ44361	Abz44361 Human ATP	C 766	12.2	43.6	50	12	ADP13010	Adp13010 50-mer ol
C 694	12.4	44.3	41	6	ABZ44362	Abz44362 Human ATP	C 767	12.2	43.6	50	8	ACD66038	AcD66038 Anti-HCV
C 695	12.4	44.3	41	6	ABZ44362	Abz44362 Human ATP	768	12.2	43.6	50	8	ACD66054	AcD66054 Anti-HCV
C 696	12.4	44.3	41	6	ABL40086	AbL40086 Human pro	C 769	12.2	43.6	50	13	ADI87698	Adi87698 Anti-HCV
C 697	12.4	44.3	41	6	ABL40085	AbL40085 Human pro	C 770	12.2	43.6	50	13	ADI87588	Adi87588 Anti-HCV
C 698	12.4	44.3	41	8	ACC00072	Acc00072 Probe #1	C 771	12.2	43.6	50	13	ADI87572	Adi87572 Hepatitis
C 699	12.4	44.3	41	12	ADL60481	AdL60481 Human org	C 772	12.2	43.6	50	13	ADI87572	Adi87572 Hepatitis
C 700	12.4	44.3	43	10	ABZ57898	Abz57898 Escherich	C 773	12.2	43.6	50	13	ADK15310	Adk15310 Hepatitis
C 701	12.4	44.3	43	2	AAV27934	Aav27934 Human GAL	C 774	12.2	43.6	50	13	ABX01759	Abx01759 Hepatitis
C 702	12.4	44.3	45	6	AAQ35877	Aaq35877 Human GAL	775	12.2	43.6	50	6	ABX01759	Abx01759 Hepatitis
C 703	12.4	44.3	45	9	AAQ28987	Aaq28987 Human gal	776	12.2	43.6	50	6	ABX01759	Abx01759 Hepatitis
C 704	12.4	44.3	45	10	ADP61153	Adp61153 Radiolabe	777	12.2	43.6	50	6	ABX01759	Abx01759 Hepatitis
C 705	12.4	44.3	47	3	ADG69463	Adg69463 Human map	778	12.2	43.6	50	17	ADH187248	Adh187248 HCV DNazY
C 706	12.4	44.3	49	10	ADOC03175	AdoC03175 Colom spe	C 779	12.2	43.6	50	18	ADH187248	Adh187248 HCV DNazY
C 707	12.4	44.3	50	6	ABZ06021	Abz06021 Human leu	C 780	12.2	43.6	50	18	ADH187248	Adh187248 HCV DNazY
C 708	12.2	43.6	17	8	ACA08213	Aca08213 NFKB sub-	C 781	12.2	43.6	50	18	ADH187248	Adh187248 HCV DNazY
C 709	12.2	43.6	18	2	AAZ21424	Aaz21424 Human MEK	C 782	12.2	43.6	50	18	ADH187248	Adh187248 HCV DNazY
C 710	12.2	43.6	19	11	ADM29453	Adm29453 Human nov	C 783	12.2	43.6	50	18	ADH187248	Adh187248 HCV DNazY
C 711	12.2	43.6	20	6	ADM36583	Adm36583 Human Her	C 784	12.2	43.6	50	18	ADH187248	Adh187248 HCV DNazY
C 712	12.2	43.6	20	12	ADH10857	Adh10857 Human cat	C 785	12.2	43.6	50	18	ADH187248	Adh10858 Human cat
C 713	12.2	43.6	20	12	ADH10857	Adh10857 Human cat	C 786	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 714	12.2	43.6	20	12	ADH10653	Ado10653 Single mu	C 787	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 715	12.2	43.6	21	4	AAQ96304	Aaq96304 Human gen	C 788	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 716	12.2	43.6	22	2	AAQ92922	Aat92922 Primer 22	C 789	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 717	12.2	43.6	24	9	ACA90118	Aca90118 Human kin	C 790	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 718	12.2	43.6	24	12	ADK98351	Adk98351 Primer of	C 791	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 719	12.2	43.6	25	4	AAH01206	Aah01206 S. pneumo	C 792	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 720	12.2	43.6	25	4	AAH01229	Aah01229 S. pneumo	C 793	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 721	12.2	43.6	25	9	ACK25919	Ack25919 Human mic	C 794	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 722	12.2	43.6	25	9	ACK17562	Ack17562 Human mic	C 795	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 723	12.2	43.6	25	9	ACK15953	Ack15953 Human mic	C 796	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 724	12.2	43.6	25	9	ACK27460	Ack27460 Human mic	C 797	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 725	12.2	43.6	25	9	ACK178781	Act178781 Human mic	C 798	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 726	12.2	43.6	26	10	ADC77572	Adc77572 Zebrafish	C 799	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 727	12.2	43.6	27	2	AAZ10608	Aaz10608 Sense PCR	C 800	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 728	12.2	43.6	28	2	AAQ46856	Aaq46856 Interleuk	C 801	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 729	12.2	43.6	33	6	ABZ23785	Abz23785 Human mac	C 802	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 730	12.2	43.6	34	10	ACC69768	Acc69768 Human H-F	C 803	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 731	12.2	43.6	35	12	ADF12121	Adf12121 ARR seque	C 804	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 732	12.2	43.6	36	2	AAQ48461	Aaq48461 catr gene	C 805	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 733	12.2	43.6	36	2	AAQ48460	Aaq48460 catr gene	C 806	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 734	12.2	43.6	37	2	AAQ52001	Aaq52001 B-cell mr	C 807	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 735	12.2	43.6	37	3	AAAL12757	Aaal12757 5' PCR pr	C 808	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 736	12.2	43.6	38	2	AAAT81930	Aat81930 Human c-m	C 809	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 737	12.2	43.6	38	12	ADP70067	Adp70067 Novel mam	C 810	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 738	12.2	43.6	39	2	AAQ46246	Aaq46246 Probe for	C 811	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 739	12.2	43.6	39	2	AAQ46245	Aaq46245 Probe for	C 812	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 740	12.2	43.6	40	10	ADC60951	Adc60951 NASBA pri	C 813	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 741	12.2	43.6	40	6	ABT112201	Abt112201 E coli ex	C 814	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 742	12.2	43.6	41	3	AAZ87872	Aaz87872 AMG varia	C 815	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 743	12.2	43.6	41	6	ABZ44861	Abz44861 Human cyt	C 816	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 744	12.2	43.6	41	6	ABZ49616	Abz49616 Human sul	C 817	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 745	12.2	43.6	41	6	ABZ50411	Abz50411 Human cyt	C 818	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 746	12.2	43.6	41	6	ABZ50411	Abz50411 Human coa	C 819	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 747	12.2	43.6	41	6	ABZ23787	Abz23787 Human mac	C 820	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 748	12.2	43.6	41	8	ABZ22572	Abz22572 Human zin	C 821	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 749	12.2	43.6	41	8	AAZ55598	Aaz55598 Probe 2 r	C 822	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 750	12.2	43.6	43	5	AAZ28334	Aaz28334 eryAI gen	C 823	12.2	43.6	50	18	ADH10858	Adh10784 Human cat
C 751	12.2	43.6	44	12	ADK41338	Adk41338 Human chr	C 824	12.2	43.6	50	18	ADH10858	Adh10784 Human cat

C 825	12	42.9	30	10	ADB79282	Adb79282 E-tag med	898	12	42.9	46	3	AAC68509	Aac68509 Periplaki
826	12	42.9	30	10	ADC22680	Adc22680 Human G p	C 899	12	42.9	46	12	ADG46560	Adg46560 pUC18 mod
827	12	42.9	30	10	ADH14153	Adh14153 Human GPC	C 900	12	42.9	47	3	AAC65934	Aac65934 Human map
828	12	42.9	30	10	ACF03426	Acf03426 Vector pG	901	12	42.9	47	3	AAZ67464	Aaz67464 Human map
829	12	42.9	30	11	ADM39449	Adm39449 Maize Zmf	C 902	12	42.9	49	6	ABL88614	AbL88614 Fungal ce
C 830	12	42.9	30	12	ADM18536	Adm18536 Human sub	C 903	12	42.9	49	1	ADC18795	Adc18795 Cell wall
831	12	42.9	30	12	ADO12772	Ado12772 Single mu	C 904	12	42.9	50	1	AAO90885	Aao90885 3'-5' pro
C 832	12	42.9	30	12	ADO12782	Ado12782 Single mu	905	12	42.9	50	3	AAZ65183	Aaz65183 Probe spe
833	12	42.9	31	2	AA339012	Aax39012 Human gen	906	12	42.9	50	3	AAC58254	Aac58254 Human PRO
834	12	42.9	32	3	AAA08336	Aaa08336 Spinach c	907	12	42.9	50	5	AAF44340	Aaf44340 Human PRO
835	12	42.9	32	2	AAT06297	Aat06297 Phage R1-	C 908	12	42.9	50	6	ABZ00733	Abz00733 Human leu
C 836	12	42.9	33	2	RAX89568	Rax89568 Forward p	C 909	12	42.9	50	6	ABZ01845	Abz01845 Human leu
837	12	42.9	33	4	AAI71682	Aai71682 Human ATP	910	12	42.9	50	6	ABZ06083	Abz06083 Human leu
838	12	42.9	33	5	AB197614	Abi97614 Endogenou	911	12	42.9	50	6	ABA202610	AbA202610 Human leu
C 839	12	42.9	33	6	ABN85225	Abn85225 Human tra	912	12	42.9	50	8	ACA64331	AcA64331 Secreted
C 840	12	42.9	33	8	ADA14822	Ada14822 Anti-idio	913	12	42.9	50	8	ACD44299	AcD44299 Human PRO
C 841	12	42.9	33	10	ADC35351	Adc35351 Monoclonal	914	12	42.9	50	8	ACD44299	AcD44299 Human PRO
C 842	12	42.9	34	6	ABK14686	Abk14686 Human IRI	915	12	42.9	50	8	ABX79470	Abx79470 Human sec
843	12	42.9	36	2	AAT97138	Aat97138 PCR prime	916	12	42.9	50	8	ACA93491	AcA93491 Novel hum
844	12	42.9	36	3	AAA94046	Aaa94046 Human HDC	917	12	42.9	50	8	ABX81173	Abx81173 Novel hum
845	12	42.9	36	6	ABX02606	Abx02606 HCV hamme	918	12	42.9	50	8	ACA92989	AcA92989 Novel hum
846	12	42.9	36	6	ABX02010	Abx02010 HCV hamme	919	12	42.9	50	8	ABX17073	Abx17073 Human PRO
847	12	42.9	36	6	ABX02092	Abx02092 HCV hamme	920	12	42.9	50	9	ACA67928	AcA67928 Novel hum
C 848	12	42.9	36	8	RA053388	Ra053388 PCR prime	921	12	42.9	50	9	ACA88377	AcA88377 Human sec
C 849	12	42.9	37	2	AAZ12403	Aaz12403 PCR prime	922	12	42.9	50	9	ACD81884	AcD81884 Human PRO
850	12	42.9	37	3	AAZ48307	Aaz48307 B. subtil	923	12	42.9	50	9	ADA37762	Ada37762 Human sec
851	12	42.9	38	4	ABK04095	Abk04095 Human NOG	924	12	42.9	50	9	ADA21448	Ada21448 Human sec
852	12	42.9	38	4	ABK03869	Abk03869 Human NOG	925	12	42.9	50	9	ADA10235	Ada10235 Human PRO
853	12	42.9	38	4	ABK05032	Abk05032 Human NOG	926	12	42.9	50	9	ADA17779	Ada17779 Human PRO
854	12	42.9	38	4	ABK08253	Abk08253 Human CD2	927	12	42.9	50	9	ADA27887	Ada27887 Human sec
855	12	42.9	38	6	ABK58046	Abk58046 Human CLC	928	12	42.9	50	9	ADA94467	Ada94467 Human sec
856	12	42.9	38	6	ACN26647	Acn26647 WNV minus	929	12	42.9	50	9	ADA38692	Ada38692 Human sec
857	12	42.9	38	6	ACN28513	Acn28513 WNV minus	930	12	42.9	50	9	ADA92813	Ada92813 Human sec
858	12	42.9	38	6	ACN18595	Acn18595 WNV Inozy	931	12	42.9	50	9	ACH65445	ACH65445 Human sec
859	12	42.9	38	6	ACN17480	Acn17480 WNV Inozy	932	12	42.9	50	9	ADA22374	Ada22374 Human sec
C 860	12	42.9	38	6	ACN16052	Acn16052 WNV Hamme	933	12	42.9	50	9	ACD339435	AcD339435 Human sec
861	12	42.9	38	6	ACN18103	Acn18103 WNV Inozy	934	12	42.9	50	9	ADA06540	Ada06540 Human sec
862	12	42.9	38	6	ACN27006	Acn27006 WNV minus	935	12	42.9	50	9	ADA39233	Ada39233 Human sec
863	12	42.9	38	6	ACN15327	Acn15327 WNV Hamme	936	12	42.9	50	9	ADB96259	AdB96259 Human PRO
864	12	42.9	38	6	ACN26671	Acn26671 WNV minus	937	12	42.9	50	10	ADC57731	AdC57731 Human PRO
865	12	42.9	38	6	ACN27305	Acn27305 WNV minus	938	12	42.9	50	10	ADC55095	AdC55095 Human PRO
866	12	42.9	38	6	ACN27305	Acn27305 WNV minus	939	12	42.9	50	10	ADC11962	AdC11962 Human sec
867	12	42.9	38	6	ACN15673	Acn15673 WNV Hamme	940	12	42.9	50	10	ADC56384	AdC56384 Human PRO
868	12	42.9	38	6	ACN15690	Acn15690 WNV Hamme	941	12	42.9	50	10	ADC07439	AdC07439 Human sec
869	12	42.9	38	6	ACN15418	Acn15418 WNV Hamme	942	12	42.9	50	10	ADC11429	AdC11429 Human sec
870	12	42.9	38	6	ACN17502	Acn17502 WNV Inozy	943	12	42.9	50	10	ADC114551	AdC114551 Novel hum
871	12	42.9	38	6	ACN15308	Acn15308 WNV Hamme	944	12	42.9	50	10	ADD08083	AdD08083 Human sec
872	12	42.9	38	6	ACN26296	Acn26296 WNV minus	945	12	42.9	50	10	ADD08083	AdD08083 Human PRO
873	12	42.9	38	6	ACN17013	Acn17013 WNV Inozy	946	12	42.9	50	10	ADD07550	AdD07550 Human sec
874	12	42.9	38	6	ACN18550	Acn18550 WNV Inozy	947	12	42.9	50	10	ADC82441	AdC82441 Human PRO
875	12	42.9	38	6	ACN16757	Acn16757 WNV Inozy	948	12	42.9	50	10	ADD08621	AdD08621 Human sec
876	12	42.9	38	6	ACN27599	Acn27599 WNV minus	949	12	42.9	50	10	ADD06870	AdD06870 Human sec
877	12	42.9	38	6	ACN15695	Acn15695 WNV Hamme	950	12	42.9	50	10	ADC83117	AdC83117 Human PRO
878	12	42.9	38	8	ACN07110	Acn07110 Necrosis	951	12	42.9	50	10	ADD31925	AdD31925 Human ret
879	12	42.9	38	8	ACN07302	Acn07302 Necrosis	C 952	12	42.9	50	10	ADD31890	AdD31890 Butterfly
C 880	12	42.9	38	12	ADM61595	Adm61595 Hepatitis	953	12	42.9	50	10	ADD55224	AdD55224 Human PRO
C 881	12	42.9	39	6	AAS96515	Aas96515 Primer #3	954	12	42.9	50	10	ADD56182	AdD56182 Human PRO
C 882	12	42.9	40	2	AAX22073	Aax22073 Probe ana	955	12	42.9	50	10	ADD54620	AdD54620 Human PRO
883	12	42.9	40	6	APT12187	Abt12187 E coli ex	956	12	42.9	50	10	ADE26774	Ade26774 Novel hum
884	12	42.9	41	2	AAV25473	Aav25473 T7 promot	957	12	42.9	50	10	ADE26241	Ade26241 Novel hum
885	12	42.9	41	6	AAV02955	Aba02955 Human nuc	958	12	42.9	50	10	ADG67178	AdG67178 Human CDN
886	12	42.9	41	6	ABA02956	AbA02956 Human nuc	959	12	42.9	50	10	ADG33646	AdG33646 Human DNA
C 887	12	42.9	41	6	ABZ070160	Abz070160 Beta lact	960	12	42.9	50	10	ADG135432	AdG135432 Human PRO
888	12	42.9	41	6	ABA01830	AbA01830 Human reg	961	12	42.9	50	10	ADH99924	AdH99924 Novel hum
C 889	12	42.9	41	6	ABZ48091	Abz48091 Human ATP	962	12	42.9	50	10	ABX77874	Abx77874 Human PRO
890	12	42.9	41	6	ABZ46311	Abz46311 Human ald	963	12	42.9	50	10	ABX80286	Abx80286 Novel hum
891	12	42.9	41	6	ABZ48822	Abz48822 Human ald	964	12	42.9	50	10	ACA69192	AcA69192 Human sec
892	12	42.9	41	6	ABA97884	AbA97884 Human NAD	965	12	42.9	50	10	ABX90263	Abx90263 Human sec
C 893	12	42.9	42	8	AD534113	Ad534113 Alpha-gal	966	12	42.9	50	10	ABX64109	Abx64109 Human PRO
894	12	42.9	42	10	ADG87147	Adg87147 CAR genom	967	12	42.9	50	12	ADF35377	AdF35377 Human PRO
895	12	42.9	45	2	AAQ81186	Aaq81186 CTLA4 ext	968	12	42.9	50	12	ADG11627	AdG11627 Human PRO
C 896	12	42.9	45	10	ADG44362	Adg44362 Anti-path	969	12	42.9	50	12	ADH19497	AdH19497 Human sec
897	12	42.9	45	10	ADG44361	Adg44361 Anti-path	970	12	42.9	50	12	ADH20990	AdH20990 Human sec

971 12 42.9 50 12 ADH20030
 972 11.8 42.1 15 4 AAF51089
 973 11.8 42.1 17 2 AAX04635
 c 974 11.8 42.1 17 8 ACC65098
 975 11.8 42.1 18 2 AAT87814
 976 11.8 42.1 18 2 AAX27644
 977 11.8 42.1 18 6 AAD24177
 c 978 11.8 42.1 18 6 AAL46928
 979 11.8 42.1 18 10 ADL24999
 c 980 11.8 42.1 18 11 ADM06741
 c 981 11.8 42.1 18 11 ADM0515
 c 982 11.8 42.1 19 11 ADM29450
 983 11.8 42.1 20 2 AAZ02396
 c 984 11.8 42.1 20 3 AAA97621
 c 985 11.8 42.1 20 4 AAH46338
 c 986 11.8 42.1 20 10 ADD01033
 c 987 11.8 42.1 20 10 ADH62993
 c 988 11.8 42.1 20 10 ADH57148
 c 989 11.8 42.1 20 12 ADK43228
 c 990 11.8 42.1 20 12 ADK43351
 c 991 11.8 42.1 20 12 ADO60079
 c 992 11.8 42.1 20 12 ADO44584
 c 993 11.8 42.1 21 11 ADM65618
 c 994 11.8 42.1 21 12 ADX98392
 c 995 11.8 42.1 22 6 AAD43483
 c 996 11.8 42.1 22 6 AAD43460
 c 997 11.8 42.1 22 6 ABK89951
 c 998 11.8 42.1 23 6 ABS63490
 c 999 11.8 42.1 23 8 ADA00131
 c1000 11.8 42.1 24 6 ABL41902

Adh20030 Human sec
 Aaf51089 IGF-I oli
 Aax04635 Probe of
 Acc65098 Murine ol
 Aat87814 Bifidobac
 Aax27644 16S rRNA
 Aad24177 Bifidobac
 Aal46928 Bifidobac
 Adl24999 Intestina
 Adm06741 Human PCR
 Adm0515 Human nov
 Adm29450 Human nov
 Aaz02396 PCR prime
 Aaa97621 Human PAR
 Aah46338 Oligonucl
 Agd01033 Human Jag
 Adh62993 Human Jag
 Adh57148 Phosphoro
 Adk43228 Antisense
 Adk43351 Human PTP
 Ado60079 CRF1 reve
 Ado44584 CRH recep
 Adm65618 NRY polym
 Adk98392 Primer of
 Aad43483 Human cal
 Aad43460 Human cal
 Abk89951 MMTV-indu
 Abs63490 Human leu
 Ada00131 Mouse mir
 Abl41902 Antisense

ALIGNMENTS

RESULT 1
 AAT67194
 ID AAT67194 standard; DNA; 28 BP.
 AC AAT67194;
 XX
 DT 13-FEB-1998 (first entry)
 XX
 DE Hepatitis C virus (HCV) RNA amplification primer ST778AA.
 XX
 KW Hepatitis C virus; HCV; ST778AA; reverse transcription PCR; RT-PCR;
 KW detection; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN EP776981-A2.
 XX
 PD 04-JUN-1997.
 XX
 XX 21-NOV-1996; 96EP-00118704.
 PF
 XX 29-NOV-1995; 95US-0007739P.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX Tsang SY;
 XX
 XX WPI; 1997-291296/27.
 DR
 XX Oligonucleotide primers for hepatitis C virus RNA amplification - by
 PT polymerase chain reaction.
 XX
 XX Claim 1; Page 12; 16pp; English.
 PS
 XX This downstream primer ST778AA is used in the amplification of the
 CC Hepatitis C virus (HCV) RNA by reverse transcription PCR. This is used to
 CC amplify a 250 base pair product from the 5' untranslated region of the
 .CC HCV genome. This can be used to detect HCV in a sample with increased

CC sensitivity. Amplification of HCV nucleic acid using this primer is up to
 CC 100 times more efficient than amplification with prior art primers
 XX
 SQ Sequence 28 BP; 10 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGCACCTATCAGGCAGTACCACAA 28
 |||||
 Db 1 GCAAGCACCTATCAGGCAGTACCACAA 28
 RESULT 2
 AAV59059
 ID AAV59059 standard; DNA; 28 BP.
 XX
 AC AAV59059;
 XX
 DT 07-JAN-1999 (first entry)
 XX
 DE Primer ST778AA for HCV fragment.
 KW PCR primer; HCV; nucleic acid amplification; ss.
 XX
 OS Synthetic.
 OS Human herpesvirus 5.
 XX
 FH Key Location/Qualifiers
 FT modified_base 25 /*tag= a
 FT /note= "optionally benzylated"
 FT modified_base 27 /*tag= b
 FT /note= "optionally benzylated"
 FT modified_base 28 /*tag= c
 FT /note= "optionally benzylated, methylated, or
 FT nitrobenzylated"
 XX
 PN EP866071-A2.
 PD 23-SEP-1998.
 XX
 PF 12-MAR-1998; 98EP-00104461.
 XX
 PR 20-MAR-1997; 97US-0041127P.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Will SG, Young KKY;
 XX
 DR WPI; 1998-482929/42.
 XX
 XX Oligo-nucleotide(s) containing N-substituted nucleotide - useful as
 PT primers for nucleic acid amplification.
 XX
 XX Example 6; Page 16; 38pp; English.
 PS
 XX This sequence represents a primer for a fragment of HCV, and is an
 CC example of an oligonucleotide of the invention. The oligonucleotides of
 CC the invention are of the formula 5'-S1-Nu-3' or 5'-S1-Nu-S2-3', where S1
 CC is a sequence of 5-50 nucleotides; S2 is a sequence of 1-3 nucleotides;
 CC and Nu is a nucleotide with a purine or pyrimidine base having an
 CC exocyclic amino group substituted by CHR2; R1, R2 are H, 1-10C alkyl,
 CC alkoxy, optionally substituted phenyl, phenoxy or optionally substituted
 CC naphthyl. The oligonucleotides are useful as primers for nucleic acid
 CC amplification, preferably by polymerase chain reaction. Use of the
 CC modified primers reduces non-specific amplification, especially primer
 CC dimer formation, with a concomitant increase in the yield of the intended
 CC target
 XX

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SQ Sequence 28 BP; 10 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTTATCAGGCGAGTACCAAA 28
Dd 1 GCAAGCACCTTATCAGGCGAGTACCAAA 28

RESULT 3
AAH25414
ID AAH25414 standard; DNA; 28 BP.
XX
AC
XX
AC AAH25414;
XX
DT 22-AUG-2001 (first entry)
XX
DE Reverse PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT modified_base 28
FT FT /*tag= a
FT FT /note= "derivatisation with a p-(t-butyl)benzyl-residue"
XX
XX WO200137291-A1.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-EP011459.
XX
XX 17-NOV-1999; 99EP-00122853.
XX
XX 12-MAY-2000; 2000EP-00110165.
XX
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
XX Weindel K, Riedling M, Geiger A;
XX
XX WPI; 2001-381247/40.
XX
XX Novel composition of magnetic glass particles for purification of DNA or
XX RNA in automated processes.
XX
XX Example 7; Page 98; 105pp; English.
XX
XX The specification describes a composition of magnetic glass particles,
XX which contain at least one magnetic object with a mean diameter between 5
XX -500 nm. The composition is useful for the purification of nucleic acids.
XX The composition can be used to process large quantities of nucleic acid
XX samples, because it does not involve the particles being centrifuged or
XX the fluids being drawn through glass fiber filters. PCR primers AAH25413-
XX 14 were used to amplify HCV DNA fragments. The amplified fragment can be
XX purified using the method of the invention.
XX
XX Sequence 28 BP; 10 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTTATCAGGCGAGTACCAAA 28
Dd 1 GCAAGCACCTTATCAGGCGAGTACCAAA 28

RESULT 4
ADC84693
ID ADC84693 standard; DNA; 28 BP.
XX
AC
XX
AC ADC84693;
XX
DT 01-JAN-2004 (first entry)
XX
DE PCR primer, #2, used to amplify HCV 5' UTR cDNA.
XX
XX RNA purification; undegraded RNA; RNA binding solution;
XX RNA-complexing salt; chaotropic substance; non-silica solid support;
XX RNA lysing solution; amphiphilic reagent; PCR; ss; primer; 5' UTR;
XX untranslated region.
XX
OS Hepatitis C virus.
XX
XX US2003073830-A1.
XX
XX 17-APR-2003.
XX
XX 12-OCT-2001; 2001US-00974798.
XX
XX 12-OCT-2001; 2001US-00974798.
XX
XX (HEAT/) HEATH E M.
XX (WAGE/) WAGES J M.
XX
XX Heath EM, Wages JM;
XX
XX WPI; 2003-786889/74.
XX
XX Purifying substantially pure and undegraded RNA from biological material
XX involves use of high pH- and strong chaotropic substance-free RNA binding
XX solution that allows RNA to preferentially bind to a solid support.
XX
XX Example 10; Page 11; 14pp; English.
XX
XX The invention discloses a method for purifying substantially pure and
XX undegraded RNA from biological material (B). The method comprises mixing
XX (B) with RNA binding solution (I) that has RNA-complexing salt and is
XX free of strong chaotropic substance, to form a mixture which is contacted
XX with to a non-silica solid support (SS) such that nucleic acids
XX comprising substantially undegraded RNA in mixture preferentially bind to
XX SS, washing SS and eluting bound substantially undegraded RNA from SS.
XX The method may also comprise mixing (B), with an RNA lysing solution (II)
XX buffered at a pH of greater than about 7, and comprising an amphiphilic
XX reagent, and RNA-complexing salt, and is free of a strong chaotropic
XX substance, lysing (B) with (II) to form a lysate comprising nucleic acids
XX comprising substantially undegraded RNA and non-nucleic acid biological
XX matter, contacting the lysate to an immobilised non-silica SS such that
XX the nucleic acids comprising substantially undegraded RNA in the lysate
XX preferentially bind to SS, washing SS and eluting bound substantially pure
XX and undegraded RNA. The methods are useful for purifying substantially pure
XX RNA, or its combinations) from biological material containing RNA. The
XX method is useful for purifying RNA from crude and partially purified
XX mixtures of nucleic acids, from (B) such as eukaryotic, prokaryotic,
XX microbial, bacterial or plant cells, mycoplasma, protozoa, bacteria,
XX fungi, viruses, yeasts, rickettsia or their homogenates. The method is
XX also useful for purifying RNA from (B) such as whole blood, bone marrow,
XX blood spots, blood serum, blood plasma, buffy coat preparations, saliva,
XX cerebrospinal fluid, solid animal tissues, faeces, urine, tears, sweat or
XX from environmental samples taken from air, water sediment or soil. The
XX purified RNA is useful in analytical and diagnostic methods such as
XX reverse transcriptase-PCR and micro array analyses. The method purifies
XX RNA from a variety of biological materials without the use of hazardous
XX substances such as phenol and chloroform or hazardous chaotropic
XX substances such as guanidinium salts, urea, etc. The method allows the
XX elution of RNA in low salt reagents thus eliminating tedious desalting
XX steps. The method is versatile and effective. The sequence presented is a
XX PCR primer which was used to amplify Hepatitis C virus (HCV) 5'
XX untranslated region (UTR) to demonstrate the integrity of the purified
XX mRNA.
XX
XX Sequence 28 BP; 10 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
```

Query Match 100.0%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGAGTACCACAA 28
DB 1 GCAAGCACCTATCAGGAGTACCACAA 28

RESULT 5
AAD43288
ID AAD43288 standard; DNA; 29 BP.
XX AC AAD43288;
XX 14-NOV-2002 (first entry)
XX HCV DNA amplifying PCR primer, ST778.
XX Amplification; target nucleic acid; PCR; primer; ss.
XX Hepatitis C virus.
XX Key Location/Qualifiers
FT stem_loop 9..17 /*tag= a
FT misc_binding 9..11 /*tag= b
FT misc_binding 15..17 /*tag= c
FT misc_binding 15..17 /bound_moiety= "Nucleotides 17-15"
FT misc_binding 15..17 /tag= c
FT misc_binding 15..17 /bound_moiety= "Nucleotides 11-9"
XX EPI236805-A1.
XX 04-SEP-2002.
XX 27-FEB-2002; 2002EP-00004483.
XX 02-MAR-2001; 2001EP-00105172.
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Jaeger S;
XX WPI; 2002-610695/66.
XX Amplification of a target nucleic acid region using a specific control sequence.
XX Example 2; Fig 3; 28pp; English.
XX The invention relates to a method for amplification of a target nucleic acid region in a sample using a specific control sequence. The invention is also directed to a method of determination of a target nucleic acid using a special control nucleic acid. Nucleic acids of the invention are used as a control in a reaction for amplifying target nucleic acids and as a control in a hybridisation reaction for determination of target nucleic acids. The present sequence is HCV (Hepatitis C virus) type I DNA amplifying PCR primer. This primer is used to illustrate the methods of the invention. Note: This sequence is stated to be same as that shown as SEQ ID NO:7 in sequence listing. However this sequence has additional A at its 3' end

XX Sequence 29 BP; 11 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGAGTACCACAA 28
DB 1 GCAAGCACCTATCAGGAGTACCACAA 28

Db 1 GCAAGCACCTATCAGGAGTACCACAA 28

RESULT 6
AAD43740
ID AAD43740 standard; DNA; 29 BP.
XX AC AAD43740;
XX 07-AUG-2003 (revised)
XX 14-NOV-2002 (first entry)
XX HCV DNA amplifying PCR primer, ST778.
XX Amplification; target nucleic acid; control nucleic acid; PCR; primer; ss.
XX Hepatitis C virus.
XX Key Location/Qualifiers
FT stem_loop 9..17 /*tag= a
FT misc_binding 9..11 /*tag= b
FT misc_binding 15..17 /*tag= c
FT misc_binding 15..17 /bound_moiety= "Nucleotides 17-15"
FT misc_binding 15..17 /tag= c
FT misc_binding 15..17 /bound_moiety= "Nucleotides 11-9"
XX EPI236804-A1.
XX 04-SEP-2002.
XX 02-MAR-2001; 2001EP-00105172.
XX 02-MAR-2001; 2001EP-00105172.
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Jaeger S;
XX WPI; 2002-610694/66.
XX Amplification of a target nucleic acid region using control sequences.
XX Example 2; Fig 3; 29pp; English.
XX The invention relates to a method for amplification of a target nucleic acid region. The method is useful for amplification of a nucleic acid molecule using control nucleic acid sequences. The control nucleic acid sequences are at least in part parallel-complementary to the sequence of the target nucleic acid. The present sequence is HCV DNA amplifying PCR primer. Note: This sequence is stated to be same as that shown as SEQ ID NO:7 in sequence listing. However this sequence has additional A at its 3' end. (Updated on 07-AUG-2003 to correct OS field.)
XX Sequence 29 BP; 11 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGAGTACCACAA 28
DB 1 GCAAGCACCTATCAGGAGTACCACAA 28

RESULT 7
AAT67195
ID AAT67195 standard; DNA; 27 BP.
XX

AC AAT67195;
 XX
 DT 13-FEB-1998 (first entry)
 XX
 DE Hepatitis C virus (HCV) RNA amplification primer ST678A.
 XX
 KW Hepatitis C virus; HCV; ST678A; reverse transcription PCR; RT-PCR;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN EP776981-A2.
 XX
 PD 04-JUN-1997.
 XX
 PF 21-NOV-1996; 96EP-00118704.
 XX
 PR 29-NOV-1995; 95US-0007739P.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Tsang SY;
 XX
 DR WPI; 1997-291296/27.
 XX
 PT Oligonucleotide primers for hepatitis C virus RNA amplification - by
 PT polymerase chain reaction.
 XX
 PS Claim 1; Page 12; 16pp; English.
 XX
 CC This downstream primer ST678A is used in the amplification of the
 CC Hepatitis C virus (HCV) RNA by reverse transcription PCR. This is used to
 CC amplify a 250 base pair product from the 5' untranslated region of the
 CC HCV genome. This can be used to detect HCV in a sample with increased
 CC sensitivity. Amplification of HCV nucleic acid using this primer is up to
 CC 100 times more efficient than amplification with prior art primers
 XX
 SQ Sequence 27 BP; 9 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 96.4%; Score 27; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCAAGCACCTATCAGGCGAGTACCACA 27
 Db 1 GCAAGCACCTATCAGGCGAGTACCACA 27
 RESULT 8
 AAA74623
 ID AAA74623 standard; DNA; 27 BP.
 AC
 AC AAA74623;
 XX
 DT 08-JAN-2001 (first entry)
 XX
 DE HCV-specific amplification primer C282R27.
 XX
 KW Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN EP1026262-A2.
 XX
 PD 09-AUG-2000.
 XX
 PF 01-FEB-2000; 2000EP-00300763.
 XX
 PR 03-FEB-1999; 99US-0118497P.
 XX
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 XX
 PI Linnen JM, Gorman KM;

XX WPI; 2000-507254/46.
 XX
 PT Detecting hepatitis C virus in biological sample involves amplifying
 PT reverse transcribed products of virus RNA using amplification primers
 PT whose sequences correspond to 5' or 3' non-coding region of the virus
 RNA.
 XX
 PS Claim 30; Page 27; 28pp; English.
 XX
 CC The present sequence is an amplification primer used in a method for
 CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA
 CC is reverse transcribed to generate cDNA. This is then amplified using
 CC primers, including the present sequence, corresponding to the 5' or 3'
 CC non-coding region of HCV. The method is useful for the diagnosis of HCV
 CC infection in patients, in testing the efficacy of anti-HCV therapeutic
 CC regimes, and in screening blood for HCV-infected samples. The method
 CC provides an improved single-round, reverse transcription/amplification
 CC assay which detects low copy levels of HCV RNA. The primers and assay
 CC system are designed to allow the co-amplification of multiple regions of
 CC the HCV genome, multiple viral species, and an internal positive control
 CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple
 CC regions of the HCV genome increases assay sensitivity and the co-
 CC amplification of an IPC decreases the likelihood of false negative
 CC results because of PCR inhibition
 XX
 SQ Sequence 27 BP; 9 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 96.4%; Score 27; DB 3; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCAAGCACCTATCAGGCGAGTACCACA 27
 Db 1 GCAAGCACCTATCAGGCGAGTACCACA 27
 RESULT 9
 ADCS4073/C
 ID ADCS4073 standard; DNA; 29 BP.
 XX
 AC ADCS4073;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE HCV 5'UTR signal amplification probe, SEQ ID NO:24.
 XX
 KW HCV; hepatitis C virus; classification; interferon therapy; 5'UTR;
 KW signal amplification; probe; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN JP2002345467-A.
 XX
 PD 03-DEC-2002.
 XX
 PF 17-APR-2001; 2001JP-00118810.
 XX
 PR 23-OCT-2000; 2000JP-00322567.
 XX
 PA (SRLS-) SRL KK.
 XX
 DR WPI; 2003-460879/44.
 XX
 PT Probe and method for classification of hepatitis C virus (HCV) types used
 PT for forecast of therapeutic effect of interferon administration.
 XX
 PS Disclosure; SEQ ID NO 24; 15pp; Japanese.
 XX
 CC The invention relates to a nucleic acid probe for the classification of
 CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1ami
 CC (type 1), MH2ami (type 2) and MHG3C+MHG3C' (type 3). The probe can be
 CC used to classify HCV type to enable prediction of the success or

CC otherwise of interferon therapy in a patient. Sequences ADC54068-ADC54073
CC represent HCV 5'UTR signal amplification probes. Note: The present
CC sequence is given in the sequence listing, but is not further referred to
CC in the specification.

XX
SQ Sequence 29 BP; 3 A; 6 C; 10 G; 10 T; 0 U; 0 Other;
Query Match 96.4%; Score 27; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGCACCCCTATCAGGCAGTACCA 28
DB 29 CAAGCACCCCTATCAGGCAGTACCA 3

RESULT 10
AAV54436
ID AAV54436 standard; DNA; 40 BP.
XX
AC AAV54436;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence of HCV PCR primer 3.
XX
KW Hepatitis C virus; HCV; PCR; primer; amplification; ss.
XX
OS Synthetic.
XX
PN JF10248579-A.
XX
PD 22-SEP-1998.
XX
PF 05-MAR-1997; 97JP-00067321.
XX
PR 05-MAR-1997; 97JP-00067321.
XX
PA (TOKR-) ZH TOKYO RINSHO IGAKU SOGO KENKYUSHO.
XX
FA (SRLS-) SRL KK.
XX
DR WPI; 1998-560731/48.
XX
PT Determination of hepatitis C virus (HCV) gene - with real time detective
PT PCR and primer and probe used for determination.
XX
PS Claim 3; Page 6; 7pp; Japanese.
XX
CC This is the nucleotide sequence of a Hepatitis C virus (HCV) PCR primer
CC used for amplification in the method of the invention. This is a useful
CC for the detection of the HCV gene
XX
SQ Sequence 40 BP; 9 A; 17 C; 9 G; 5 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCACCCCTATCAGGCAGTACCA 25
DB 16 GCAGCACCCCTATCAGGCAGTACCA 40

RESULT 11
ABZ81791/c
ID ABZ81791 standard; RNA; 47 BP.
XX
AC ABZ81791;
XX
DT 11-JUN-2003 (first entry)
XX
XX HCV 5' UTR molecular interaction site 7 polynucleotide 2.
XX
XX

KW HCV; 5' untranslated region; 5' UTR; molecular interaction;
KW secondary structure; combinatorial library; screening; virucide; ss.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT misc_binding 1..4
FT /tag= a
FT /bound_moiety= "Polynucleotide 1"
FT /note= "forms double-stranded region with bases 14-17 of
FT sequence in ABZ81790"
FT misc_structure 5
FT /tag= b
FT /note= "forms internal loop with base 13 of sequence in
FT ABZ81790"
FT misc_binding 6..7
FT /tag= c
FT /bound_moiety= "Polynucleotide 1"
FT /note= "forms double-stranded region with bases 11-12 of
FT sequence in ABZ81790"
FT stem_loop 8..19
FT /tag= d
FT misc_binding 20..21
FT /tag= e
FT /bound_moiety= "Bases 30-31"
FT /note= "forms double-stranded stem region with bases 30-
FT 31"
FT misc_structure 22..29
FT /tag= f
FT /note= "internal loop"
FT misc_binding 23..28
FT /tag= g
FT /bound_moiety= "Bases 42-47"
FT /note= "forms double-stranded dangling structure"
FT misc_binding 30..31
FT /tag= h
FT /bound_moiety= "Bases 20-21"
FT /note= "forms double-stranded stem region with bases 20-
FT 21"
FT misc_binding 32..40
FT /tag= i
FT /bound_moiety= "Polynucleotide 1"
FT /note= "forms double-stranded region with bases 2-10 of
FT sequence in ABZ81790"
FT misc_binding 42..47
FT /tag= g
FT /bound_moiety= "Bases 23-28"
FT /note= "forms double-stranded dangling structure"
XX WO2003018747-A2.
XX 06-MAR-2003.
XX 19-AUG-2002; 2002WO-US026219.
XX 22-AUG-2001; 2001US-0314236P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ;
XX WPI; 2003-300721/29.
XX
XX Polynucleotides useful for screening combinatorial libraries of compounds
XX that inhibit or stimulate viral replication, comprise molecular
XX interaction sites of hepatitis C virus RNA having a defined secondary
XX structure.
XX Claim 26; Page 38; 63pp; English.
XX The present sequence is that of the second polynucleotide of a molecular
XX interaction site (number 7) that has been identified in the 5',
XX untranslated region (5' UTR) of hepatitis C virus (HCV) RNA (see
XX

CC AB281793). The first polynucleotide forming site 7 is given in AB281790.
 CC The 2 polynucleotides together form a double-stranded RNA including
 CC internal and terminal loops and 2 dangling structures. The 8 molecular
 CC interaction sites identified in the HCV 5' UTR each have a secondary
 CC structure capable of interacting with cellular components, such as
 CC factors and proteins required for translation and other cellular
 CC processes. Nucleic acid molecules, polynucleotides or oligonucleotides
 CC comprising the molecular interaction sites can be used to screen,
 CC virtually or actually, combinatorial libraries of compounds that bind to
 CC them. Such compounds can be used to modulate the activity of HCV RNA and
 CC hence to modulate (inhibit or stimulate) viral replication. Thus, novel
 CC drugs, and agricultural and industrial chemicals, that operate through
 CC the modulation of HCV RNA can be identified

XX SQ Sequence 47 BP; 6 A; 11 C; 18 G; 0 T; 12 U; 0 Other;

Query Match 89.3%; Score 25; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGAGTACCA 25
 Db 25 GCAAGCACCTATCAGGCGAGTACCA 1

RESULT 12
 AAT05222
 ID AAT05222 standard; DNA; 28 BP.

AC AAT05222;

XX 13-JUN-1996 (first entry)

DE Hepatitis C virus antisense oligonucleotide A312.

XX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
 KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
 KW infection; antisense; non coding; region; NCR; core region; ss.
 XX Synthetic.

XX WO9530746-A1.

XX 16-NOV-1995.

XX 08-MAY-1995; 95WO-US005812.

XX 10-MAY-1994; 94US-00240382.

XX (GEHO) GEN HOSPITAL CORP.

XX Wakita T, Wands JR;

XX WPI; 1995-404113/51.

XX New anti-sense hepatitis C virus oligo:nucleotide(s) - used for
 PT inhibiting HCV RNA translation, for the treatment or prevention of HCV
 PT infection.

XX Claim 1; Page 29; 50pp; English.

XX The present oligonucleotide (ON) inhibits the expression of hepatitis C
 CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis
 CC is inhibited by 45% and 18%, respectively. The ONs of the invention
 CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,
 CC and can therefore be used to treat or prevent HCV infection. The
 CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV
 CC 5'-non-coding and part of the core region. The A or S in the ONs name
 CC denotes antisense or sense, and the no. indicates the position of the 5'-
 CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA

XX Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 85.7%; Score 24; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGAGTACC 24
 Db 5 GCAAGCACCTATCAGGCGAGTACC 28

RESULT 13
 AA257757
 ID AA257757 standard; DNA; 28 BP.

XX AA257757;

XX 05-APR-2000 (first entry)

DE Hepatitis C virus antisense inhibitor oligonucleotide A312.

XX Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
 KW anti-inflammatory; translation inhibition; HCV infection; virucide.

XX Hepatitis C virus.

XX US6001990-A.

XX 14-DEC-1999.

XX 07-JUN-1995; 95US-00474700.

XX 10-MAY-1994; 94US-00240382.

XX (GEHO) GEN HOSPITAL CORP.

XX Moradpour D, Wands JR, Wakita T;

XX WPI; 2000-104900/09.

XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
 PT Hepatitis C virus infections.

XX Claim 1; Col 23; 31pp; English.

XX This sequence is an antisense oligonucleotide that hybridises to
 CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
 CC invention relates to HCV antisense oligonucleotides, and also for a
 CC vector comprising a nucleotide sequence which is transcribed in an animal
 CC cell to generate an antisense oligonucleotide. The oligonucleotides have
 CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
 CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
 CC Hepatitis C virus is a positive strand RNA virus, and is the major
 CC causative agent of post-transfusion hepatitis. Persistent HCV infection
 CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma

XX SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 85.7%; Score 24; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGAGTACC 24
 Db 5 GCAAGCACCTATCAGGCGAGTACC 28

RESULT 14
 AAQ55728
 ID AAQ55728 standard; DNA; 30 BP.

XX AAQ55728;

XX 13-OCT-1994 (first entry)

XX

DE Hepatitis C detection primer 2.
XX Key.
XX Synthetic.
OS JP06014800-A.
XX PN
XX PD
XX 25-JAN-1994.
XX PF 02-JUL-1992; 92JP-00197407.
XX PR 02-JUL-1992; 92JP-00197407.
XX (TOXJ) TOSOH CORP.
PA WPI; 1994-061488/08.
XX
XX Detection of human hepatitis C virus - using primer contg. at least 15
PT continuous bases.
XX
XX Claim 1; Page 1; 5pp; Japanese.
XX
XX The primers (AAQ55727-728) are used to detect hepatitis C virus. The
CC method can amplify and detect specifically the nucleic acid sequence
CC originated from a trace amount of HCV contained in a sample
XX
XX Sequence 30 BP; 8 A; 12 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 85.7%; Score 24; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGCACCCCTATCAGGCAGTACC 24
DB 7 GCAAGCACCCCTATCAGGCAGTACC 30
RESULT 15
AAQ31158
ID AAQ31158 standard; DNA; 33 BP.
XX
XX AAQ31158;
AC
XX 25-MAR-2003 (revised)
DT 24-MAR-1993 (first entry)
XX
XX Probe 127 for genotyping analysis of HCV-1.
DE Hepatitis C virus; non-A, non-B hepatitis; polymerase chain reaction;
XX amplified solution phase nucleic acid sandwich assay;
KW genotyping analysis; capture probe; detection probe; ss.
XX
XX Synthetic.
OS
XX WO9219743-A2.
PN
XX 12-NOV-1992.
PD
XX 08-MAY-1992; 92WO-US004036.
PF
XX 08-MAY-1991; 91US-00697326.
PR
XX (CHIR) CHIRON CORP.
PA
XX Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
PI WPI; 1992-398869/48.
XX
XX Compan. comprising a non-hepatitis C virus-1 nucleotide sequence -
PT related to HCV-1, useful for treating and detecting HCV-1 infections and
PT as a vaccine.
XX

PS Claim 63; Page 140; 186pp; English.
XX
XX A sandwich hybridisation assay can be used for HCV-1 genotyping analysis.
CC One example uses nucleotide sequences which correspond to sequences in
CC the C gene and the 5' UT region of HCV isolates as either capture or
CC detection probes. Probe 127 is preferably used as a capture probe.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 85.7%; Score 24; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGCACCCCTATCAGGCAGTACC 24
DB 10 GCAAGCACCCCTATCAGGCAGTACC 33
RESULT 16
AAQ46464
ID AAQ46464 standard; DNA; 33 BP.
XX
XX AAQ46464;
AC
XX 25-MAR-2003 (revised)
DT 13-DEC-1993 (first entry)
XX
XX Hepatitis C virus RNA assay capture probe HCV.33.9.
DE
XX Detection; HCV; reduced background signal; improved reproducibility;
KW hybridisation; 5'-untranslated region; C gene; ss.
XX
XX Synthetic.
OS
XX WO9313224-A1.
PN
XX 08-JUL-1993.
PD
XX 22-DEC-1992; 92WO-US011343.
PF
XX 23-DEC-1991; 91US-00813338.
PR
XX (CHIR) CHIRON CORP.
PA
XX Sheridan P, Chang C, Running J;
PI
XX WPI; 1993-227338/28.
DR
XX Immobilising nucleic acid probe on styreneI, useful for HCV sequence
PT detection - by using intermediate passively adsorbed polymer having
PT functional gps. for covalently bonding to probe via its base-stable
PT linkages.
XX
XX Example; Fig 3.1; 34pp; English.
PS
XX The sequence is that of a synthetic capture probe which is complementary
CC to nucleotide sequences in the hepatitis C virus C gene and the 5' -
CC untranslated region. It may be used in an assay for the detection of HCV
CC RNA. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 85.7%; Score 24; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGCACCCCTATCAGGCAGTACC 24
DB 10 GCAAGCACCCCTATCAGGCAGTACC 33
RESULT 17

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AAV07838
ID AAV07838 standard; DNA; 33 BP.
XX AC AAV07838;
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 10-DEC-1998 (first entry)
XX DE HCV.33.9 amplifier probe.
XX KW Comb-type branched polynucleotide; amplification multimer; analyte;
XX KW hybridisation assay; hepatitis c virus; HCV; amplifier probe; ss.
XX OS Synthetic.
XX OS Hepatitis C virus.
XX PN US5710264-A.
XX PD 20-JAN-1998.
XX PF 07-JUN-1995; 95US-00478085.
XX PR 27-JUL-1990; 90US-00558897.
XX PR 23-DEC-1991; 91US-00813588.
XX PA (CHIR ) CHIRON CORP.
XX PI Chang C, Fultz TJ, Warner B, Urdea MS, Horn T;
XX WPI; 1998-109872/10.
XX DR New large comb-type branched polynucleotides - useful as amplification
XX PT multimers in nucleic acid hybridisation assays.
XX PS Example 6; Col 25; 33pp; English.
XX CC The invention relates to a large comb-type branched polynucleotide of
XX CC formula: 3'-A-S-(S'-X'm-S''-5'; where X' is a branched site joined to -
XX CC (R)n-S''-E-L; A = an oligonucleotide complementary to an analyte nucleic
XX CC acid sequence; S = a first spacer segment of 1-50 linked monomers where
XX CC each monomer is selected from nucleotides and a cleavable linker R; S' =
XX CC a branching site spacer segment of 0-15 linked monomers where each of the
XX CC monomers is selected from nucleotides and cleavable linker R; X' = a
XX CC multifunctional nucleotide that provides a branch site; m = 1-100; S'' =
XX CC a second spacer segment of 0-10 linked monomers where each of the
XX CC monomers is selected from nucleotides and cleavable linker R; R = a
XX CC cleavable linker molecule; n = 0 or 1; S''' = a third spacer segment of 0
XX CC -10 linked monomers where each of the monomers is selected from
XX CC nucleotides and cleavable linker R; E = an oligonucleotide segment of 5-
XX CC 10 nucleotides; L = an oligonucleotide containing 2-10 iterations of a
XX CC nucleotide sequence complementary to a labelled nucleic acid probe. The
XX CC invention also relates to a branched nucleic acid polymer. The poly-
XX CC nucleotides are useful as amplification multimers in nucleic acid
XX CC hybridisation assays used for genetic research, biomedical research and
XX CC clinical diagnostics. Since the polynucleotide multimers include a large
XX CC number (at least 20) iterations of a sequence that are available for
XX CC specific hybridisation, they permit a greater degree of amplification and
XX CC decrease the threshold level of a detectable analyte. The present
XX CC sequence represents a hepatitis c virus (HCV) amplifier probe. (Updated
XX CC on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct
XX CC OS field.)
XX SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 85.7%; Score 24; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCAAGCACCTATCAGGCAGTACC 24
DB 10 GCAAGCACCTATCAGGCAGTACC 33
RESULT 19
ADF52816/c
ID ADF52816 standard; RNA; 23 BP.
XX AC ADF52816;
```

```
RESULT 18 -
AAV83066
ID AAV83066 standard; DNA; 33 BP.
XX AC AAV83066;
XX DT 24-FEB-1999 (first entry)
XX DE Amplifier probe HCV.33.9.
XX KW Comb-type branched polynucleotide; amplifier probe;
XX KW multifunctional nucleotide; pendant polynucleotide sidechain;
XX KW hybridisation assay; amplification multimer; sandwich assay; ss.
XX OS Synthetic.
XX OS Hepatitis C virus.
XX PN US5849481-A.
XX PD 15-DEC-1998.
XX PF 05-JUN-1995; 95US-00470124.
XX PR 27-JUL-1990; 90US-00558897.
XX PR 23-DEC-1991; 91US-00813588.
XX PA (CHIR ) CHIRON CORP.
XX PI Warner B, Horn T, Fultz TJ, Urdea MS, Chang C;
XX WPI; 1999-069715/06.
XX DR Improved nucleic acid hybridisation assays - using large comb-type
XX PT polypeptide(s).
XX PS Example 6; Col 24; 31pp; English.
XX CC Oligonucleotides AAV83063-80 represent amplifier probes, used in a
XX CC sandwich hybridisation assay for Hepatitis C virus (HCV) DNA. The
XX CC sandwich hybridisation assay utilises the comb-type branched
XX CC polynucleotide amplification multimer of the invention. This large comb-
XX CC type branched polynucleotide comprises a polynucleotide backbone having
XX CC at least 15 multifunctional nucleotides each defining a sidechain site
XX CC and pendant polynucleotide sidechains extending from the multifunctional
XX CC nucleotides, each comprising iterations of an single stranded
XX CC oligonucleotide unit capable of binding specifically to a second single-
XX CC stranded polynucleotide sequence. The total number of iterations in all
XX CC sidechains is at least 20. The first single-stranded polynucleotide
XX CC sequence is a labelled polynucleotide, directly or indirectly linked to a
XX CC nucleic acid analyte. In the nucleic acid hybridisation assay of the
XX CC invention, the labelled nucleic acid probe is hybridised to the branched
XX CC polymeric nucleotide via the second single-stranded oligonucleotide unit.
XX CC The comb-type branched polynucleotides are used as amplification
XX CC multimers in nucleic acid hybridisation assays and other assays such as
XX CC direct, indirect and sandwich assays
XX SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 85.7%; Score 24; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCAAGCACCTATCAGGCAGTACC 24
DB 10 GCAAGCACCTATCAGGCAGTACC 33
RESULT 19
ADF52816/c
ID ADF52816 standard; RNA; 23 BP.
XX AC ADF52816;
```

XX DT 12-FEB-2004 (first entry)
XX DE Hepatitis C virus siNA target sequence SeqID1406.
XX short interfering nucleic acid; siNA; virus replication inhibition;
KW Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX OS Hepatitis C virus.
XX PN WO2003070750-A2.
XX PD 28-AUG-2003.
XX PF 20-FEB-2003; 2003WO-US005043.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 26-MAR-2002; 2002WO-US009187.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 05-AUG-2002; 2002US-0401104P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (SIRN-) SIRNA THERAPEUTICS INC.
XX PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WI; 2003-689778/65.
XX DR New double-stranded short interfering nucleic acid comprises sugar-
XX PT modified pyrimidine bases useful for treating infection with hepatitis C
XX PT virus.
XX PS Example 3; SEQ ID NO 1406; 183pp; English.
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX SQ Sequence 23 BP; 3 A; 4 C; 8 G; 0 T; 8 U; 0 Other;
Query Match 82.1%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AGCACCCCTATCAGGCAGTACCA 25
|||||
Db 23 AAGCACCCCTATCAGGCAGTACCA 1
RESULT 20
ADFS2808/c
.ID ADFS2808 standard; RNA; 23 BP.

XX AC ADFS2808;
XX DT 12-FEB-2004 (first entry)
XX DE Hepatitis C virus siNA target sequence SeqID1398.
XX short interfering nucleic acid; siNA; virus replication inhibition;
KW Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX OS Hepatitis C virus.
XX PN WO2003070750-A2.
XX PD 28-AUG-2003.
XX PF 20-FEB-2003; 2003WO-US005043.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 26-MAR-2002; 2002WO-US009187.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 05-AUG-2002; 2002US-0401104P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (SIRN-) SIRNA THERAPEUTICS INC.
XX PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WI; 2003-689778/65.
XX DR New double-stranded short interfering nucleic acid comprises sugar-
XX PT modified pyrimidine bases useful for treating infection with hepatitis C
XX PT virus.
XX PS Example 3; SEQ ID NO 1398; 183pp; English.
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX SQ Sequence 23 BP; 3 A; 3 C; 9 G; 0 T; 8 U; 0 Other;
Query Match 82.1%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CACCCTATCAGGCAGTACCA 28
|||||
Db 23 CACCCTATCAGGCAGTACCA 1
RESULT 21

```
ADFS2814/c
ID ADF52814 standard; RNA; 23 BP.
AC ADF52814;
XX
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus siNA target sequence SeqID1404.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
XX OS
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 1404; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX
XX Sequence 23 BP; 3 A; 4 C; 9 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 82.1%; Score 23; DB 10; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 1.1;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 GCACCCCTATCAGGCAGTACCACA 27
XX
XX 23 GCACCCCTATCAGGCAGTACCACA 1
XX
```

```
RESULT 22
ADFS2817/c
ID ADF52817 standard; RNA; 23 BP.
XX
XX ADF52817;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus siNA target sequence SeqID1407.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
XX OS
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 1407; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX
XX Sequence 23 BP; 3 A; 4 C; 9 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 82.1%; Score 23; DB 10; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 1.1;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 CAAGCACCCCTATCAGGCAGTACC 24
XX
XX |||||
```

Db 23 CAAGCACCTATCAGGAGTACC 1

RESULT 23

ADFS2815/c
ID ADFS2815 standard; RNA; 23 BP.

XX ADFS2815;
AC ADFS2815;
XX 12-FEB-2004 (first entry)
DT
XX Hepatitis C virus siRNA target sequence SeqID1405.
DE
XX short interfering nucleic acid; siRNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX

OS Hepatitis C virus.

XX WO2003070750-A2.

PN 28-AUG-2003.

PD 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.

PA Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-modified pyrimidine bases useful for treating infection with hepatitis C virus.

XX Example 3; SEQ ID NO 1405; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (ASS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to ASS, and where most of the pyrimidine nucleotides comprise a sugar modification. The invention may allow development of compounds with virucide, antiinflammatory, hepatotropic or cytostatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siRNA's of the invention may be used to inhibit replication of HCV, in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure, hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity, cellular uptake and/or binding affinity. The siRNA can be directed to conserved regions of HCV genes, so are active against many different strains.

XX Sequence 23 BP; 3 A; 4 C; 9 G; 0 T; 7 U; 0 Other;

XX Query Match 82.1%; Score 23; DB 10; Length 23;

XX Best Local Similarity 100.0%; Pred. No. 1.1;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGCACCTATCAGGAGTACC 26
Db 23 AGCACCTATCAGGAGTACC 1

RESULT 24

AAD19057
ID AAD19057 standard; DNA; 24 BP.

XX AAD19057;

XX 18-DEC-2001 (first entry)

DT Hepatitis viral DNA amplifying reverse PCR primer #31.

DE
XX Hepatitis virus; bacterial infection; fungi; protozoa; PCR primer;
KW amplification; blood-borne pathogen; sexually transmitted disease;
KW respiratory disease; ss.

XX Hepatitis virus.

XX WO200168921-A2.

PN 20-SEP-2001.

PD 14-MAR-2001; 2001WO-US008110.

PR 14-MAR-2000; 2000US-0189344P.

XX (INVE-) INVESTIGEN.

XX Koshinsky H, Zwick MS, Mccue KP;

XX WPI; 2001-611396/70.

XX Simultaneous detection of biological entities such as bacteria, fungi and viruses by specific nucleic acid amplification.

XX Disclosure; Page 31; 55pp; English.

XX The invention relates to a method and apparatus for the simultaneous detection of multiple biological entities such as bacteria, fungi and viruses by specific nucleic acid amplification. The invention also relates to a kit for simultaneous detection of biological entities. The kit is employed for detecting blood-borne pathogens, associated with a variety of infectious diseases such as respiratory and sexually transmitted diseases. The methods and apparatus are used for the simultaneous detection of biological entities present in biological and environment samples. In particular, they are used for monitoring diseases caused by microorganisms associated with a respiratory or sexually transmitted disease such as a bacterium (Staphylococcus, Pneumococcus, Gonococcus, Haemophilus, Bacteroides, Escherichia or Salmonella), virus (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV, HDV, HEV, HGV or TTV), fungus (Aspergillus fumigatus, Blastomycosis, dermatitis, Candida albicans) or protozoa (Entamoeba histolytica). The present sequence is a PCR primer used for amplifying Hepatitis viral DNA

XX Sequence 24 BP; 7 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

XX Query Match 82.1%; Score 23; DB 4; Length 24;

XX Best Local Similarity 100.0%; Pred. No. 1.1;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCACCTATCAGGAGTACC 23

Db 2 GCAAGCACCTATCAGGAGTACC 24

RESULT 25

AZ87367
ID AZ87367 standard; cDNA; 27 BP.

XX AZ87367;

```

XX DT 22-MAY-2000 (first entry)
XX DE Hepatitis C virus 5'NCR RT-PCR primer NC4.
XX KW Hepatitis C virus; HCV; in vitro culture; primary mammalian hepatocyte;
XX KW culture medium; replication; drug screening; antibody testing; diagnosis;
XX KW vaccine development; 5'NCR; reverse transcriptase-PCR; RT-PCR primer; ss.
XX OS Hepatitis C virus.
XX PN WO9967362-A1.
XX PD 29-DEC-1999.
XX PF 23-JUN-1999; 99WO-EP004337.
XX PR 24-JUN-1998; 98EP-00401554.
XX FA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Rumin S, Inchauspe G, Trepo C, Gripon P;
XX DR WPI; 2000-160580/14.
XX Use of a culture medium comprising at least one mammalian plasma or sera
PT and antioxidants and/or corticoids, for in vitro replication of hepatitis
PT C virus in hepatocytes.
XX Example 3; Page 18; 39pp; English.
XX The invention relates to a novel process and cell culture medium for in
CC vitro replication of hepatitis C virus (HCV) in primary mammalian
CC hepatocytes. The culture medium comprising one or more mammalian plasma
CC or sera, a chemical or biological compound with an anti-oxidative
CC property and/or a differentiating property, such as dimethyl sulphoxide
CC (DMSO), retinoic acid, vitamin (e.g., vitamin E), or selenium, and/or at
CC least one corticoid. The culture medium may be used in an in vitro HCV
CC infection and culture system. This would allow the mechanisms of viral
CC replication to be studied, and could also be used for in vitro screening
CC of anti-HCV drugs; to test neutralising antibodies; for in vitro
CC diagnosis of HCV; and for the preparation of vaccines against HCV. The
CC HCV-infected hepatocytes survive for at least 4 months in the culture
CC medium. Previously, a reliable and robust in vitro HCV culture method has
CC not been available. Sequences AA287367-287375 represent reverse
CC transcriptase-PCR (RT-PCR) primers used in an exemplification of the
CC present invention
XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 82.1%; Score 23; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGTAC 23
Db 5 GCAAGCACCTTATCAGGCAGTAC 27

RESULT 26
AAH78439
ID AAH78439 standard; DNA; 27 BP.
XX AC AAH78439;
XX DT 10-DEC-2001 (first entry)
XX PCR primer used to amplify HCV cDNA fragment.
XX Protein isolation; magnetic colloidal particle; polymer envelope;
XX KW vaccine; HCV; PCR primer; ss.
XX OS Hepatitis C virus.

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XX WO200152612-A2.
XX 26-JUL-2001.
XX 22-JAN-2001; 2001WO-FR000205.
XX 21-JAN-2000; 2000FR-00000862.
XX (INMR ) BIO MERIEUX.
XX Elaissari A, Mandrand B, Delair T, Spencer D, Arkis A;
XX WPI; 2001-596423/67.
XX Isolation of protein and protein-nucleic acid complexes, useful e.g. for
PT subsequent analysis or transport, by binding to magnetic beads coated
PT with functionalized polymer.
XX Example 4; Page 13; 29pp; French.
XX The specification describes a method for the isolation of proteins and/or
CC their complexes with nucleic acid. The method comprises treating a sample
CC with magnetic colloidal particles that comprise a magnetic core and an
CC envelope of a polymer (P1) containing ionizable functional groups. The
CC mixture is incubated then the proteins or complexes are recovered by
CC application of a magnetic field. The core is covered by at least one
CC polymer (P2) containing functional groups, at least some of which have
CC reacted with groups in (P1). Functional groups in P1 and P2 are the same
CC or different, and are amino, hydroxy thiol, formyl, ester, anhydride,
CC acyl chloride, carbonate, carbamate and/or isothio) cyanate. The method
CC is used for extraction, identification, detection and/or quantification
CC of protein and their complexes. It is also used for establishing cell
CC cultures and biological samples. The complexes formed between magnetic
CC colloidal particles and the proteins are useful for transfer, transport
CC and/or storage of infectious agents (virus, bacterium or yeast) and for
CC preparation of vaccines. PCR primers AAH78438-39 were used to amplify a
CC fragment of HCV cDNA. The amplified fragment was used to demonstrate the
CC use of the method of the invention for capture of HCV particles by
CC magnetic latex
XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 82.1%; Score 23; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGTAC 23
Db 5 GCAAGCACCTTATCAGGCAGTAC 27

RESULT 27
AAH78441
ID AAH78441 standard; DNA; 27 BP.
XX AC AAH78441;
XX DT 10-DEC-2001 (first entry)
XX PCR primer used to amplify HCV cDNA fragment.
XX Protein isolation; magnetic colloidal particle; polymer envelope;
XX KW vaccine; HCV; PCR primer; ss.
XX OS Hepatitis C virus.
XX PN WO200152612-A2.
XX 26-JUL-2001.
XX 22-JAN-2001; 2001WO-FR000205.
XX

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PR 21-JAN-2000; 2000FR-00000862.
XX (INNR ) BIO MERIEUX.
PA Elaissari A, Mandrand B, Delair T, Spencer D, Arkis A;
XX WPI; 2001-596423/67.
DR
XX
XX Isolation of protein and protein-nucleic acid complexes, useful e.g. for
PT subsequent analysis or transport, by binding to magnetic beads coated
PT with functionalized polymer.
XX
XX Example 4; Page 13; 29pp; French.
XX
XX The specification describes a method for the isolation of proteins and/or
CC their complexes with nucleic acid. The method comprises treating a sample
CC with magnetic colloidal particles that comprise a magnetic core and an
CC envelope of a polymer (P1) containing ionizable functional groups. The
CC mixture is incubated then the proteins or complexes are recovered by
CC application of a magnetic field. The core is covered by at least one
CC polymer (P2) containing functional groups, at least some of which have
CC reacted with groups in (P1). Functional groups in P1 and P2 are the same
CC or different, and are amino, hydroxy thiol, formyl, ester, anhydride,
CC acyl chloride, carbonate, carbamate and/or isothiolocyanate. The method
CC is used for extraction, identification, detection and/or quantification
CC of protein and their complexes. It is also used for establishing cell
CC cultures and biological samples. The complexes formed between magnetic
CC colloidal particles and the proteins are useful for transfer, transport
CC and/or storage of infectious agents (virus, bacterium or yeast) and for
CC preparation of vaccines. PCR primers AAH78440-41 were used to amplify a
CC fragment of HCV cDNA. The amplified fragment was used to demonstrate the
CC use of the method of the invention for capture of HCV particles by
CC magnetic latex
XX
XX Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 82.1%; Score 23; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCACCCTATCAGGCGATAC 23
DB 5 GCAAGCACCCCTATCAGGCGATAC 27
RESULT 28
ADFS2809/C
XX ADFS2809 standard; RNA; 23 BP.
XX
XX ADFS2809;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus siRNA target sequence SeqID1399.
XX
XX short interfering nucleic acid; siRNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
OS
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
PR
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PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1399; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
XX Sequence 23 BP; 3 A; 4 C; 8 G; 0 T; 8 U; 0 Other;
SQ
Query Match 78.6%; Score 22; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ACCCTATCAGGCGATACCACAA 28
DB 23 ACCCTATCAGGCGATACCACAA 2
RESULT 29
ADFS2818/C
XX ADFS2818 standard; RNA; 23 BP.
XX
XX ADFS2818;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus siRNA target sequence SeqID1408.
XX
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
OS
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
PR
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PR 06-JUN-2002; 2002US-0386782P.
 PR 09-AUG-2002; 2002US-0401104P.
 PR 05-SEP-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
 PI WPI; 2003-689778/65.
 DR
 XX
 XX New double-stranded short interfering nucleic acid comprises sugar-
 PT modified pyrimidine bases useful for treating infection with hepatitis C
 PT virus.
 XX
 XX Example 3; SEQ ID NO 1408; 183pp; English.
 PS
 XX This invention relates to novel double-stranded short interfering nucleic
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
 CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
 CC interference. The siNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains.
 XX
 XX Sequence 23 BP; 3 A; 5 C; 8 G; 0 T; 7 U; 0 Other;
 SQ
 Query Match 78.6%; Score 22; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred.No. 3.1;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGCACCCTATCAGGCAGTA 22
 Db 22 GCAGCACCCTATCAGGCAGTA 1
 RESULT 30
 ID AAQ71839 standard; DNA; 27 BP.
 XX
 AC AAQ71839;
 XX
 XX 25-MAR-2003 (revised)
 DT 25-MAR-1995 (first entry)
 XX
 XX PCR primer for hepatitis G virus.
 DE
 XX DNA primer; sense; polymerase chain reaction; hepatitis G virus;
 KW diagnostic; ss.
 KW
 OS Synthetic.
 XX
 XX WO9418217-A1.
 FN
 XX 18-AUG-1994.
 PD
 XX 03-FEB-1993; 93WO-US000928.
 PF
 XX 03-FEB-1993; 93WO-US000928.
 PR
 XX

PA (ABBO) ABBOTT LAB.
 XX
 PI Tassopoulos NC, Hatzakis AE, Troonen H, Kuhns MC;
 XX
 DR WPI; 1994-279671/34.
 XX
 XX Hepatitis G virus polypeptides, nucleic acids, antibodies and cell
 PT cultures - used to detect the virus in a test sample and to screen
 PT antiviral agents.
 XX
 XX Disclosure; Page 60; 67pp; English.
 PS
 XX The sense primer is used with an antisense primer (AAQ71840) in a reverse
 CC transcription-polymerase chain reaction assay for hepatitis E virus. A
 CC DNA probe (AAQ71841) is used to detect the PCR products generated by the
 CC 2 primers. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 78.6%; Score 22; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred.No. 3.1;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGCACCCTATCAGGCAGTA 22
 Db 6 GCAGCACCCTATCAGGCAGTA 27
 RESULT 31
 ID AAA74624 standard; DNA; 27 BP.
 XX
 AC AAA74624;
 XX
 XX 08-JAN-2001 (first entry)
 DT
 XX HCV-specific amplification primer C287R27.
 DE
 XX Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
 KW
 XX Hepatitis C virus.
 OS
 XX EP1026262-A2.
 FN
 XX 09-AUG-2000.
 PD
 XX 01-FEB-2000; 2000EP-00300763.
 PF
 XX 03-FEB-1999; 99US-0118497P.
 PR
 XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 PA
 PI Linnen JM, Gorman KM;
 XX
 DR WPI; 2000-507254/46.
 XX
 XX Detecting hepatitis C virus in biological sample involves amplifying
 PT reverse transcribed products of virus RNA using amplification primers
 PT whose sequences correspond to 5' or 3' non-coding region of the virus
 PT RNA.
 XX
 XX Claim 30; Page 27; 28pp; English.
 PS
 XX The present sequence is an amplification primer used in a method for
 CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA
 CC is reverse transcribed to generate cDNA. This is then amplified using
 CC primers, including the present sequence, corresponding to the 5' or 3'
 CC non-coding region of HCV. The method is useful for the diagnosis of HCV
 CC infection in patients, in testing the efficacy of anti-HCV therapeutic
 CC regimes, and in screening blood for HCV-infected samples. The method
 CC provides an improved single-round, reverse transcription/amplification
 CC assay which detects low copy levels of HCV RNA. The primers and assay
 CC system are designed to allow the co-amplification of multiple regions of

CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

XX
11

DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberyze (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^{2+} . Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an enzymatic nucleic acid with trans-acting inhibitory sequences (S- are substrate sequences, Rz- are enzymatic nucleic acid and I- are inhibitory sequences)

PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (CHOW/) CHOWRIRA B M.
XX
XX PI Blatt L, Mcswiggen J, Chowrira BM;
XX
XX WPT; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
XX Example 7; Page 170; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOMO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOMO-
CC targeting nucleic acid is used to cleave RNA of the NOMO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOMO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOMO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOMO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOMO expression. The present
CC sequence is an enzymatic nucleic acid with trans-acting inhibitory
CC sequences (S- are substrate sequences, RZ- are enzymatic nucleic acid and
CC I- are inhibitory sequences)
XX
XX SQ Sequence 27 BP; 4 A; 5 C; 10 G; 0 T; 8 U; 0 Other;
Query Match 78.6%; Score 22; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCAAGCACCCCTATCAGGCAGTA 22
Db 22 GCAAGCACCCCTATCAGGCAGTA 1
RESULT 34
ABA02736
ID ABA02736 standard; RNA; 27 BP.
XX
XX AC ABA02736;
XX
XX DT 12-FEB-2002 (first entry)
XX

DE Nucleic acid sensor molecule SEQ ID NO 8.
XX
XX Nucleic acid sensor molecule; detection; infection; disease diagnosis;
KW physiological abnormality; electronic; signalling molecule;
KW nucleoside analogue; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..27
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methyl nucleotides"
XX
XX WO200166721-A2.
XX
XX PD 13-SEP-2001.
XX
XX PF 06-MAR-2001; 2001WO-US007163.
XX
XX PR 06-MAR-2000; 2000US-0187128P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Usman N, Mcswiggen JA, Zinnen S, Seiwert S, Haerberli P;
XX Chowrira B, Blatt L;
XX WPT; 2001-616242/71.
XX
XX PT New nucleic acid sensor molecule useful in diagnostic applications,
XX nucleic acid-based electronics and functional genomics, comprises an
XX enzymatic nucleic acid and one or more sensors.
XX
XX Example 1; Page 69; 115pp; English.
XX
XX The invention relates to a nucleic acid sensor molecule (I) comprising an
XX enzymatic nucleic acid component and one or more sensor components. (I)
XX is useful in diagnostic applications to identify the presence of genes
XX and/or gene products indicative of a particular genotype and/or
XX phenotype, e.g. a disease state or infection and for diagnosis of disease
XX states or physiological abnormalities related to the expression of viral,
XX bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based
XX electronics, for the detection of specific target signalling molecules,
XX in assays to assess the specificity, toxicity and effectiveness of
XX various small molecules, nucleoside analogues or non-nucleic acid drugs
XX or for detection of pathogens, biochemicals, organic or inorganic
XX compounds. The present sequence is that of a nucleic acid sensor molecule
XX of the invention
XX
XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 78.6%; Score 22; DB 4; Length 27;
Best Local Similarity 86.4%; Pred. No. 3.1;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCAAGCACCCCTATCAGGCAGTA 22
Db 6 GCAAGCACCCCTATCAGGCAGTA 27
RESULT 35
ABA02738/c
ID ABA02738 standard; RNA; 27 BP.
XX
XX AC ABA02738;
XX
XX DT 12-FEB-2002 (first entry)
XX
XX DE Nucleic acid sensor molecule SEQ ID NO 10.
XX
XX KW Nucleic acid sensor molecule; detection; infection; disease diagnosis;
KW physiological abnormality; electronic; signalling molecule;
KW nucleoside analogue; ss.

XX OS Synthetic.
 XX PN WO200166721-A2.
 XX PD 13-SEP-2001.
 XX PF 06-MAR-2001; 2001WO-US007163.
 XX PR 06-MAR-2000; 2000US-0187128P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Usman N, Mcswiggen JA, Zinnen S, Seiwert S, Haerberli P;
 PI Chowrira B, Blatt L;
 XX WIPI; 2001-616242/71.
 XX DR New nucleic acid sensor molecule useful in diagnostic applications,
 XX PT nucleic acid-based electronics and functional genomics, comprises an
 XX PT enzymatic nucleic acid and one or more sensors.
 XX PS Example 1; Page 69; 115pp; English.
 XX CC The invention relates to a nucleic acid sensor molecule (I) comprising an
 XX CC enzymatic nucleic acid component and one or more sensor components. (I)
 XX CC is useful in diagnostic applications to identify the presence of genes
 XX CC and/or gene products indicative of a particular genotype and/or
 XX CC phenotype, e.g. a disease state or infection and for diagnosis of disease
 XX CC states or physiological abnormalities related to the expression of viral,
 XX CC bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based
 XX CC electronics, for the detection of specific target signalling molecules,
 XX CC in assays to assess the specificity, toxicity and effectiveness of
 XX CC various small molecules, nucleoside analogues or non-nucleic acid drugs
 XX CC or for detection of pathogens, biochemicals, organic or inorganic
 XX CC compounds. The present sequence is that of a nucleic acid sensor molecule
 XX CC of the invention
 XX SQ Sequence 27 BP; 4 A; 5 C; 10 G; 0 T; 8 U; 0 Other;
 Query Match 78.6%; Score 22; DB 4; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAAGCACCCCTATCAGGCAGTA 22
 DB 22 GCAAGCACCCCTATCAGGCAGTA 1
 RESULT 36
 AAF58265
 ID AAF58265 standard; DNA; 46 BP.
 XX AC AAF58265;
 XX DT 24-APR-2001 (first entry)
 XX DE Hepatitis C virus primer #1.
 XX XX Primer; fluorescence polarization; detection; ss.
 XX OS Hepatitis C virus.
 XX PN JP2000333699-A.
 XX PD 05-DEC-2000.
 XX PF 31-MAY-1999; 99JP-00152109.
 XX PR 31-MAY-1999; 99JP-00152109.
 XX PA (KARO/) KAROE M.
 XX PA (TSUR/) TSURUOKA M.

PA (TOWA-) TOWA KAGAKU KK.
 XX WIPI; 2001-172352/18.
 XX DR
 XX PT Detecting ribonucleic acid (RNA) comprises transcription with RNA
 XX PT polymerase, contacting with a fluorescently labelled probe and detecting
 XX PT changes in fluorescent polarization.
 XX PS Example 1; Page 4; 8pp; Japanese.
 XX CC The present invention relates to detection of ribonucleic acid (RNA) with
 XX CC fluorescence polarization. The method gives sensitive and specific
 XX CC detection of RNA
 XX SQ Sequence 46 BP; 16 A; 12 C; 8 G; 10 T; 0 U; 0 Other;
 Query Match 78.6%; Score 22; DB 4; Length 46;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAAGCACCCCTATCAGGCAGTA'22
 DB 25 GCAAGCACCCCTATCAGGCAGTA 46
 RESULT 37
 AAQ58380
 ID AAQ58380 standard; DNA; 21 BP.
 XX AC AAQ58380;
 XX DT 25-MAR-2003 (revised)
 XX DT 04-OCT-1994 (first entry)
 XX DE Antisense oligonucleotide targetted to HCV 5'untranslated region.
 XX KW Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
 XX KW antisense oligonucleotide; translation inhibition; therapy; ss.
 XX OS Synthetic.
 XX PN WO9405813-A1.
 XX PD 17-MAR-1994.
 XX PF 10-SEP-1993; 93WO-JP001293.
 XX PR 10-SEP-1992; 92US-00945289.
 XX PR 14-APR-1993; 93JP-00087195.
 XX PA (MOCH) MOCHIDA PHARM CO LTD.
 XX PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;
 PI Nakatake H, Hamada F, Eto T, Furukawa S;
 XX WIPI; 1994-101217/12.
 XX PT Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome
 XX PT - useful for inhibiting HCV replication, to treat related diseases.
 XX PS Claim 5; Page 14; 91pp; English.
 XX CC Oligonucleotides which are complementary to part of the hepatitis C virus
 XX CC genomic or messenger RNA are claimed. Preferred antisense
 XX CC oligonucleotides (see AAQ58364-Q58387) are complementary to RNA
 XX CC comprising the 5' end hairpin loop, 5' end 6bp repeat, 5' end untranslated
 XX CC region, polypeptide translation initiation codon, ORF3 translation, R2
 XX CC initiation codon, 3' untranslated region, 3' end palindromic region, R2
 XX CC sequence or 3' end hairpin loop of HCV. (Updated on 25-MAR-2003 to
 XX CC correct PN field.)

```
SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 75.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCCTATCAGGCAGTACCACAA 28
DB 1 CCCTATCAGGCAGTACCACAA 21

RESULT 38
AAQ75034
ID AAQ75034 standard; DNA; 21 BP.
XX AC AAQ75034;
XX DT 25-MAR-2003 (revised)
XX DT 04-AUG-1995 (first entry)
XX DE PCR primer for the amplification of a peptide-streptavidin-oligo.
XX KW Synthetic peptide; solid phase immunoassay; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_difference 1
XX FT /*tag= a
XX FT /note= "linked to digoxigenin"
XX PN WO9426932-A1.
XX PD 24-NOV-1994.
XX PF 13-MAY-1994; 94WO-US005407.
XX PR 13-MAY-1993; 93US-00061694.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Fields HA, Khudyakov YE;
XX DR WPI; 1995-006819/01.
XX PT Solid phase immunoassay using oligo:nucleotide as label - also new
XX PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
XX PT diagnosing hepatitis C or E virus infection.
XX PS Example; Page 19; 34pp; English.
XX CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
XX CC They are used in a method for detecting an antigen in a subject. The
XX CC method involves binding the antigen to a solid support and then reacting
XX CC it with an immunoreactive ligand (L) bound to an oligo; removing any
XX CC unreacted L, and then detecting the presence of the oligo. A similar
XX CC method can be used to detect Abs, in which case the ligand is an oligo-
XX CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
XX CC to be detected at very low levels. In the example, anti-human antibodies
XX CC are adsorbed on the surface of microcentrifuge tubes and used to capture
XX CC antibodies from human sera specimens. Then the tubes are incubated with a
XX CC peptide- streptavidin-oligo complex. After washing, PCR is performed,
XX CC using primers AAQ75034 and AAQ75035. AAQ75034 could be labelled with
XX CC another moiety, for example, biotin. (Updated on 25-MAR-2003 to correct
XX CC PN field.)
XX SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 75.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCCTATCAGGCAGTACCACAA 28
DB 1 CCCTATCAGGCAGTACCACAA 21

RESULT 39
AAQ85921
ID AAQ85921 standard; DNA; 21 BP.
XX AC AAQ85921;
XX DT 25-MAR-2003 (revised)
XX DT 02-NOV-1995 (first entry)
XX DE Hepatitis C virus genome internal PCR primer YK-106B.
XX KW Hepatitis C virus; HCV; non-A non-B; external PCR primer; YK-106B;
XX OS primer specific detection; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /label= biotinylated
XX PN WO9506753-A1.
XX PD 09-MAR-1995.
XX PF 02-SEP-1994; 94WO-US009869.
XX PR 03-SEP-1993; 93US-00116344.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Fields HA, Khudyakov YE;
XX DR WPI; 1995-115465/15.
XX PT New method and kit for primer-specific detection of nucleic acids - using
XX PT two primers having a known sequence and a marker, resp for solid-phase
XX PT detection of amplification prods.
XX PS Example 1; Page 12; 20pp; English.
XX CC AAQ85918/19 are external, and AAQ85820/21 are internal PCR primers for
XX CC the Hepatitis C virus (HCV) genome. They were used to demonstrate a new
XX CC method for the primer specific detection of nucleic acids. (Updated on 25
XX CC -MAR-2003 to correct PN field.)
XX SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 75.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCCTATCAGGCAGTACCACAA 28
DB 1 CCCTATCAGGCAGTACCACAA 21

RESULT 40
AAZ25792
ID AAZ25792 standard; DNA; 21 BP.
XX AC AAZ25792;
XX DT 11-JAN-2000 (first entry)
XX DE Hepatitis C virus PCR primer #4.
XX KW Hepatitis C virus; HCV; PCR primer; ribavirin; interferon alpha;
XX KW antiviral; detection; infection; ss.
```

XX OS Synthetic.
OS Hepatitis C virus.
XX PN EP956861-A1.
XX PD 17-NOV-1999.
XX PF 13-MAY-1999; 99EP-00303729.
XX PR 15-MAY-1998; 98US-00079566.
XX PA (SCHE) SCHERING CORP.
XX PI Albrecht JK;
XX DR WPI; 1999-612821/53.
XX PT Use of ribavirin and/or interferon-alpha for composition for treating
XX PT chronic hepatitis C.
XX PS Disclosure; Page 6; 26pp; English.
XX CC The present invention describes the use of ribavirin and/or interferon-
CC alpha (IFN-alpha) for the manufacture of a pharmaceutical composition,
CC for treating an antiviral treatment naive patient having chronic
CC hepatitis C infection to eradicate detectable HCV-RNA. The method
CC comprises administering ribavirin with IFN-alpha for a period of 20-50
CC weeks. If the antiviral treatment naive patient has an HCV genotype 1
CC infection, the patient is administered ribavirin in association with IFN-
CC alpha for 40-50 (especially 48) weeks and if the antiviral treatment
CC naive patient has an HCV genotype 2 or 3 infection, the patient is
CC administered ribavirin in association with IFN-alpha for 20-30
CC (especially 24) weeks. The composition of ribavirin and/or IFN-alpha is
CC useful for the preparation of a pharmaceutical composition for treating
CC antiviral treatment naive patient having chronic hepatitis C. The
CC composition eradicates HCV-RNA in a long-term and effective manner.
CC AA225789 to AA225792 represent PCR primers which can amplify all known
CC subtypes of HCV
XX SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 75.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CCTATCAGGCGAGTACCACAA 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCTATCAGGCGAGTACCACAA 21

Search completed: November 23, 2004, 17:29:30
Job time : 167.277 secs

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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1	28	100.0	28	2	US-08-738-928-2
2	28	100.0	28	3	US-09-039-866-4
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4	27	96.4	27	2	US-08-738-928-3
5	27	96.4	27	4	US-09-493-353-5
6	24	85.7	28	3	US-08-474-700B-12
7	24	85.7	28	5	PCT-US95-05812-12
8	24	85.7	33	1	US-08-438-639-51
9	24	85.7	33	1	US-07-811-338A-51
10	24	85.7	33	2	US-08-470-124-61
11	24	85.7	33	3	US-08-441-971-137
12	24	85.7	33	3	US-08-221-653-137
13	24	85.7	33	3	US-08-442-144A-127
14	24	85.7	33	3	US-08-441-970-127
15	22	78.6	27	4	US-09-493-353-6
16	22	78.6	27	5	PCT-US93-00928-1
17	21	75.0	21	3	US-09-078-290A-10
18	21	75.0	21	3	US-08-938-033-4
19	21	75.0	21	3	US-08-397-220B-17
20	21	75.0	21	3	US-08-650-093C-17
21	21	75.0	21	4	US-08-823-895A-17
22	21	75.0	21	4	US-09-311-487-4
23	21	75.0	21	5	PCT-US94-05407-13
24	21	75.0	23	1	US-08-356-287-25
25	21	75.0	23	5	PCT-US93-04863-25
26	21	75.0	24	1	US-08-240-547-18
27	21	75.0	24	1	US-08-449-050-16

28	21	75.0	24	1	US-08-332-616A-8	Sequence 8, Appli
29	21	75.0	24	1	US-08-317-220-8	Sequence 8, Appli
30	21	75.0	24	1	US-08-675-153-8	Sequence 8, Appli
31	21	75.0	24	1	US-08-244-116B-51	Sequence 51, Appli
32	21	75.0	24	2	US-08-738-928-5	Sequence 5, Appli
33	21	75.0	24	2	US-08-841-252-8	Sequence 8, Appli
34	21	75.0	24	2	US-08-881-571-8	Sequence 8, Appli
35	21	75.0	24	3	US-09-282-054-8	Sequence 8, Appli
36	21	75.0	24	3	US-09-665-638-8	Sequence 8, Appli
37	21	75.0	24	4	US-10-007-389-5	Sequence 5, Appli
38	21	75.0	26	1	US-08-240-547-19	Sequence 19, Appli
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54	19	67.9	22	5	PCT-US93-04863-27	Sequence 27, Appli
55	18.4	65.7	26	1	US-08-244-116B-23	Sequence 23, Appli
56	18	64.3	28	3	US-08-474-700B-11	Sequence 11, Appli
57	18	64.3	28	3	US-08-474-700B-34	Sequence 34, Appli
58	18	64.3	28	3	US-08-474-700B-35	Sequence 35, Appli
59	18	64.3	28	5	PCT-US95-05812-11	Sequence 11, Appli
60	18	64.3	28	5	PCT-US95-05812-34	Sequence 34, Appli
61	18	64.3	28	5	PCT-US95-05812-35	Sequence 35, Appli
62	17.4	62.1	34	4	US-09-770-158-22	Sequence 22, Appli
63	17.4	62.1	34	4	US-09-770-158-24	Sequence 24, Appli
64	17.4	62.1	35	4	US-09-770-158-26	Sequence 26, Appli
65	17	60.7	30	4	US-10-029-907-18	Sequence 18, Appli
66	17	60.7	30	4	US-10-029-907-18	Sequence 18, Appli
67	16.4	58.6	33	4	US-09-770-158-23	Sequence 23, Appli
68	16.4	58.6	33	4	US-09-770-158-25	Sequence 25, Appli
69	16	57.1	16	4	US-09-474-432B-34	Sequence 34, Appli
70	16	57.1	16	4	US-09-476-387-34	Sequence 34, Appli
71	15.4	55.0	22	4	US-09-706-649-4	Sequence 4, Appli
72	15	53.6	15	1	US-08-182-968A-13	Sequence 13, Appli
73	15	53.6	15	1	US-08-182-968A-14	Sequence 14, Appli
74	15	53.6	15	2	US-08-774-306A-13	Sequence 13, Appli
75	15	53.6	15	2	US-08-774-306A-14	Sequence 14, Appli
76	15	53.6	15	3	US-09-064-156A-13	Sequence 13, Appli
77	15	53.6	15	3	US-09-064-156A-14	Sequence 14, Appli
78	15	53.6	16	4	US-09-474-432B-18	Sequence 18, Appli
79	15	53.6	16	4	US-09-476-387-18	Sequence 18, Appli
80	15	53.6	18	3	US-09-034-205-24	Sequence 24, Appli
81	15	53.6	18	3	US-08-934-097A-24	Sequence 24, Appli
82	15	53.6	18	3	US-08-851-588-24	Sequence 24, Appli
83	15	53.6	18	3	US-09-677-218B-24	Sequence 24, Appli
84	15	53.6	18	3	US-09-677-192-24	Sequence 24, Appli
85	15	53.6	18	4	US-09-402-618B-24	Sequence 24, Appli
86	15	53.6	18	4	US-09-825-574-24	Sequence 24, Appli
87	15	53.6	18	4	US-09-676-768-24	Sequence 24, Appli
88	15	53.6	19	1	US-09-798-641-37	Sequence 37, Appli
89	15	53.6	19	2	US-08-690-495-37	Sequence 37, Appli
90	15	53.6	19	2	US-08-690-494-37	Sequence 37, Appli
91	15	53.6	19	3	US-09-220-848A-3	Sequence 3, Appli
92	15	53.6	19	4	US-09-702-758A-3	Sequence 3, Appli
93	15	53.6	19	4	US-09-299-217-37	Sequence 37, Appli
94	15	53.6	19	4	US-09-728-265-37	Sequence 37, Appli
95	15	53.6	20	3	US-09-214-471-2	Sequence 2, Appli
96	15	53.6	20	4	US-09-661-364-2	Sequence 2, Appli
97	15	53.6	21	3	US-09-012-573-4	Sequence 4, Appli
98	15	53.6	25	4	US-09-494-332A-2	Sequence 2, Appli
99	15	53.6	25	4	US-09-494-332A-11	Sequence 11, Appli
100	15	53.6	25	4	US-09-493-353-7	Sequence 7, Appli

101	14.6	52.1	30	2	US-08-859-998-151	Sequence 151, Appl	174	12.4	44.3	32	5	PCT-US96-07496-18	Sequence 18, Appl
102	14.6	52.1	30	3	US-09-225-928-151	Sequence 151, Appl	c 175	12.4	44.3	32	5	PCT-US96-07496-19	Sequence 19, Appl
103	14.6	52.1	30	4	US-09-225-201B-151	Sequence 151, Appl	c 176	12.4	44.3	38	4	US-09-371-772B-7206	Sequence 7206, Ap
c 104	14.4	51.4	31	4	US-09-417-197-32	Sequence 32, Appl	c 177	12.4	44.3	38	4	US-09-371-772B-8954	Sequence 8954, Ap
c 105	14	50.0	16	4	US-09-474-432B-19	Sequence 19, Appl	c 178	12.4	44.3	38	4	US-09-371-772B-11675	Sequence 11675, A
c 106	14	50.0	16	4	US-09-476-387-19	Sequence 19, Appl	c 179	12.4	44.3	39	1	US-08-399-696-42	Sequence 42, Appl
107	14	50.0	18	3	US-09-012-573-1	Sequence 1, Appl	180	12.4	44.3	45	3	US-09-199-737-53	Sequence 53, Appl
108	14	50.0	19	3	US-09-165-264-10	Sequence 10, Appl	181	12.4	44.3	45	3	US-09-058-333A-53	Sequence 53, Appl
c 109	14	50.0	30	1	US-08-468-557-24	Sequence 24, Appl	182	12.4	44.3	47	4	US-09-422-978-777	Sequence 777, App
c 110	14	50.0	30	1	US-08-451-715A-63	Sequence 63, Appl	c 183	12.4	44.3	47	4	US-09-422-978-3819	Sequence 3819, Ap
c 111	14	50.0	30	2	US-08-743-130A-35	Sequence 35, Appl	c 184	12.2	43.6	18	2	US-09-157-378-27	Sequence 27, Appl
c 112	14	50.0	30	2	US-08-742-026-15	Sequence 15, Appl	c 185	12.2	43.6	20	4	US-09-676-610B-97	Sequence 97, Appl
c 113	14	50.0	30	2	US-08-415-593-23	Sequence 23, Appl	c 186	12.2	43.6	22	4	US-08-822-445-27	Sequence 27, Appl
c 114	13.6	48.6	21	3	US-08-927-219-33	Sequence 33, Appl	c 187	12.2	43.6	22	3	US-09-396-540-37	Sequence 37, Appl
c 115	13.2	47.1	20	2	US-08-888-982A-40	Sequence 40, Appl	c 188	12.2	43.6	29	2	US-08-450-905B-31	Sequence 31, Appl
c 116	13.2	47.1	20	2	US-08-888-982A-41	Sequence 41, Appl	c 189	12.2	43.6	29	3	US-07-982-759F-31	Sequence 31, Appl
c 117	13.2	47.1	20	3	US-09-462-261-40	Sequence 40, Appl	c 190	12.2	43.6	32	2	US-08-450-905B-30	Sequence 30, Appl
c 118	13.2	47.1	20	3	US-09-462-261-41	Sequence 41, Appl	c 191	12.2	43.6	32	3	US-07-982-759F-30	Sequence 30, Appl
c 119	13.2	47.1	20	4	US-09-506-073-129	Sequence 129, App	c 192	12.2	43.6	36	2	US-08-868-162A-3	Sequence 3, Appl
c 120	13.2	47.1	20	4	US-09-506-073-130	Sequence 130, App	c 193	12.2	43.6	38	1	US-07-598-737C-14	Sequence 14, Appl
121	13.2	47.1	29	2	US-08-799-825-1	Sequence 1, Appl	194	12.2	43.6	38	1	US-08-084-718-27	Sequence 27, Appl
122	13.2	47.1	29	3	US-09-280-068-1	Sequence 1, Appl	195	12.2	43.6	38	1	US-08-443-976-27	Sequence 27, Appl
123	13.2	47.1	30	2	US-08-716-284-15	Sequence 15, Appl	c 196	12.2	43.6	38	1	US-08-443-977-27	Sequence 27, Appl
c 124	13.2	47.1	30	4	US-09-929-922-29	Sequence 29, Appl	c 197	12.2	43.6	38	1	US-08-373-124A-635	Sequence 635, App
c 125	13.2	47.1	43	2	US-08-850-049-107	Sequence 107, App	c 198	12.2	43.6	38	1	US-08-435-628-635	Sequence 635, App
126	13.2	47.1	43	2	US-08-050-478-107	Sequence 107, App	c 199	12.2	43.6	39	1	US-07-846-181-7	Sequence 7, Appl
127	13.2	47.1	43	3	US-09-414-117-107	Sequence 107, App	c 200	12.2	43.6	39	1	US-07-846-181-8	Sequence 8, Appl
128	13.2	47.1	43	4	US-09-678-437-107	Sequence 107, App	c 201	12.2	43.6	39	1	US-07-845-989-7	Sequence 7, Appl
129	13.2	47.1	43	4	US-09-943-722-107	Sequence 107, App	c 202	12.2	43.6	39	1	US-07-845-989-8	Sequence 8, Appl
c 130	13	46.4	19	3	US-08-745-310-4	Sequence 4, Appl	c 203	12.2	43.6	39	1	US-07-598-737C-13	Sequence 13, Appl
c 131	13	46.4	24	1	US-08-484-557C-16	Sequence 16, Appl	c 204	12.2	43.6	39	1	US-08-084-718-26	Sequence 26, Appl
c 132	13	46.4	24	1	US-08-487-426B-16	Sequence 16, Appl	c 205	12.2	43.6	39	1	US-08-443-976-26	Sequence 26, Appl
c 133	13	46.4	24	2	US-08-487-720A-16	Sequence 16, Appl	c 206	12.2	43.6	39	1	US-08-443-977-26	Sequence 26, Appl
c 134	13	46.4	38	4	US-09-371-772B-9976	Sequence 9976, Ap	c 207	12.2	43.6	41	3	US-08-813-507-109	Sequence 109, App
c 135	13	46.4	38	4	US-09-371-772B-11318	Sequence 11318, A	c 208	12.2	43.6	41	3	US-09-351-814-42	Sequence 42, Appl
c 136	13	46.4	45	2	US-08-882-756-2	Sequence 2, Appl	c 209	12.2	43.6	41	3	US-09-464-453-109	Sequence 109, App
c 137	13	46.4	45	2	US-08-882-756-1	Sequence 1, Appl	c 210	12.2	43.6	42	2	US-08-716-284-3	Sequence 3, Appl
c 138	13	46.4	45	2	US-08-882-756-5	Sequence 5, Appl	c 211	12	42.9	20	1	US-07-752-101A-31	Sequence 31, Appl
c 139	13	46.4	45	3	US-09-301-153-1	Sequence 1, Appl	c 212	12	42.9	20	1	US-07-752-101A-49	Sequence 49, Appl
c 140	13	46.4	45	3	US-09-301-153-2	Sequence 2, Appl	c 213	12	42.9	20	2	US-08-117-952-168	Sequence 168, App
c 141	12.8	45.7	18	4	US-09-614-748A-31	Sequence 31, Appl	c 214	12	42.9	20	3	US-09-418-641-67	Sequence 67, Appl
c 142	12.8	45.7	26	4	US-09-127-578-15	Sequence 15, Appl	c 215	12	42.9	25	4	US-08-647-563-30	Sequence 30, Appl
c 143	12.8	45.7	26	4	US-09-127-578-17	Sequence 17, Appl	c 216	12	42.9	27	3	US-08-513-974B-165	Sequence 165, App
c 144	12.8	45.7	31	4	US-09-648-667-2	Sequence 2, Appl	c 217	12	42.9	29	4	US-09-807-784B-13	Sequence 13, Appl
c 145	12.8	45.7	31	4	US-09-648-667-8	Sequence 8, Appl	c 218	12	42.9	30	3	US-09-338-907-170	Sequence 170, App
c 146	12.8	45.7	44	3	US-08-617-454-11	Sequence 11, Appl	c 219	12	42.9	30	3	US-09-218-207-170	Sequence 170, App
c 147	12.8	45.7	47	4	US-09-422-978-2844	Sequence 2844, Ap	c 220	12	42.9	30	4	US-09-170-496D-161	Sequence 161, App
c 148	12.8	45.7	50	4	US-09-613-263-12	Sequence 12, Appl	c 221	12	42.9	33	2	US-08-752-844-60	Sequence 60, Appl
c 149	12.8	45.7	50	4	US-09-613-263-13	Sequence 13, Appl	c 222	12	42.9	33	4	US-09-293-533-60	Sequence 60, Appl
c 150	12.6	45.0	24	4	US-08-952-899-10	Sequence 10, Appl	c 223	12	42.9	36	1	US-08-639-256-10	Sequence 10, Appl
c 151	12.6	45.0	25	4	US-09-615-095-1	Sequence 1, Appl	c 224	12	42.9	37	3	US-09-311-626B-53	Sequence 53, Appl
c 152	12.6	45.0	30	4	US-09-929-922-30	Sequence 30, Appl	c 225	12	42.9	45	3	US-08-894-727-7	Sequence 7, Appl
c 153	12.6	45.0	31	3	US-08-351-923-19	Sequence 19, Appl	c 226	12	42.9	46	4	US-09-552-322-23	Sequence 23, Appl
c 154	12.6	45.0	35	4	US-09-736-116-56	Sequence 56, Appl	c 227	12	42.9	46	4	US-10-150-048-5	Sequence 5, Appl
c 155	12.6	45.0	36	2	US-08-829-876-60	Sequence 60, Appl	c 228	12	42.9	46	4	US-09-422-978-281	Sequence 281, App
c 156	12.6	45.0	36	3	US-09-234-874A-60	Sequence 60, Appl	c 229	12	42.9	47	4	US-09-280-181B-2	Sequence 2, Appl
c 157	12.6	45.0	36	4	US-09-234-873A-60	Sequence 60, Appl	c 230	11.8	42.1	20	3	US-09-657-472-1069	Sequence 1069, Ap
c 158	12.6	45.0	38	4	US-09-371-772B-7868	Sequence 7868, Ap	c 231	11.8	42.1	21	4	US-09-989-002-3	Sequence 3, Appl
c 159	12.6	45.0	38	4	US-09-371-772B-10726	Sequence 10726, A	c 232	11.8	42.1	22	4	US-09-989-002-26	Sequence 26, Appl
c 160	12.6	45.0	41	2	US-08-386-198A-8	Sequence 8, Appl	c 233	11.8	42.1	25	4	US-09-579-692B-56	Sequence 56, Appl
c 161	12.6	45.0	42	3	US-08-679-645-7	Sequence 7, Appl	c 234	11.8	42.1	26	4	US-09-641-259B-35	Sequence 35, Appl
c 162	12.4	44.3	18	1	US-08-487-135B-15	Sequence 15, Appl	c 235	11.8	42.1	27	2	US-08-442-010-2	Sequence 2, Appl
c 163	12.4	44.3	18	2	US-08-443-342A-19	Sequence 19, Appl	c 236	11.8	42.1	28	1	US-08-123-761A-3	Sequence 3, Appl
c 164	12.4	44.3	18	2	US-08-915-972B-15	Sequence 15, Appl	c 237	11.8	42.1	28	3	US-09-006-636-19	Sequence 19, Appl
c 165	12.4	44.3	18	2	US-09-177-909-15	Sequence 15, Appl	c 238	11.8	42.1	28	3	US-09-006-632-19	Sequence 19, Appl
c 166	12.4	44.3	24	1	US-08-487-135B-4	Sequence 4, Appl	c 239	11.8	42.1	30	1	US-09-325-274-19	Sequence 19, Appl
c 167	12.4	44.3	24	2	US-08-915-972A-4	Sequence 4, Appl	c 240	11.8	42.1	30	1	US-08-219-012-31	Sequence 31, Appl
c 168	12.4	44.3	24	2	US-09-177-909-4	Sequence 4, Appl	c 241	11.8	42.1	30	3	US-08-687-421-219	Sequence 219, App
c 169	12.4	44.3	30	3	US-09-423-744A-8	Sequence 8, Appl	c 242	11.8	42.1	30	4	US-09-270-957-52	Sequence 52, Appl
c 170	12.4	44.3	32	2	US-08-454-028-18	Sequence 18, Appl	c 243	11.8	42.1	31	3	US-08-679-645-355	Sequence 355, App
c 171	12.4	44.3	32	5	US-08-454-028-19	Sequence 19, Appl	c 244	11.8	42.1	32	2	US-08-811-492-54	Sequence 54, Appl
c 172	12.4	44.3	32	5	PCT-US94-05388-18	Sequence 18, Appl	c 245	11.8	42.1	32	2	US-08-859-998-1208	Sequence 1208, Ap
c 173	12.4	44.3	32	5	PCT-US94-05388-19	Sequence 19, Appl	c 246	11.8	42.1	32	2		

c 247	11.8	42.1	32	3	US-09-225-928-1208	Sequence 1208, Ap	c 320	11.6	41.4	39	2	US-08-752-844-50	Sequence 50, Appl
c 248	11.8	42.1	32	4	US-09-225-201B-1208	Sequence 1208, Ap	c 321	11.6	41.4	39	2	US-08-591-196-50	Sequence 50, Appl
c 249	11.8	42.1	32	5	PCT-US96-10545A-54	Sequence 54, Appl	c 322	11.6	41.4	39	3	US-09-140-804-47	Sequence 47, Appl
c 250	11.8	42.1	33	2	US-08-868-162A-15	Sequence 15, Appl	c 323	11.6	41.4	39	3	US-09-173-043-23	Sequence 23, Appl
c 251	11.8	42.1	33	2	PCT-US96-06224-4	Sequence 4, Appl	c 324	11.6	41.4	39	3	US-08-973-124-177	Sequence 177, Appl
c 252	11.8	42.1	36	1	US-08-455-860-5	Sequence 5, Appl	c 325	11.6	41.4	39	3	US-08-931-743C-88	Sequence 88, Appl
c 253	11.8	42.1	36	1	US-08-383-749-5	Sequence 5, Appl	c 326	11.6	41.4	39	3	US-09-209-525-41	Sequence 41, Appl
c 254	11.8	42.1	36	2	US-08-780-370A-6	Sequence 6, Appl	c 327	11.6	41.4	39	3	US-08-976-288A-7	Sequence 7, Appl
c 255	11.8	42.1	36	4	US-09-251-330-6	Sequence 6, Appl	c 328	11.6	41.4	39	4	US-09-569-572C-7	Sequence 7, Appl
c 256	11.8	42.1	39	3	US-09-011-540-9	Sequence 9, Appl	c 329	11.6	41.4	39	4	US-09-686-838B-47	Sequence 47, Appl
c 257	11.8	42.1	39	4	US-09-989-002-37	Sequence 37, Appl	c 330	11.6	41.4	39	4	US-09-293-533-50	Sequence 50, Appl
c 258	11.8	42.1	42	4	US-09-119-507B-87	Sequence 87, Appl	c 331	11.6	41.4	39	4	US-09-851-486-88	Sequence 88, Appl
c 259	11.8	42.1	42	4	US-08-897-556A-87	Sequence 87, Appl	c 332	11.6	41.4	39	5	PCT-US96-08014-177	Sequence 177, Appl
c 260	11.8	42.1	42	4	US-09-547-693-87	Sequence 87, Appl	c 333	11.6	41.4	40	1	US-07-977-696C-14	Sequence 14, Appl
c 261	11.8	42.1	45	4	US-09-291-874-11	Sequence 11, Appl	c 334	11.6	41.4	40	1	US-08-137-117D-1	Sequence 1, Appl
c 262	11.8	42.1	45	4	US-09-344-783C-28	Sequence 28, Appl	c 335	11.6	41.4	40	1	US-08-129-930B-14	Sequence 14, Appl
c 263	11.8	42.1	45	4	US-09-422-978B-1138	Sequence 1138, Ap	c 336	11.6	41.4	40	1	US-08-436-717-1	Sequence 1, Appl
c 264	11.8	42.1	47	4	US-09-422-978-2425	Sequence 2425, Ap	c 337	11.6	41.4	40	2	US-08-553-501A-1	Sequence 1, Appl
c 265	11.8	42.1	47	4	US-09-422-978-3338	Sequence 3338, Ap	c 338	11.6	41.4	40	2	US-08-765-783A-1	Sequence 1, Appl
c 266	11.8	42.1	47	4	US-09-422-978-3776	Sequence 3776, Ap	c 339	11.6	41.4	40	3	US-08-434-465-9	Sequence 9, Appl
c 267	11.8	42.1	49	4	US-09-388-089B-3	Sequence 3, Appl	c 340	11.6	41.4	40	3	US-08-434-465-13	Sequence 13, Appl
c 268	11.8	42.1	50	3	US-09-298-886-22	Sequence 22, Appl	c 341	11.6	41.4	40	3	US-08-921-100-1	Sequence 1, Appl
c 269	11.8	42.1	50	4	US-09-999-672-22	Sequence 22, Appl	c 342	11.6	41.4	40	3	US-08-880-142-1	Sequence 1, Appl
c 270	11.8	42.1	50	4	US-09-513-989C-15492	Sequence 15492, A	c 343	11.6	41.4	40	3	US-08-902-201-1	Sequence 1, Appl
c 271	11.6	41.4	20	2	US-08-985-090-25	Sequence 25, Appl	c 344	11.6	41.4	40	3	US-09-205-231-1	Sequence 1, Appl
c 272	11.6	41.4	20	2	US-08-888-982A-22	Sequence 22, Appl	c 345	11.6	41.4	40	3	US-08-646-265A-1	Sequence 1, Appl
c 273	11.6	41.4	20	3	US-09-165-543-27	Sequence 27, Appl	c 346	11.6	41.4	40	3	US-09-091-814-19	Sequence 19, Appl
c 274	11.6	41.4	20	3	US-09-462-261-22	Sequence 22, Appl	c 347	11.6	41.4	40	3	US-09-091-814-82	Sequence 82, Appl
c 275	11.6	41.4	20	4	US-09-506-073-111	Sequence 111, App	c 348	11.6	41.4	40	3	US-09-416-557-1	Sequence 1, Appl
c 276	11.6	41.4	20	4	US-09-668-313A-142	Sequence 142, App	c 349	11.6	41.4	40	3	US-08-134-346A-1	Sequence 1, Appl
c 277	11.6	41.4	20	4	US-09-422-978-5198	Sequence 5198, Ap	c 350	11.6	41.4	40	3	US-08-976-288A-14	Sequence 14, Appl
c 278	11.6	41.4	24	4	US-09-854-140-1	Sequence 1, Appl	c 351	11.6	41.4	40	4	US-09-569-572C-5	Sequence 5, Appl
c 279	11.6	41.4	24	4	US-09-445-174B-18	Sequence 18, Appl	c 352	11.6	41.4	40	4	US-09-569-572C-8	Sequence 8, Appl
c 280	11.6	41.4	25	3	US-07-705-490-9	Sequence 9, Appl	c 353	11.6	41.4	40	4	US-09-569-572C-12	Sequence 12, Appl
c 281	11.6	41.4	25	3	US-09-075-272-7	Sequence 7, Appl	c 354	11.6	41.4	40	4	US-09-269-921-29	Sequence 29, Appl
c 282	11.6	41.4	25	3	US-07-751-891B-9	Sequence 9, Appl	c 355	11.6	41.4	40	6	5256558-14	Parent No. 5256558
c 283	11.6	41.4	27	3	US-09-253-396A-62	Sequence 62, Appl	c 356	11.6	41.4	41	1	US-08-330-638D-10	Sequence 10, Appl
c 284	11.6	41.4	27	3	US-08-584-040-564	Sequence 564, App	c 357	11.6	41.4	41	2	US-08-906-746A-10	Sequence 10, Appl
c 285	11.6	41.4	28	2	US-08-418-848A-55	Sequence 55, Appl	c 358	11.6	41.4	41	3	US-08-434-465-7	Sequence 7, Appl
c 286	11.6	41.4	28	3	US-09-183-412-40	Sequence 40, Appl	c 359	11.6	41.4	41	3	US-08-434-465-12	Sequence 12, Appl
c 287	11.6	41.4	28	4	US-09-920-759-5	Sequence 5, Appl	c 360	11.6	41.4	41	3	US-08-434-465-15	Sequence 15, Appl
c 288	11.6	41.4	28	4	US-09-769-864-40	Sequence 40, Appl	c 361	11.6	41.4	41	4	US-09-586-216C-2	Sequence 2, Appl
c 289	11.6	41.4	30	3	US-09-550-338-9	Sequence 9, Appl	c 362	11.6	41.4	42	2	US-08-124-961A-8	Sequence 8, Appl
c 290	11.6	41.4	30	3	US-09-767-878-9	Sequence 9, Appl	c 363	11.6	41.4	42	3	US-08-434-465-5	Sequence 5, Appl
c 291	11.6	41.4	32	2	US-08-618-911-7	Sequence 7, Appl	c 364	11.6	41.4	42	3	US-08-434-465-8	Sequence 8, Appl
c 292	11.6	41.4	32	4	US-09-595-344-14	Sequence 14, Appl	c 365	11.6	41.4	42	3	US-08-589-939-13	Sequence 13, Appl
c 293	11.6	41.4	33	1	US-08-417-476-14	Sequence 14, Appl	c 366	11.6	41.4	42	3	US-09-037-190-6	Sequence 6, Appl
c 294	11.6	41.4	33	3	US-08-427-569-52	Sequence 52, Appl	c 367	11.6	41.4	42	3	US-09-037-192-6	Sequence 6, Appl
c 295	11.6	41.4	33	6	5316943-2	Patent No. 5316943	c 368	11.6	41.4	42	3	US-09-037-192-6	Sequence 6, Appl
c 296	11.6	41.4	36	2	US-08-418-085-16	Sequence 16, Appl	c 369	11.6	41.4	42	3	US-09-049-691-6	Sequence 6, Appl
c 297	11.6	41.4	36	3	US-08-434-465-3	Sequence 3, Appl	c 370	11.6	41.4	42	3	US-08-174-6	Sequence 6, Appl
c 298	11.6	41.4	36	3	US-09-099-011A-16	Sequence 16, Appl	c 371	11.6	41.4	42	3	US-08-260-174-6	Sequence 6, Appl
c 299	11.6	41.4	36	4	US-09-569-572C-3	Sequence 3, Appl	c 372	11.6	41.4	42	3	US-09-338-128A-6	Sequence 6, Appl
c 300	11.6	41.4	36	4	US-07-955-726A-40	Sequence 40, Appl	c 373	11.6	41.4	42	3	US-09-232-346-6	Sequence 6, Appl
c 301	11.6	41.4	36	4	US-09-569-572C-9	Sequence 9, Appl	c 374	11.6	41.4	43	2	US-09-037-192-6	Sequence 6, Appl
c 302	11.6	41.4	37	2	US-08-455-968E-38	Sequence 38, Appl	c 375	11.6	41.4	43	2	US-08-418-897-8	Sequence 8, Appl
c 303	11.6	41.4	38	1	US-08-219-012-91	Sequence 91, Appl	c 376	11.6	41.4	43	2	US-08-418-897-28	Sequence 28, Appl
c 304	11.6	41.4	38	1	US-08-376-329-2	Sequence 2, Appl	c 377	11.6	41.4	43	2	US-08-418-897-32	Sequence 32, Appl
c 305	11.6	41.4	38	1	US-08-276-271-2	Sequence 2, Appl	c 378	11.6	41.4	44	2	US-07-624-299-7	Sequence 7, Appl
c 306	11.6	41.4	38	3	US-08-434-465-6	Sequence 6, Appl	c 379	11.6	41.4	44	2	US-08-951-822-17	Sequence 17, Appl
c 307	11.6	41.4	38	3	US-08-687-421-279	Sequence 279, App	c 380	11.6	41.4	44	3	US-08-793-418-15	Sequence 15, Appl
c 308	11.6	41.4	38	4	US-09-569-572C-6	Sequence 6, Appl	c 381	11.6	41.4	44	3	US-09-173-043-33	Sequence 33, Appl
c 309	11.6	41.4	38	4	US-09-569-572C-9	Sequence 9, Appl	c 382	11.6	41.4	44	3	US-09-368-951-17	Sequence 17, Appl
c 310	11.6	41.4	38	4	US-09-569-572C-13	Sequence 13, Appl	c 383	11.6	41.4	44	4	US-09-229-947-17	Sequence 17, Appl
c 311	11.6	41.4	38	4	US-09-569-572C-15	Sequence 15, Appl	c 384	11.6	41.4	45	2	US-08-039-198B-3	Sequence 3, Appl
c 312	11.6	41.4	38	4	US-09-569-572C-18	Sequence 18, Appl	c 385	11.6	41.4	45	2	US-08-455-695B-22	Sequence 22, Appl
c 313	11.6	41.4	38	5	PCT-US95-09237-2	Sequence 2, Appl	c 386	11.6	41.4	45	3	US-09-091-814-16	Sequence 16, Appl
c 314	11.6	41.4	39	1	US-08-527-734-8	Sequence 8, Appl	c 387	11.6	41.4	45	3	US-09-091-814-104	Sequence 104, App
c 315	11.6	41.4	39	1	US-08-479-783A-90	Sequence 90, Appl	c 388	11.6	41.4	45	5	PCT-US94-14436-22	Sequence 22, Appl
c 316	11.6	41.4	39	1	US-08-479-725-90	Sequence 90, Appl	c 389	11.6	41.4	47	3	US-08-589-939-59	Sequence 59, Appl
c 317	11.6	41.4	39	1	US-08-618-693-88	Sequence 88, Appl	c 390	11.6	41.4	47	4	US-09-422-978-1811	Sequence 1811, Ap
c 318	11.6	41.4	39	1	US-07-977-696C-7	Sequence 7, Appl	c 391	11.6	41.4	47	4	US-09-422-978-2253	Sequence 2253, Ap
c 319	11.6	41.4	39	1	US-08-129-930B-7	Sequence 7, Appl	c 392	11.6	41.4	48	1	US-08-040-548-12	Sequence 12, Appl

393	11.6	41.4	48	1	US-08-466-344-12	Sequence 12, Appl	C 466	11.4	40.7	38	4	US-09-371-772B-8869	Sequence 8869, Ap
C 394	11.6	41.4	48	3	US-09-091-814-12	Sequence 12, Appl	C 467	11.4	40.7	38	4	US-09-371-772B-9046	Sequence 9046, Ap
395	11.6	41.4	48	4	US-09-119-507B-92	Sequence 92, Appl	C 468	11.4	40.7	38	4	US-09-371-772B-9198	Sequence 9198, Ap
396	11.6	41.4	48	4	US-08-897-556A-92	Sequence 92, Appl	C 469	11.4	40.7	38	4	US-09-371-772B-9287	Sequence 9287, Ap
397	11.6	41.4	48	4	US-09-547-693-92	Sequence 92, Appl	C 470	11.4	40.7	38	4	US-09-371-772B-9540	Sequence 9540, Ap
398	11.6	41.4	48	4	US-09-091-814-58	Sequence 58, Appl	C 471	11.4	40.7	38	4	US-09-371-772B-9847	Sequence 9847, Ap
399	11.6	41.4	49	3	US-08-687-580B-20	Sequence 20, Appl	C 472	11.4	40.7	38	4	US-09-371-772B-9907	Sequence 9907, Ap
C 400	11.6	41.4	50	1	US-08-146-422-19	Sequence 19, Appl	C 473	11.4	40.7	38	4	US-09-371-772B-10741	Sequence 10741, A
C 401	11.6	41.4	50	1	US-08-146-424-21	Sequence 21, Appl	C 474	11.4	40.7	38	4	US-09-371-772B-11014	Sequence 11014, A
C 402	11.6	41.4	50	1	US-08-047-413-16	Sequence 16, Appl	C 475	11.4	40.7	38	4	US-09-371-772B-11269	Sequence 11269, A
C 403	11.6	41.4	50	1	US-08-047-413-17	Sequence 17, Appl	C 476	11.4	40.7	38	4	US-09-371-772B-11645	Sequence 11645, A
C 404	11.6	41.4	50	1	US-08-626-554-1	Sequence 1, Appl	C 477	11.4	40.7	38	4	US-09-371-772B-11841	Sequence 11841, A
C 405	11.6	41.4	50	1	US-08-693-709-3	Sequence 3, Appl	C 478	11.4	40.7	38	4	US-09-371-772B-11930	Sequence 11930, A
C 406	11.6	41.4	50	2	US-08-253-877C-42	Sequence 42, Appl	C 479	11.4	40.7	38	4	US-09-371-772B-12015	Sequence 12015, A
C 407	11.6	41.4	50	2	US-08-452-164A-42	Sequence 42, Appl	C 480	11.4	40.7	38	4	US-09-371-772B-12913	Sequence 12913, A
C 408	11.6	41.4	50	3	US-08-229-050-16	Sequence 16, Appl	C 481	11.4	40.7	38	4	US-09-371-772B-13902	Sequence 13902, A
C 409	11.6	41.4	50	3	US-08-801-563-17	Sequence 17, Appl	C 482	11.4	40.7	39	1	US-07-834-539A-47	Sequence 47, Appl
C 410	11.6	41.4	50	3	US-08-801-563-16	Sequence 16, Appl	C 483	11.4	40.7	39	1	US-08-053-131-59	Sequence 59, Appl
C 411	11.6	41.4	50	3	US-08-801-563-17	Sequence 17, Appl	C 484	11.4	40.7	39	1	US-08-645-641-59	Sequence 59, Appl
C 412	11.6	41.4	50	3	US-08-569-147-23	Sequence 23, Appl	C 485	11.4	40.7	39	1	US-07-853-408B-59	Sequence 59, Appl
C 413	11.6	41.4	50	3	US-08-976-183A-18	Sequence 18, Appl	C 486	11.4	40.7	39	1	US-08-096-762-59	Sequence 59, Appl
C 414	11.6	41.4	50	4	US-09-270-767-26445	Sequence 26445, A	C 487	11.4	40.7	39	2	US-08-800-353-47	Sequence 47, Appl
C 415	11.6	41.4	15	4	US-09-935-194-15	Sequence 15, Appl	C 488	11.4	40.7	39	2	US-08-308-855-59	Sequence 59, Appl
C 416	11.4	40.7	21	4	US-09-409-096-13	Sequence 13, Appl	C 489	11.4	40.7	39	2	US-08-807-332B-24	Sequence 24, Appl
C 417	11.4	40.7	25	4	US-09-206-942-75	Sequence 75, Appl	C 490	11.4	40.7	39	2	US-08-807-332B-25	Sequence 25, Appl
C 418	11.4	40.7	25	4	US-09-437-568A-31	Sequence 31, Appl	C 491	11.4	40.7	39	3	US-09-338-876-24	Sequence 24, Appl
C 419	11.4	40.7	25	4	US-09-980-777-21	Sequence 21, Appl	C 492	11.4	40.7	39	3	US-09-338-876-25	Sequence 25, Appl
C 420	11.4	40.7	26	3	US-09-814-134A-10	Sequence 10, Appl	C 493	11.4	40.7	39	3	US-09-042-353-222	Sequence 222, App
C 421	11.4	40.7	26	4	US-09-789-556A-17	Sequence 17, Appl	C 494	11.4	40.7	39	3	US-08-758-417A-70	Sequence 70, Appl
C 422	11.4	40.7	27	2	US-08-330-394A-24	Sequence 24, Appl	C 495	11.4	40.7	39	5	PCT-US92-06185-47	Sequence 47, Appl
C 423	11.4	40.7	27	2	US-08-330-394A-31	Sequence 31, Appl	C 496	11.4	40.7	39	5	PCT-US92-10983-59	Sequence 59, Appl
C 424	11.4	40.7	27	3	US-08-985-162-1123	Sequence 1123, Ap	C 497	11.4	40.7	41	3	US-08-813-507-69	Sequence 69, Appl
C 425	11.4	40.7	27	3	US-08-584-040-88	Sequence 88, Appl	C 498	11.4	40.7	41	3	US-09-464-453-69	Sequence 69, Appl
C 426	11.4	40.7	27	3	US-08-584-040-88	Sequence 88, Appl	C 499	11.4	40.7	41	3	US-08-962-281-34	Sequence 34, Appl
C 427	11.4	40.7	27	4	US-09-401-063-1123	Sequence 1123, Ap	C 500	11.4	40.7	44	3	US-09-367-890-2	Sequence 2, Appl
C 428	11.4	40.7	28	4	US-09-878-756-7	Sequence 7, Appl	C 501	11.4	40.7	44	3	US-08-157-185-8	Sequence 8, Appl
C 429	11.4	40.7	29	4	US-09-599-220-2	Sequence 2, Appl	C 502	11.4	40.7	45	2	US-08-281-526B-8	Sequence 8, Appl
C 430	11.4	40.7	30	4	US-08-388-857B-5	Sequence 5, Appl	C 503	11.4	40.7	45	3	US-09-450-797-8	Sequence 8, Appl
C 431	11.4	40.7	32	1	US-08-591-070A-31	Sequence 31, Appl	C 504	11.4	40.7	45	3	US-09-450-790A-8	Sequence 8, Appl
C 432	11.4	40.7	32	2	US-08-927-855-31	Sequence 31, Appl	C 505	11.4	40.7	45	4	US-09-332-837-8	Sequence 8, Appl
C 433	11.4	40.7	33	1	US-08-068-945A-46	Sequence 46, Appl	C 506	11.4	40.7	45	4	US-09-592-480-14	Sequence 14, Appl
C 434	11.4	40.7	33	2	US-08-442-806-46	Sequence 46, Appl	C 507	11.4	40.7	46	3	US-09-453-702B-221	Sequence 221, App
C 435	11.4	40.7	33	2	US-08-394-177-9	Sequence 9, Appl	C 508	11.4	40.7	47	3	US-09-338-907-188	Sequence 188, App
C 436	11.4	40.7	33	3	US-09-333-636-9	Sequence 9, Appl	C 509	11.4	40.7	47	3	US-09-338-907-265	Sequence 265, App
C 437	11.4	40.7	34	3	US-09-079-812E-27	Sequence 27, Appl	C 510	11.4	40.7	47	3	US-09-218-207-188	Sequence 188, App
C 438	11.4	40.7	35	3	US-08-433-263B-7	Sequence 7, Appl	C 511	11.4	40.7	47	3	US-09-218-207-265	Sequence 265, App
C 439	11.4	40.7	36	1	US-07-834-539A-10	Sequence 10, Appl	C 512	11.4	40.7	47	4	US-09-641-638-750	Sequence 750, App
C 440	11.4	40.7	36	1	US-08-053-131-18	Sequence 18, Appl	C 513	11.4	40.7	47	4	US-09-641-638-750	Sequence 1090, Ap
C 441	11.4	40.7	36	1	US-08-334-847-183	Sequence 183, App	C 514	11.4	40.7	47	4	US-09-641-638-1206	Sequence 1206, Ap
C 442	11.4	40.7	36	1	US-08-334-847-185	Sequence 185, App	C 515	11.4	40.7	47	4	US-09-422-978-2836	Sequence 2836, Ap
C 443	11.4	40.7	36	1	US-08-645-641-18	Sequence 18, Appl	C 516	11.4	40.7	47	4	US-09-422-978-2836	Sequence 750, App
C 444	11.4	40.7	36	1	US-07-853-408B-18	Sequence 18, Appl	C 517	11.4	40.7	47	4	US-10-170-097-1090	Sequence 1090, Ap
C 445	11.4	40.7	36	1	US-08-311-486C-803	Sequence 803, Appl	C 518	11.4	40.7	47	4	US-10-170-097-1206	Sequence 1206, Ap
C 446	11.4	40.7	36	1	US-08-096-762-18	Sequence 18, Appl	C 519	11.4	40.7	49	2	US-08-299-074A-13	Sequence 13, Appl
C 447	11.4	40.7	36	2	US-08-800-353-10	Sequence 10, Appl	C 520	11.4	40.7	49	3	US-09-398-773-13	Sequence 13, Appl
C 448	11.4	40.7	36	2	US-08-585-684B-1568	Sequence 1568, Ap	C 521	11.4	40.7	50	3	US-08-848-567A-61	Sequence 61, Appl
C 449	11.4	40.7	36	2	US-08-585-684B-2450	Sequence 2450, Ap	C 522	11.2	40.0	18	2	US-08-585-684B-2636	Sequence 2636, Ap
C 450	11.4	40.7	36	2	US-08-308-865-18	Sequence 18, Appl	C 523	11.2	40.0	18	3	US-09-161-443-44	Sequence 44, Appl
C 451	11.4	40.7	36	3	US-09-038-073-1568	Sequence 1568, Ap	C 524	11.2	40.0	18	3	US-09-339-964-15	Sequence 15, Appl
C 452	11.4	40.7	36	3	US-09-038-073-2450	Sequence 2450, Ap	C 525	11.2	40.0	18	3	US-09-038-073-2636	Sequence 32, Appl
C 453	11.4	40.7	36	3	US-09-042-353-186	Sequence 186, App	C 526	11.2	40.0	18	4	US-09-614-748A-32	Sequence 32, Appl
C 454	11.4	40.7	36	3	US-08-758-417A-34	Sequence 34, Appl	C 527	11.2	40.0	19	3	US-09-050-791-3380	Sequence 3380, Ap
C 455	11.4	40.7	36	5	PCT-US92-06185-10	Sequence 10, Appl	C 528	11.2	40.0	19	4	US-09-696-791-28	Sequence 54, Appl
C 456	11.4	40.7	36	5	PCT-US92-10983-17	Sequence 18, Appl	C 529	11.2	40.0	19	4	US-10-071-411A-54	Sequence 54, Appl
C 457	11.4	40.7	38	1	US-08-435-350-117	Sequence 117, App	C 530	11.2	40.0	20	3	US-09-338-907-90	Sequence 90, Appl
C 458	11.4	40.7	38	1	US-08-373-124A-259	Sequence 259, App	C 531	11.2	40.0	20	3	US-09-428-583-45	Sequence 45, Appl
C 459	11.4	40.7	38	1	US-08-373-124A-2292	Sequence 2292, Ap	C 532	11.2	40.0	20	3	US-09-218-207-90	Sequence 90, Appl
C 460	11.4	40.7	38	1	US-08-373-124A-2976	Sequence 2476, Ap	C 533	11.2	40.0	20	3	US-09-659-791A-41	Sequence 41, Appl
C 461	11.4	40.7	38	1	US-08-435-628-259	Sequence 259, App	C 534	11.2	40.0	20	3	US-09-198-452A-1493	Sequence 42, Appl
C 462	11.4	40.7	38	1	US-08-435-628-2292	Sequence 2292, Ap	C 535	11.2	40.0	20	4	US-09-198-452A-1493	Sequence 1493, Ap
C 463	11.4	40.7	38	1	US-08-435-628-2476	Sequence 2476, Ap	C 536	11.2	40.0	20	4	US-09-068-821-8	Sequence 8, Appl
C 464	11.4	40.7	38	4	US-09-371-772B-7682	Sequence 7682, Ap	C 537	11.2	40.0	20	4	US-08-793-107-3	Sequence 3, Appl
C 465	11.4	40.7	38	4	US-09-371-772B-7733	Sequence 7733, Ap	C 538	11.2	40.0	21	2		

c 539	11.2	40.0	21	3	US-08-793-110-3	Sequence 3, Appli	612	11.2	40.0	44	1	US-07-931-473B-232	Sequence 232, App
540	11.2	40.0	23	1	US-08-227-689-4	Sequence 4, Appli	613	11.2	40.0	44	1	US-07-714-131C-232	Sequence 232, App
541	11.2	40.0	23	3	US-09-368-169-4	Sequence 4, Appli	614	11.2	40.0	44	1	US-08-412-110-232	Sequence 232, App
542	11.2	40.0	24	3	US-08-995-369-11	Sequence 11, Appl	615	11.2	40.0	44	1	US-08-409-442A-232	Sequence 232, App
543	11.2	40.0	24	5	PCT-US95-10075-11	Sequence 11, Appl	616	11.2	40.0	44	2	US-08-469-609A-232	Sequence 232, App
c 544	11.2	40.0	25	4	US-09-289-180-7	Sequence 7, Appli	617	11.2	40.0	44	3	US-08-143-190-232	Sequence 232, App
545	11.2	40.0	26	1	US-08-608-881A-5	Sequence 5, Appli	618	11.2	40.0	44	3	US-09-502-344-232	Sequence 232, App
c 546	11.2	40.0	26	1	US-08-608-881A-6	Sequence 6, Appli	c 619	11.2	40.0	47	4	US-09-641-638-232	Sequence 232, App
c 547	11.2	40.0	26	2	US-08-089-974B-24	Sequence 24, Appl	c 620	11.2	40.0	47	4	US-08-641-638-1197	Sequence 1197, Ap
548	11.2	40.0	26	3	US-08-804-439A-98	Sequence 98, Appl	621	11.2	40.0	47	4	US-08-585-593A-7	Sequence 7, Appli
549	11.2	40.0	26	3	US-08-720-229-98	Sequence 98, Appl	622	11.2	40.0	47	4	US-09-422-978-1779	Sequence 1779, Ap
c 550	11.2	40.0	26	4	US-09-390-134B-6	Sequence 6, Appli	623	11.2	40.0	47	4	US-09-422-978-2165	Sequence 2165, Ap
551	11.2	40.0	26	4	US-09-727-758-2	Sequence 2, Appli	c 624	11.2	40.0	47	4	US-09-422-978-3007	Sequence 3007, Ap
552	11.2	40.0	27	3	US-09-253-396A-55	Sequence 55, Appl	c 625	11.2	40.0	47	4	US-09-422-978-3508	Sequence 3508, Ap
553	11.2	40.0	28	2	US-08-995-998-622	Sequence 622, App	c 626	11.2	40.0	47	4	US-10-170-097-933	Sequence 933, App
554	11.2	40.0	28	3	US-09-225-928-622	Sequence 622, App	c 627	11.2	40.0	47	4	US-10-170-097-933	Sequence 933, App
555	11.2	40.0	28	4	US-09-225-201B-622	Sequence 622, App	c 628	11.2	40.0	47	4	US-10-170-097-1197	Sequence 1197, Ap
c 556	11.2	40.0	29	4	US-09-304-232-408	Sequence 408, App	c 629	11.2	40.0	48	2	US-08-479-275D-14	Sequence 14, Appl
557	11.2	40.0	30	3	US-09-593-012-25	Sequence 25, Appl	c 630	11.2	40.0	48	2	US-08-488-271B-14	Sequence 14, Appl
c 558	11.2	40.0	30	3	US-09-318-786-13	Sequence 13, Appl	c 631	11.2	40.0	48	3	US-08-488-551B-802	Sequence 802, App
c 559	11.2	40.0	31	1	US-08-350-884-46	Sequence 46, Appl	632	11.2	40.0	48	4	US-10-007-073-5	Sequence 5, Appli
c 560	11.2	40.0	31	1	US-08-440-548-46	Sequence 46, Appl	c 633	11.2	40.0	49	4	US-09-935-916B-66	Sequence 66, Appl
c 561	11.2	40.0	31	1	US-08-709-173-46	Sequence 46, Appl	c 634	11.2	40.0	50	1	US-08-374-641-27	Sequence 27, Appl
c 562	11.2	40.0	31	1	US-08-191-866D-87	Sequence 87, Appl	c 635	11	39.3	16	4	US-09-474-432B-20	Sequence 20, Appl
c 563	11.2	40.0	31	2	US-08-185-949B-95	Sequence 95, Appl	c 636	11	39.3	16	4	US-08-476-373-20	Sequence 20, Appl
c 564	11.2	40.0	31	2	US-08-709-177-46	Sequence 95, Appl	c 637	11	39.3	18	1	US-08-363-240A-1081	Sequence 1081, Ap
c 565	11.2	40.0	31	3	US-08-480-640A-137	Sequence 137, App	638	11	39.3	19	3	US-09-338-907-363	Sequence 363, App
c 566	11.2	40.0	31	3	US-08-295-802-137	Sequence 137, App	c 639	11	39.3	19	3	US-09-218-207-363	Sequence 363, App
c 567	11.2	40.0	31	3	US-08-444-818-194	Sequence 194, App	c 640	11	39.3	20	3	US-09-422-978-6231	Sequence 6231, Ap
c 568	11.2	40.0	31	3	US-08-686-968C-64	Sequence 64, Appl	641	11	39.3	20	3	US-09-468-872-77	Sequence 77, Appl
c 569	11.2	40.0	31	3	US-08-488-237A-137	Sequence 137, App	642	11	39.3	20	4	US-09-198-452A-6236	Sequence 6236, Ap
c 570	11.2	40.0	31	3	US-08-375-992A-137	Sequence 137, App	c 643	11	39.3	21	1	US-08-368-870-7	Sequence 7, Appli
c 571	11.2	40.0	31	4	US-09-545-481-2	Sequence 2, Appli	644	11	39.3	21	4	US-09-657-472-1153	Sequence 1153, Ap
c 572	11.2	40.0	31	4	US-08-472-679B-137	Sequence 137, App	c 645	11	39.3	21	4	US-09-657-472-763	Sequence 763, App
c 573	11.2	40.0	32	1	US-08-410-739-4	Sequence 4, Appli	c 646	11	39.3	21	4	US-09-657-472-2525	Sequence 2525, Ap
574	11.2	40.0	32	2	US-08-997-080-67	Sequence 67, Appl	c 647	11	39.3	22	5	PCT-US96-00108-7	Sequence 7, Appli
575	11.2	40.0	32	2	US-08-997-362-67	Sequence 67, Appl	c 648	11	39.3	22	3	US-08-765-332-191	Sequence 191, App
576	11.2	40.0	32	3	US-08-873-970-67	Sequence 67, Appl	649	11	39.3	22	3	US-09-047-347-3	Sequence 3, Appli
577	11.2	40.0	32	3	US-09-095-855-67	Sequence 67, Appl	c 650	11	39.3	22	3	US-09-448-894-191	Sequence 191, App
578	11.2	40.0	32	3	US-09-324-542-67	Sequence 67, Appl	651	11	39.3	23	1	US-08-297-299B-86	Sequence 86, Appl
579	11.2	40.0	32	4	US-09-205-426-67	Sequence 67, Appl	652	11	39.3	23	2	US-08-858-083-86	Sequence 86, Appl
580	11.2	40.0	33	2	US-08-417-435-10	Sequence 10, Appl	653	11	39.3	23	5	PCT-US95-11029-86	Sequence 86, Appl
581	11.2	40.0	33	2	US-08-284-391B-10	Sequence 10, Appl	654	11	39.3	24	3	US-08-868-033-17	Sequence 17, Appl
582	11.2	40.0	33	2	US-08-394-177-4	Sequence 4, Appli	c 655	11	39.3	25	1	US-08-466-033-9	Sequence 9, Appli
583	11.2	40.0	33	3	US-08-394-912A-4	Sequence 4, Appli	c 656	11	39.3	25	1	US-08-444-733-9	Sequence 9, Appli
584	11.2	40.0	33	3	US-09-218-950-10	Sequence 10, Appl	c 657	11	39.3	25	2	US-08-464-134-9	Sequence 9, Appli
585	11.2	40.0	33	4	US-09-333-636-4	Sequence 4, Appli	c 658	11	39.3	25	2	US-08-461-361-9	Sequence 9, Appli
586	11.2	40.0	33	4	US-08-394-388A-10	Sequence 10, Appl	c 659	11	39.3	25	2	US-08-485-910-9	Sequence 9, Appli
587	11.2	40.0	33	4	PCT-US92-01785-10	Sequence 9, Appli	c 660	11	39.3	25	5	PCT-US95-06266-9	Sequence 9, Appli
588	11.2	40.0	33	5	US-08-910-408-52	Sequence 10, Appl	c 661	11	39.3	27	1	US-08-678-304-8	Sequence 8, Appli
589	11.2	40.0	35	3	US-08-715-628B-8	Sequence 8, Appli	c 662	11	39.3	27	3	US-08-886-886-4	Sequence 4, Appli
c 590	11.2	40.0	36	1	US-08-291-932A-478	Sequence 478, App	663	11	39.3	27	3	US-09-253-396A-169	Sequence 169, App
c 591	11.2	40.0	36	1	US-08-291-932A-667	Sequence 667, App	c 664	11	39.3	28	2	US-08-859-998-724	Sequence 724, App
c 592	11.2	40.0	36	1	US-08-363-240A-505	Sequence 505, App	c 665	11	39.3	28	2	US-08-859-998-1075	Sequence 1075, Ap
c 593	11.2	40.0	36	2	US-08-868-162A-7	Sequence 7, Appli	c 666	11	39.3	28	3	US-09-225-928-724	Sequence 724, App
c 594	11.2	40.0	37	1	US-07-977-696C-22	Sequence 22, Appl	c 667	11	39.3	28	3	US-09-225-928-1075	Sequence 1075, Ap
c 595	11.2	40.0	37	1	US-08-129-930B-22	Sequence 22, Appl	c 668	11	39.3	28	3	US-09-368-770-6	Sequence 6, Appli
c 596	11.2	40.0	37	3	US-08-134-346A-9	Sequence 9, Appli	c 669	11	39.3	28	4	US-09-225-201B-724	Sequence 724, App
c 597	11.2	40.0	37	3	US-08-976-288A-22	Sequence 22, Appl	c 670	11	39.3	28	4	US-09-225-201B-1075	Sequence 1075, Ap
c 598	11.2	40.0	38	4	US-09-757-207-9	Sequence 9, Appli	c 671	11	39.3	29	3	US-09-304-232-402	Sequence 402, App
c 599	11.2	40.0	39	1	US-08-682-218-24	Sequence 24, Appl	c 672	11	39.3	29	4	US-09-304-232-878	Sequence 878, App
c 600	11.2	40.0	39	4	US-09-219-797-9	Sequence 9, Appli	c 673	11	39.3	30	3	US-07-661-370-2	Sequence 2, Appli
c 601	11.2	40.0	41	3	US-08-813-507-111	Sequence 111, App	c 674	11	39.3	31	1	US-08-390-850-151	Sequence 151, App
c 602	11.2	40.0	41	3	US-09-464-453-111	Sequence 111, App	675	11	39.3	31	1	US-08-390-850-152	Sequence 152, App
c 603	11.2	40.0	42	1	US-08-271-880A-52	Sequence 52, Appl	676	11	39.3	31	1	US-08-435-634-151	Sequence 151, App
c 604	11.2	40.0	42	2	US-08-910-408-52	Sequence 52, Appl	677	11	39.3	31	1	US-08-435-634-152	Sequence 152, App
c 605	11.2	40.0	42	3	US-09-249-215-52	Sequence 52, Appl	c 678	11	39.3	33	1	US-08-639-256-13	Sequence 13, App
c 606	11.2	40.0	42	3	US-08-850-049-108	Sequence 108, App	c 679	11	39.3	33	4	US-08-677-970-5	Sequence 5, Appli
c 607	11.2	40.0	43	2	US-08-050-478-108	Sequence 108, App	680	11	39.3	33	4	US-08-675-499A-22	Sequence 22, Appl
608	11.2	40.0	43	2	US-08-050-478-108	Sequence 108, App	681	11	39.3	33	4	US-08-812-008-22	Sequence 22, Appl
609	11.2	40.0	43	3	US-09-414-117-108	Sequence 108, App	682	11	39.3	33	4	US-08-933-821-11	Sequence 11, Appl
610	11.2	40.0	43	4	US-09-678-437-108	Sequence 108, App	c 683	11	39.3	34	2	US-08-960-507-11	Sequence 11, Appl
611	11.2	40.0	43	4	US-09-943-722-108	Sequence 108, App	c 684	11	39.3	34	3		

c 685	11	39.3	34	3	US-08-966-341-8	Sequence 8, Appli	758	11	39.3	50	1	US-08-171-389-229	Sequence 229, App
c 686	11	39.3	34	3	US-08-966-341-9	Sequence 9, Appli	759	11	39.3	50	1	US-08-530-492-55	Sequence 55, Appl
c 687	11	39.3	34	3	US-09-064-411A-30	Sequence 30, Appl	760	11	39.3	50	1	US-08-123-936-229	Sequence 229, App
c 688	11	39.3	34	3	US-09-136-828-11	Sequence 11, Appl	761	11	39.3	50	2	US-08-475-288A-229	Sequence 229, App
c 689	11	39.3	34	3	US-09-332-928A-11	Sequence 11, Appl	762	11	39.3	50	2	US-08-482-080A-229	Sequence 229, App
c 690	11	39.3	34	3	US-09-136-801-11	Sequence 11, Appl	763	11	39.3	50	3	US-08-906-517-55	Sequence 55, Appl
c 691	11	39.3	34	4	US-09-332-923-11	Sequence 11, Appl	764	11	39.3	50	3	US-09-354-947-229	Sequence 229, App
c 692	11	39.3	34	4	US-09-333-075-11	Sequence 11, Appl	765	11	39.3	50	5	PCT-US93-12388-229	Sequence 229, App
c 693	11	39.3	34	4	US-09-202-088A-11	Sequence 11, Appl	766	10.8	38.6	16	4	US-09-649-747A-32	Sequence 32, Appl
c 694	11	39.3	34	4	US-09-333-077-11	Sequence 11, Appl	767	10.8	38.6	17	3	US-08-584-040-5349	Sequence 5349, Ap
c 695	11	39.3	35	4	US-09-284-100A-43	Sequence 43, Appl	768	10.8	38.6	17	3	US-08-584-040-5350	Sequence 5350, Ap
c 696	11	39.3	35	4	US-09-284-100A-47	Sequence 47, Appl	769	10.8	38.6	17	3	Sequence 8021, Ap	
c 697	11	39.3	35	4	US-09-284-100A-49	Sequence 49, Appl	770	10.8	38.6	17	4	Sequence 8021, Ap	
c 698	11	39.3	35	4	US-09-284-100A-51	Sequence 51, Appl	771	10.8	38.6	17	4	Sequence 2251, Ap	
c 699	11	39.3	36	1	US-08-363-240A-920	Sequence 920, App	772	10.8	38.6	18	2	Sequence 2252, Ap	
c 700	11	39.3	36	1	US-08-363-240A-921	Sequence 921, App	773	10.8	38.6	18	2	Sequence 3804, Ap	
c 701	11	39.3	36	2	US-08-585-684B-1002	Sequence 1002, Ap	774	10.8	38.6	18	1	Sequence 12, Appl	
c 702	11	39.3	36	2	US-09-038-073-1002	Sequence 34, Appl	775	10.8	38.6	18	1	Sequence 12, Appl	
c 703	11	39.3	36	4	US-09-897-425-34	Sequence 2320, Ap	776	10.8	38.6	18	2	Sequence 12, Appl	
c 704	11	39.3	38	2	US-08-292-620A-2320	Sequence 1, Appli	777	10.8	38.6	18	4	Sequence 4, Appli	
c 705	11	39.3	38	3	US-08-876-078-1	Sequence 2320, Ap	778	10.8	38.6	18	4	Sequence 11, Appl	
c 706	11	39.3	38	3	US-09-071-843-2320	Sequence 1, Appli	779	10.8	38.6	20	1	Sequence 12, Appl	
c 707	11	39.3	38	3	US-08-831-823-1	Sequence 7262, Ap	780	10.8	38.6	20	1	Sequence 143, App	
c 708	11	39.3	38	4	US-09-371-772B-7262	Sequence 7262, Ap	781	10.8	38.6	20	3	Sequence 26, Appl	
c 709	11	39.3	38	4	US-09-371-772B-7679	Sequence 7679, Ap	782	10.8	38.6	20	3	Sequence 143, App	
c 710	11	39.3	38	4	US-09-371-772B-7721	Sequence 7721, Ap	783	10.8	38.6	20	3	Sequence 20, Appl	
c 711	11	39.3	38	4	US-09-371-772B-7860	Sequence 7860, Ap	784	10.8	38.6	20	3	Sequence 53, Appl	
c 712	11	39.3	38	4	US-09-371-772B-8356	Sequence 8356, Ap	785	10.8	38.6	20	3	Sequence 8, Appli	
c 713	11	39.3	38	4	US-09-371-772B-8653	Sequence 8653, Ap	786	10.8	38.6	20	4	Sequence 91, Appl	
c 714	11	39.3	38	4	US-09-371-772B-8708	Sequence 8708, Ap	787	10.8	38.6	20	4	Sequence 3426, Ap	
c 715	11	39.3	38	4	US-09-371-772B-9047	Sequence 9047, Ap	788	10.8	38.6	20	4	Sequence 56, Appl	
c 716	11	39.3	38	4	US-09-371-772B-10685	Sequence 10685, A	789	10.8	38.6	21	1	Sequence 1, Appli	
c 717	11	39.3	38	4	US-09-371-772B-11069	Sequence 11069, A	790	10.8	38.6	21	1	Sequence 1, Appli	
c 718	11	39.3	38	4	US-09-371-772B-11319	Sequence 11319, A	791	10.8	38.6	21	3	Sequence 1, Appli	
c 719	11	39.3	38	4	US-09-371-772B-11468	Sequence 11468, A	792	10.8	38.6	21	3	Sequence 4, Appli	
c 720	11	39.3	38	4	US-09-371-772B-12425	Sequence 12425, A	793	10.8	38.6	21	3	Sequence 8249, Ap	
c 721	11	39.3	38	4	US-09-371-772B-12582	Sequence 12582, A	794	10.8	38.6	21	3	Sequence 71, Appl	
c 722	11	39.3	39	4	US-09-155-989A-10	Sequence 10, Appl	795	10.8	38.6	22	3	Sequence 63, Appl	
c 723	11	39.3	40	1	US-08-447-169A-227	Sequence 227, App	796	10.8	38.6	24	4	Sequence 7, Appli	
c 724	11	39.3	40	3	US-09-091-814-83	Sequence 83, Appl	797	10.8	38.6	24	4	Sequence 10, Appl	
c 725	11	39.3	40	3	US-09-672-609-45	Sequence 45, Appl	798	10.8	38.6	24	4	Sequence 351, App	
c 726	11	39.3	40	3	US-08-956-653A-29	Sequence 29, Appl	799	10.8	38.6	25	3	Sequence 10, Appl	
c 727	11	39.3	40	4	US-09-025-403A-45	Sequence 45, Appl	800	10.8	38.6	25	3	Sequence 11047, A	
c 728	11	39.3	40	4	US-09-789-556A-33	Sequence 33, Appl	801	10.8	38.6	25	4	Sequence 11048, A	
c 729	11	39.3	40	4	US-09-860-474-227	Sequence 227, App	802	10.8	38.6	25	4	Sequence 11049, A	
c 730	11	39.3	41	3	US-08-813-507-159	Sequence 159, App	803	10.8	38.6	25	4	Sequence 11050, A	
c 731	11	39.3	41	3	US-09-464-453-159	Sequence 159, App	804	10.8	38.6	26	4	Sequence 21, Appl	
c 732	11	39.3	42	3	US-08-679-645-6	Sequence 6, Appli	805	10.8	38.6	26	4	Sequence 648, App	
c 733	11	39.3	44	2	US-08-353-372A-5	Sequence 5, Appli	806	10.8	38.6	27	1	Sequence 3502, Ap	
c 734	11	39.3	45	2	US-08-629-039-8	Sequence 8, Appli	807	10.8	38.6	27	3	Sequence 4921, Ap	
c 735	11	39.3	46	1	US-08-283-067-55	Sequence 55, Appl	808	10.8	38.6	27	3	Sequence 5193, Ap	
c 736	11	39.3	46	1	US-08-271-880A-98	Sequence 98, Appl	809	10.8	38.6	27	3	Sequence 6840, Ap	
c 737	11	39.3	46	2	US-08-910-008-98	Sequence 98, Appl	810	10.8	38.6	27	3	Sequence 5, Appli	
c 738	11	39.3	46	3	US-09-249-215-98	Sequence 16, Appl	811	10.8	38.6	28	4	Sequence 20, Appl	
c 739	11	39.3	47	1	US-09-486-241-16	Sequence 23, Appl	812	10.8	38.6	28	4	Sequence 4, Appli	
c 740	11	39.3	47	1	US-07-972-032-23	Sequence 32, Appl	813	10.8	38.6	28	4	Sequence 6, Appli	
c 741	11	39.3	47	1	US-08-175-155-56	Sequence 56, Appl	814	10.8	38.6	29	1	Sequence 7, Appli	
c 742	11	39.3	47	1	US-08-477-509B-91	Sequence 91, Appl	815	10.8	38.6	29	1	Sequence 6, Appli	
c 743	11	39.3	47	1	US-08-642-255-37	Sequence 37, Appl	816	10.8	38.6	29	1	Sequence 7, Appli	
c 744	11	39.3	47	2	US-08-707-237A-63	Sequence 63, Appl	817	10.8	38.6	29	1	Sequence 6, Appli	
c 745	11	39.3	47	3	US-09-444-791A-91	Sequence 91, Appl	818	10.8	38.6	29	1	Sequence 7, Appli	
c 746	11	39.3	47	4	US-09-422-978-765	Sequence 765, App	819	10.8	38.6	29	1	Sequence 6, Appli	
c 747	11	39.3	47	4	US-09-422-978-897	Sequence 897, App	820	10.8	38.6	29	1	Sequence 7, Appli	
c 748	11	39.3	47	4	US-09-422-978-1339	Sequence 1339, Ap	821	10.8	38.6	29	1	Sequence 6, Appli	
c 749	11	39.3	47	4	US-09-422-978-1876	Sequence 1876, Ap	822	10.8	38.6	29	2	Sequence 7, Appli	
c 750	11	39.3	47	4	US-09-422-978-2358	Sequence 2358, Ap	823	10.8	38.6	29	2	Sequence 6, Appli	
c 751	11	39.3	47	4	US-09-422-978-2756	Sequence 2756, Ap	824	10.8	38.6	29	2	Sequence 7, Appli	
c 752	11	39.3	47	4	US-09-422-978-2787	Sequence 2787, Ap	825	10.8	38.6	29	2	Sequence 6, Appli	
c 753	11	39.3	47	4	US-09-422-978-3349	Sequence 3349, Ap	826	10.8	38.6	29	4	Sequence 12, Appl	
c 754	11	39.3	47	4	US-09-306-417-7	Sequence 7, Appli	827	10.8	38.6	29	4	Sequence 29, Appl	
c 755	11	39.3	48	2	US-09-438-954-7	Sequence 9, Appli	828	10.8	38.6	30	1	Sequence 4, Appli	
c 756	11	39.3	49	2	US-08-417-210A-92	Sequence 92, Appl	829	10.8	38.6	30	3	Sequence 2, Appli	
c 757	11	39.3	49	4	US-09-136-159A-92	Sequence 92, Appl	830	10.8	38.6	30	3	Sequence 2, Appli	

C 831	10.8	38.6	31	1	US-08-073-384C-18	Sequence 18, Appl	904	10.8	38.6	40	4	US-09-626-595-19	Sequence 19, Appl
C 832	10.8	38.6	31	1	US-08-390-850-153	Sequence 153, Appl	905	10.8	38.6	40	4	US-09-694-863-19	Sequence 19, Appl
C 833	10.8	38.6	31	1	US-08-254-359A-18	Sequence 18, Appl	906	10.8	38.6	42	1	US-08-416-872-3	Sequence 3, Appl
C 834	10.8	38.6	31	1	US-08-373-124A-44	Sequence 44, Appl	907	10.8	38.6	42	2	US-09-035-241-3	Sequence 3, Appl
C 835	10.8	38.6	31	1	US-08-483-043-18	Sequence 18, Appl	c 908	10.8	38.6	42	3	US-08-952-973-19	Sequence 19, Appl
C 836	10.8	38.6	31	1	US-08-435-624-153	Sequence 153, Appl	909	10.8	38.6	42	3	US-08-990-140-7	Sequence 7, Appl
C 837	10.8	38.6	31	1	US-08-481-238-18	Sequence 18, Appl	910	10.8	38.6	42	3	US-09-546-238-7	Sequence 7, Appl
C 838	10.8	38.6	31	1	US-08-435-628-44	Sequence 44, Appl	911	10.8	38.6	42	3	US-09-578-634A-58	Sequence 58, Appl
C 839	10.8	38.6	31	2	US-08-471-066B-18	Sequence 18, Appl	912	10.8	38.6	42	5	PCT-US94-06197-3	Sequence 3, Appl
C 840	10.8	38.6	31	2	US-08-484-956-18	Sequence 18, Appl	913	10.8	38.6	44	3	US-08-864-473-67	Sequence 67, Appl
C 841	10.8	38.6	31	2	US-08-757-653-18	Sequence 18, Appl	914	10.8	38.6	44	3	US-09-440-523-67	Sequence 67, Appl
C 842	10.8	38.6	31	2	US-08-599-431-18	Sequence 18, Appl	915	10.8	38.6	44	4	US-09-360-376-41	Sequence 41, Appl
C 843	10.8	38.6	31	2	US-08-956-047-3	Sequence 3, Appl	916	10.8	38.6	44	4	US-09-918-156-67	Sequence 67, Appl
C 844	10.8	38.6	31	2	US-08-956-047-37	Sequence 37, Appl	c 917	10.8	38.6	45	4	US-09-518-914-13	Sequence 13, Appl
C 845	10.8	38.6	31	2	US-08-756-386-18	Sequence 18, Appl	918	10.8	38.6	45	4	US-09-478-189-160	Sequence 160, Appl
C 846	10.8	38.6	31	2	US-08-823-516-18	Sequence 18, Appl	919	10.8	38.6	45	4	US-09-636-215-790	Sequence 790, Appl
C 847	10.8	38.6	31	3	US-08-682-853A-18	Sequence 18, Appl	920	10.8	38.6	45	4	US-09-685-166A-790	Sequence 790, Appl
C 848	10.8	38.6	31	3	US-08-759-038-18	Sequence 18, Appl	c 921	10.8	38.6	45	4	US-09-679-426-790	Sequence 790, Appl
C 849	10.8	38.6	31	3	US-08-758-314-18	Sequence 18, Appl	922	10.8	38.6	46	1	US-08-271-880A-91	Sequence 91, Appl
C 850	10.8	38.6	31	3	US-09-350-309-18	Sequence 18, Appl	923	10.8	38.6	46	1	US-08-271-880A-93	Sequence 93, Appl
C 851	10.8	38.6	31	3	US-08-520-946-18	Sequence 18, Appl	924	10.8	38.6	46	1	US-08-271-880A-114	Sequence 114, Appl
C 852	10.8	38.6	31	4	US-09-684-938-18	Sequence 18, Appl	925	10.8	38.6	46	1	US-08-271-880A-116	Sequence 116, Appl
C 853	10.8	38.6	31	4	US-09-308-825A-18	Sequence 18, Appl	926	10.8	38.6	46	2	US-08-910-408-91	Sequence 91, Appl
C 854	10.8	38.6	31	4	US-09-097-055B-80	Sequence 80, Appl	927	10.8	38.6	46	2	US-08-910-408-93	Sequence 93, Appl
C 855	10.8	38.6	31	4	US-09-655-378A-18	Sequence 18, Appl	928	10.8	38.6	46	2	US-08-910-408-114	Sequence 114, Appl
C 856	10.8	38.6	31	4	US-09-940-244-18	Sequence 18, Appl	929	10.8	38.6	46	2	US-08-910-408-116	Sequence 116, Appl
C 857	10.8	38.6	31	4	US-09-333-145-18	Sequence 18, Appl	930	10.8	38.6	46	3	US-09-249-215-91	Sequence 91, Appl
C 858	10.8	38.6	32	1	US-08-246-704-4	Sequence 4, Appl	931	10.8	38.6	46	3	US-09-249-215-93	Sequence 93, Appl
C 859	10.8	38.6	32	3	US-09-014-416-21	Sequence 21, Appl	932	10.8	38.6	46	3	US-09-249-215-114	Sequence 114, Appl
C 860	10.8	38.6	32	4	US-09-206-551-3	Sequence 3, Appl	933	10.8	38.6	46	3	US-09-249-215-116	Sequence 116, Appl
C 861	10.8	38.6	33	1	US-08-073-807A-13	Sequence 13, Appl	934	10.8	38.6	46	3	US-09-199-737-40	Sequence 40, Appl
C 862	10.8	38.6	34	3	US-09-038-909-8	Sequence 8, Appl	c 935	10.8	38.6	46	3	US-09-302-620B-72	Sequence 72, Appl
C 863	10.8	38.6	34	3	US-08-762-428A-8	Sequence 8, Appl	936	10.8	38.6	46	3	US-09-453-702B-216	Sequence 216, Appl
C 864	10.8	38.6	34	4	US-09-543-141-8	Sequence 8, Appl	937	10.8	38.6	47	4	US-09-474-432B-72	Sequence 72, Appl
C 865	10.8	38.6	34	4	US-09-254-180C-12	Sequence 12, Appl	938	10.8	38.6	47	4	US-09-422-978-1137	Sequence 1137, Ap
C 866	10.8	38.6	36	1	US-08-095-726-40	Sequence 40, Appl	939	10.8	38.6	47	4	US-09-422-978-1216	Sequence 1216, Ap
C 867	10.8	38.6	36	1	US-08-096-043-37	Sequence 37, Appl	c 940	10.8	38.6	47	4	US-09-422-978-1582	Sequence 1582, Ap
C 868	10.8	38.6	36	1	US-08-093-577-33	Sequence 33, Appl	941	10.8	38.6	47	4	US-09-422-978-1622	Sequence 1622, Ap
C 869	10.8	38.6	36	1	US-08-331-004A-7	Sequence 7, Appl	942	10.8	38.6	47	4	US-09-422-978-1701	Sequence 1701, Ap
C 870	10.8	38.6	36	1	US-08-411-796-364	Sequence 364, Appl	943	10.8	38.6	47	4	US-09-422-978-1961	Sequence 1961, Ap
C 871	10.8	38.6	36	1	US-08-096-623A-45	Sequence 45, Appl	c 944	10.8	38.6	47	4	US-09-422-978-3440	Sequence 3440, Ap
C 872	10.8	38.6	36	3	US-08-471-039-364	Sequence 364, Appl	945	10.8	38.6	47	4	US-09-422-978-3573	Sequence 3573, Ap
C 873	10.8	38.6	36	4	US-08-593-390-364	Sequence 364, Appl	946	10.8	38.6	47	4	US-09-422-978-3772	Sequence 3772, Ap
C 874	10.8	38.6	36	5	PCT-US93-11198-364	Sequence 364, Appl	947	10.8	38.6	47	4	US-09-422-978-3785	Sequence 3785, Ap
C 875	10.8	38.6	36	5	PCT-US95-13937A-7	Sequence 7, Appl	c 948	10.8	38.6	48	3	US-09-453-702B-216	Sequence 216, Appl
C 876	10.8	38.6	37	3	US-08-995-156A-14	Sequence 14, Appl	949	10.8	38.6	48	4	US-09-301-511A-34	Sequence 34, Appl
C 877	10.8	38.6	37	3	US-09-419-281-14	Sequence 14, Appl	950	10.8	38.6	48	4	US-09-476-387-72	Sequence 72, Appl
C 878	10.8	38.6	37	6	5310667-23	Patent No. 5310667	951	10.8	38.6	48	2	US-09-002-177-21	Sequence 21, Appl
C 879	10.8	38.6	38	1	US-08-373-124A-221	Sequence 221, Appl	952	10.8	38.6	49	3	US-09-374-584-21	Sequence 21, Appl
C 880	10.8	38.6	38	1	US-08-373-124A-1354	Sequence 1354, Appl	953	10.8	38.6	49	4	US-09-538-709-1085	Sequence 1085, Ap
C 881	10.8	38.6	38	1	US-08-591-070A-18	Sequence 18, Appl	c 954	10.8	38.6	50	2	US-08-556-424-5	Sequence 5, Appl
C 882	10.8	38.6	38	1	US-08-435-628-221	Sequence 221, Appl	c 955	10.8	38.6	50	3	US-09-263-914-5	Sequence 5, Appl
C 883	10.8	38.6	38	1	US-08-435-628-1354	Sequence 1354, Appl	956	10.8	38.6	50	4	US-09-613-263-5	Sequence 5, Appl
C 884	10.8	38.6	38	2	US-08-927-855-18	Sequence 18, Appl	957	10.8	38.6	50	4	US-09-613-263-6	Sequence 6, Appl
C 885	10.8	38.6	38	4	US-09-371-772B-9234	Sequence 9234, Appl	958	10.8	38.6	50	4	US-09-613-263-9	Sequence 9, Appl
C 886	10.8	38.6	38	4	US-09-371-772B-9947	Sequence 9947, Appl	959	10.8	38.6	50	4	US-09-613-263-10	Sequence 10, Appl
C 887	10.8	38.6	38	4	US-09-371-772B-10643	Sequence 10643, Appl	960	10.8	38.6	50	4	US-09-554-929-8	Sequence 8, Appl
C 888	10.8	38.6	38	4	US-09-371-772B-10886	Sequence 10886, A	c 961	10.8	38.6	50	4	US-09-554-929-187	Sequence 187, Appl
C 889	10.8	38.6	38	4	US-09-371-772B-11647	Sequence 11647, A	962	10.8	38.6	50	4	US-08-956-171E-1789	Sequence 1789, Ap
C 890	10.8	38.6	38	4	US-09-371-772B-11914	Sequence 11914, A	963	10.8	38.6	50	4	US-09-909-496-5	Sequence 5, Appl
C 891	10.8	38.6	38	4	US-09-371-772B-12046	Sequence 12046, A	964	10.8	38.6	50	4	US-09-909-496-6	Sequence 6, Appl
C 892	10.8	38.6	38	4	US-09-371-772B-12221	Sequence 12221, A	965	10.8	38.6	50	4	US-09-909-496-7	Sequence 7, Appl
C 893	10.8	38.6	38	4	US-09-371-772B-12417	Sequence 12417, A	966	10.8	38.6	50	4	US-09-909-496-11	Sequence 11, Appl
C 894	10.8	38.6	38	4	US-09-371-772B-13754	Sequence 13754, A	967	10.8	38.6	50	4	US-09-270-767-25222	Sequence 25222, A
C 895	10.8	38.6	38	4	US-09-371-772B-13756	Sequence 13756, A	968	10.8	38.6	50	4	US-08-781-986A-1789	Sequence 1789, Ap
C 896	10.8	38.6	38	4	US-09-968-255-15	Sequence 15, Appl	969	10.8	38.6	50	4	US-09-533-999C-15243	Sequence 15243, A
C 897	10.8	38.6	39	2	US-08-570-155-10	Sequence 10, Appl	970	10.6	37.9	17	1	US-08-373-124A-558	Sequence 558, App
C 898	10.8	38.6	39	5	PCT-US95-02861-10	Sequence 10, Appl	971	10.6	37.9	17	1	US-08-435-628-558	Sequence 558, App
C 899	10.8	38.6	40	3	US-09-626-929-19	Sequence 19, Appl	972	10.6	37.9	17	4	US-09-866-108A-8927	Sequence 8927, Ap
C 900	10.8	38.6	40	3	US-09-484-850-19	Sequence 19, Appl	c 973	10.6	37.9	18	3	US-09-102-528-17	Sequence 17, Appl
C 901	10.8	38.6	40	3	US-09-408-392-19	Sequence 19, Appl	974	10.6	37.9	18	4	US-09-658-679A-5	Sequence 5, Appl
C 902	10.8	38.6	40	4	US-09-626-930-19	Sequence 19, Appl	975	10.6	37.9	18	4	US-09-422-978-4437	Sequence 4437, Ap
C 903	10.8	38.6	40	4	US-09-626-930-19	Sequence 19, Appl	c 976	10.6	37.9	18	4	US-09-422-978-6382	Sequence 6382, Ap


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US-09-547-757-1
Query Match      100.0%; Score 28; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACCACAA 28
Db 36 GCAAGCACCTTATCAGGCGAGTACCACAA 9

RESULT 4
US-08-738-928-3
; Sequence 3, Application US/08738928
; Patent No. 5837442
; GENERAL INFORMATION:
; APPLICANT: Tsang, Sue Y.
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
; TITLE OF INVENTION: HCV Nucleic Acid
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-738-928-3

Query Match      96.4%; Score 27; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACCACA 27
Db 1 GCAAGCACCTTATCAGGCGAGTACCACA 27

RESULT 5
US-09-493-353-5
; Sequence 5, Application US/09493353
; Patent No. 6638714
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; APPLICANT: Linnen, J.M.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT
; TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2094/1E286-US1

US-09-547-757-1
; CURRENT APPLICATION NUMBER: US/09/493,353
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/118,497
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-493-353-5

Query Match      96.4%; Score 27; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACCACA 27
Db 1 GCAAGCACCTTATCAGGCGAGTACCACA 27

RESULT 6
US-08-474-700B-12
; Sequence 12, Application US/08474700B
; Patent No. 6001990
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Wakita, Takaji
; APPLICANT: Moradpour, Darius
; TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,700B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,382
; FILING DATE: 10 May 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/279001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-474-700B-12

Query Match      85.7%; Score 24; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACC 24
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Db

|||||

5 GCAAGCACCTATCAGGAGTACC 28

RESULT 7

PCT-US95-05812-12

Sequence 12, Application PC/TUS9505812

GENERAL INFORMATION:

APPLICANT: Wakiita, Takaji

APPLICANT: Wands, Jack

TITLE OF INVENTION: ANTISENSE INHIBITION OF

TITLE OF INVENTION: HEPATITIS C VIRUS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05812

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/240,382

FILING DATE: 10 May 1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/221001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US95-05812-12

Query Match 85.7%; Score 24; DB 5; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.016;

Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0;

Qy

1 GCAAGCACCTATCAGGAGTACC 24

|||||

Db

5 GCAAGCACCTATCAGGAGTACC 28

RESULT 8

US-08-438-639-51

Sequence 51, Application US/08438639

Patent No. 5712383

GENERAL INFORMATION:

APPLICANT: Sheridan, Patrick

APPLICANT: Chang, Chu-An

APPLICANT: Running, Joyce

APPLICANT: Urdea, Michael S.

TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID

TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION - R440

STREET: P.O. Box 8097

CITY: Emeryville

STATE: CA

ZIP: 94662-8097

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/813,338A

FILING DATE: 23-DEC-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Kenneth, M.

REGISTRATION NUMBER: 34,174

REFERENCE/DOCKET NUMBER: 0232.001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-813-338A-51

Query Match 85.7%; Score 24; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGATACC 24
|||||
Db 10 GCAAGCACCTATCAGGCGATACC 33

RESULT 10

US-08-470-124-61
Sequence 61, Application US/08470124
Patent No. 5849481

GENERAL INFORMATION:

APPLICANT: Urdea, Michael S.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
APPLICANT: Warner, Brian
APPLICANT: Fultz, Timothy J.
TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
TITLE OF INVENTION: POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.125
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,124
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/813,588

FILING DATE: 23 December 1991

ATTORNEY/AGENT INFORMATION:

NAME: Ciotti, Thomas E.

REGISTRATION NUMBER: 21,013

REFERENCE/DOCKET NUMBER: 22300-20104.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-813-5600

TELEFAX: 415-327-2951

TELEX: 706141

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-470-124-61

Query Match 85.7%; Score 24; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGATACC 24

Db 10 GCAAGCACCTATCAGGCGATACC 33
|||||

RESULT 11

US-08-441-971-127

Sequence 127, Application US/08441971

Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janiuk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 127:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-441-971-127

Query Match 85.7%; Score 24; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGATACC 24
|||||

Db 10 GCAAGCACCTATCAGGCGATACC 33
|||||

RESULT 12

US-08-221-653-127

Sequence 127, Application US/08221653

Patent No. 6190864

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,653
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/881,528
FILING DATE:
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-221-653-127

Query Match 85.7%; Score 24; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24
DB 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 13
US-08-442-144A-127
Sequence 127, Application US/08442144A
Patent No. 6214583
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
APPLICANT: Eileen Beall
APPLICANT: Bruce Irvine
APPLICANT: Janice Kolberg
APPLICANT: Michael S. Urdea
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,144A
FILING DATE: MAY 16, 1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,653
FILING DATE: APRIL 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yanko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CHIR-0121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
TELEX:
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 Nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
US-08-442-144A-127

Query Match 85.7%; Score 24; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24
DB 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 14
US-08-441-970-127
Sequence 127, Application US/08441970
Patent No. 6297370
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,970
FILING DATE: 16-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/881,528
FILING DATE: 08-MAY-1992
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single

```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-441-970-127

Query Match      85.7%; Score 24; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGTACC 24
Db 10 GCAAGCACCTTATCAGGCAGTACC 33

RESULT 15
US-09-493-353-6
; Sequence 6, Application US/094933353
; Patent No. 6638714
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; APPLICANT: Linnen, J.M.
; APPLICANT: Gorman, K.M.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT
; TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2094/1E286-US1
; CURRENT APPLICATION NUMBER: US/09/493,353
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/118,497
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-493-353-6

Query Match      78.6%; Score 22; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGTA 22
Db 6 GCAAGCACCTTATCAGGCAGTA 27

RESULT 16
PCT-US93-00928-1
; Sequence 1, Application PC/TUS9300928
; GENERAL INFORMATION:
; APPLICANT: TASSOPOULOS, NIC C.
; APPLICANT: HATZAKIS, ANGELOS E.
; APPLICANT: KUHN, MARY C.
; APPLICANT: TROONEN, HUGO
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METH
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00928
; FILING DATE: 19930203
```

```
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5132.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-00928-1

Query Match      78.6%; Score 22; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGTA 22
Db 6 GCAAGCACCTTATCAGGCAGTA 27

RESULT 17
US-09-078-290A-10
; Sequence 10, Application US/09078290A
; Patent No. 6048696
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Leslie M.
; APPLICANT: Hawkins, Gregory A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,290A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 310307.90100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
US-09-078-290A-10

Query Match      75.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 8 CCCTATCAGGCAGTACCACAA 28
```

Db 1 CCCTATCAGGCGTACCACAA 21

RESULT 18

US-08-938-033-4

Sequence 4, Application US/08938033

Patent No. 6172046

GENERAL INFORMATION:

APPLICANT: Albrecht, Janice K.

TITLE OF INVENTION: Detectable HCV-RNA In Patients Having Chronic Hepatitis C Infection

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation

STREET: 2000 Galloping Hill Road

CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA

ZIP: 07033

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: 7.5.3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,033

FILING DATE: 21-Sep-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hoffman, Thomas D.

REGISTRATION NUMBER: 28,221

REFERENCE/DOCKET NUMBER: IN0783-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-298-5037

TELEFAX: 908-298-5388

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (oligonucleotide)

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-08-938-033-4

Query Match 75.0%; Score 21; DB 3; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.42;

Mismatches 21; Conservative 0; Indels 0; Gaps 0;

QY 8 CCCTATCAGGCGTACCACAA 28

DB 1 CCCTATCAGGCGTACCACAA 21

RESULT 19

US-08-397-220B-17

Sequence 17, Application US/08397220B

Patent No. 6284458

GENERAL INFORMATION:

APPLICANT: Anderson et al.

TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jane Massey Licata, Esq. 201

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/397,220B

FILING DATE: 09-Mar-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/01293

FILING DATE: 10-Sep-93

APPLICATION NUMBER: JP 5-87195

FILING DATE: 14-Apr-93

APPLICATION NUMBER: 07/945,289

FILING DATE: 10-Sep-92

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-8488

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-08-397-220B-17

Query Match 75.0%; Score 21; DB 3; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.42;

Mismatches 21; Conservative 0; Indels 0; Gaps 0;

QY 8 CCCTATCAGGCGTACCACAA 28

DB 1 CCCTATCAGGCGTACCACAA 21

RESULT 20

US-08-650-093C-17

Sequence 17, Application US/08650093C

Patent No. 6391542

GENERAL INFORMATION:

APPLICANT: Kevin P. Anderson et al.

TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: LICATA & TYRRELL P.C.

STREET: 66 E. Main Street

CITY: Marlton

STATE: NJ

COUNTRY: USA

ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WORDPERFECT 6.1 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/650,093C

FILING DATE: 17-May-1996

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/452,841

FILING DATE: May 30, 1995

APPLICATION NUMBER: 08/397,220

FILING DATE: March 9, 1995

APPLICATION NUMBER: 07/945,289

FILING DATE: September 10, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

```
;
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-650-093C-17

Query Match 75.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 21
US-08-823-895A-17
; Sequence 17, Application US/08823895A
; Patent No. 6433159
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson
; TITLE OF INVENTION: Compositions And Methods For
; TREATMENT OF HEPATITIS C VIRUS-ASSOCIATED DISEASES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,895A
; FILING DATE: March 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/453,085
; FILING DATE: May 30, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/945,289
; FILING DATE: September 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: Nucleic
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-823-895A-17

Query Match 75.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
```

```
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 22
US-09-311-487-4
; Sequence 4, Application US/09311487
; Patent No. 6472373
; GENERAL INFORMATION:
; APPLICANT: Albrecht, Janice K.
; TITLE OF INVENTION: Combination Therapy For Eradicating
; TITLE OF INVENTION: Detectable HCV-RNA In Patients
; TITLE OF INVENTION: Having Chronic Hepatitis C Infection
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,487
; FILING DATE: May 13, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoffman, Thomas D.
; REGISTRATION NUMBER: 28,221
; REFERENCE/DOCKET NUMBER: IN0878K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-5388
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-09-311-487-4

Query Match 75.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 23
PCT-US94-05407-13
; Sequence 13, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05407

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/061,694

FILING DATE: 13-MAY-1993

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: oligonucleotide

PCT-US94-05407-13

Query Match

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

8 CCCTATCAGCAGTACACAA 28

|||||

Db

1 CCCTATCAGCAGTACACAA 21

RESULT 24

US-08-356-287-25

; Sequence 25, Application US/08356287

; Patent No. 5686272

; GENERAL INFORMATION:

; APPLICANT: Ronald L. Marshall

; APPLICANT: John J. Carrino

; APPLICANT: Joann Sustachek

; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING

; TITLE OF INVENTION: THE LIGASE CHAIN REACTION

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,287

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/891,543

; FILING DATE: 29 MAY 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul D. Yeager

; REGISTRATION NUMBER: 37,477

; REFERENCE/DOCKET NUMBER: 5172.US.P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-2341

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid (synthetic DNA)

US-08-356-287-25

Query Match

75.0%; Score 21; DB 1; Length 23;

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05407

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/061,694

FILING DATE: 13-MAY-1993

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: oligonucleotide

PCT-US94-05407-13

Query Match

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

8 CCCTATCAGCAGTACACAA 28

|||||

Db

1 CCCTATCAGCAGTACACAA 21

RESULT 24

US-08-356-287-25

; Sequence 25, Application US/08356287

; Patent No. 5686272

; GENERAL INFORMATION:

; APPLICANT: Ronald L. Marshall

; APPLICANT: John J. Carrino

; APPLICANT: Joann Sustachek

; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING

; TITLE OF INVENTION: THE LIGASE CHAIN REACTION

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy diskette

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.0.1

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,287

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/891,543

; FILING DATE: 29 MAY 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul D. Yeager

; REGISTRATION NUMBER: 37,477

; REFERENCE/DOCKET NUMBER: 5172.US.P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-2341

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid (synthetic DNA)

US-08-356-287-25

Query Match

75.0%; Score 21; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.43;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GCAAGCACCTATCAGGCAGT 21

|||||

Db

3 GCAAGCACCTATCAGGCAGT 23

RESULT 25

PCT-US93-04863-25

; Sequence 25, Application PC/TUS9304863

; GENERAL INFORMATION:

; APPLICANT: Ronald L. Marshall

; APPLICANT: John J. Carrino

; APPLICANT: Joann C. Sustachek

; APPLICANT: ABBOTT LABORATORIES

; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES

; TITLE OF INVENTION: USING THE LIGASE CHAIN REACTION

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: One Abbott Park Road

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/04863

; FILING DATE: 19930524

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/891,543

; FILING DATE: 29 MAY 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Thomas D. Brainard

; REGISTRATION NUMBER: 32,459

; REFERENCE/DOCKET NUMBER: 5172.PC.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-4884

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid (synthetic DNA)

PCT-US93-04863-25

Query Match

Best Local Similarity 100.0%; Pred. No. 0.43;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.43;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GCAAGCACCTATCAGGCAGT 21

|||||

Db

3 GCAAGCACCTATCAGGCAGT 23

RESULT 26

US-08-240-547-18

; Sequence 18, Application US/08240547

; Patent No. 5527669

; GENERAL INFORMATION:

; APPLICANT: Resnick, Robert M.

; APPLICANT: Young, Karen K.Y.

; TITLE OF INVENTION: Primers and Probes for Detection of

; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants

; NUMBER OF SEQUENCES: 43

Query Match

75.0%; Score 21; DB 5; Length 23;

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-240-547-18

Query Match          75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 27
US-08-449-050-16
; Sequence 16, Application US/08449050
; Patent No. 5561058
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David
; APPLICANT: Myers, Thomas
; APPLICANT: Sigua, Christopher
; TITLE OF INVENTION: Reagents and Methods for Coupled High
; TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain
; TITLE OF INVENTION: Reactions
; NUMBER OF INVENTION: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,050
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 16:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-08-449-050-16

Query Match          75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 28
US-08-332-616A-8
; Sequence 8, Application US/08332616A
; Patent No. 5620852
; GENERAL INFORMATION:
; APPLICANT: LIN, LILY
; APPLICANT: CIMINO, GEORGE
; APPLICANT: ZHU, YU SHENG
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,616A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,545
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: HRI-01202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-332-616A-8

Query Match          75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 29
US-08-317-220-8
```

; Sequence 8, Application US/08317220
; Patent No. 5654179
; GENERAL INFORMATION:
; APPLICANT: LIN, LILY
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETER G. CARROLL
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,220
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,649
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,545
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/614,921
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: HRI-00542
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-317-220-8

Query Match 75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 30
US-08-675-153-8
; Sequence 8, Application US/08675153
; Patent No. 5677124
; GENERAL INFORMATION:
; APPLICANT: DuBois, Dwight
; APPLICANT: Winkler, Matthew
; APPLICANT: Pasloske, Brittan L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America

; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,153
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-675-153-8

Query Match 75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 31
US-08-244-116B-51/c
; Sequence 51, Application US/08244116B
; Patent No. 5763159
; GENERAL INFORMATION:
; APPLICANT: Simmonds, Peter
; APPLICANT: Chan, Shiu-Wan
; APPLICANT: Yap, Peng L.
; TITLE OF INVENTION: Hepatitis-C Virus Testing
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 5763159th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,116B
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02143
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs


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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA
; DESCRIPTION: oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis-C virus
US-08-244-116B-51

Query Match 75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
Db 21 GCAAGCACCTATCAGGCAGT 1

RESULT 32
US-08-738-928-5
; Sequence 5, Application US/08738928
; Patent No. 5637442
; GENERAL INFORMATION:
; APPLICANT: Teang, Sue Y.
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
; TITLE OF INVENTION: HCV Nucleic Acid
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-738-928-5

Query Match 75.0%; Score 21; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 33
US-08-841-252-8

; Sequence 8, Application US/08841252
; Patent No. 5919625
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, DWIGHT
; APPLICANT: WINKLER, MATTHEW
; APPLICANT: PASLOSKE, BRITTAN L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
; TITLE OF INVENTION: STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,252
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,677,124
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMB1:026--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-300
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-841-252-8

Query Match 75.0%; Score 21; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 34
US-08-861-571-8
; Sequence 8, Application US/08861571
; Patent No. 5939262
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; TITLE OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-282-054-8

Query Match 75.0%; Score 21; DB 3; Length 24;
Best Local Similarity 100.0%; Pred No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0;

QY 1 GCAAGCACCTATCAGGCAGT 21
DDB 4 GCAAGCACCTATCAGGCAGT 24
|||||
|||||

RESULT 36
US-09-665-638-8
; Sequence 8, Application US/09665638
; Patent No. 6399307
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; Brown, Dwight
; Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/665,638
; FILING DATE: 19-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-665-638-8

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Query Match      75.0%; Score 21; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
    |||||
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 37
US-10-007-389-5
; Sequence 5, Application US/10007389
; Patent No. 6727067
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehres, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-007-389-5

Query Match      75.0%; Score 21; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
    |||||
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 38
US-08-240-547-19
; Sequence 19, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and probes for detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
```

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-19

Query Match      75.0%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
    |||||
Db 6 GCAAGCACCTATCAGGCAGT 26

RESULT 39
US-08-256-568B-4
; Sequence 4, Application US/08256568B
; Patent No. 5846704
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,568B
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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Wed Nov 24 08:46:08 2004

us-10-087-631b-7.max.rni

```

; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -29 of 5' end
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..26
; OTHER INFORMATION: /standard name=
; OTHER INFORMATION: "Universal HCV primer HcPr96"
; US-08-256-568B-4

Query Match          75.0%; Score 21; DB 2; Length 26;
Best Local Similarity 100.0%; Pred.No. 0.44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21
   |||||
Db 6 GCAAGCACCTATCAGGCAGT 26

STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HCV
POSITION IN GENOME:
CHROMOSOME/SEGMENT: HCV
MAP POSITION: Position -29 of 5' end
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..26
OTHER INFORMATION: /standard name=
OTHER INFORMATION: "Universal HCV primer HcPr96"
US-09-038-369B-4

Query Match          75.0%; Score 21; DB 3; Length 26;
Best Local Similarity 100.0%; Pred.No. 0.44;
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RESULT 40
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; Sequence 4, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,369B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
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OM nucleic - nucleic search, using sw model

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Title: US-10-087-631B-7

Perfect score: 28

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Scoring table: IDENTITY_NUC

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Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 235	15	53.6	15	10	US-09-740-332-4591	Sequence 4591, Ap	c 308	14	50.0	17	17	US-10-669-841-2660	Sequence 2660, Ap
c 236	15	53.6	15	10	US-09-740-332-4657	Sequence 4697, Ap	c 309	14	50.0	19	18	US-10-667-271-14	Sequence 14, Appl
c 237	15	53.6	15	10	US-09-740-332-4698	Sequence 4698, Ap	c 310	14	50.0	19	18	US-10-667-271-45	Sequence 45, Appl
c 238	15	53.6	15	10	US-09-740-332-4711	Sequence 4711, Ap	c 311	14	50.0	19	18	US-10-667-271-710	Sequence 710, Appl
c 239	15	53.6	15	10	US-09-740-332-4712	Sequence 4712, Ap	c 312	14	50.0	19	18	US-10-667-271-741	Sequence 741, Appl
c 240	15	53.6	15	10	US-09-740-332-4728	Sequence 4728, Ap	c 313	14	50.0	21	18	US-10-667-271-1511	Sequence 1511, Ap
c 241	15	53.6	15	10	US-09-740-332-4729	Sequence 4729, Ap	c 314	14	50.0	21	18	US-10-667-271-1523	Sequence 1523, Ap
c 242	15	53.6	15	10	US-09-740-332-4753	Sequence 4753, Ap	c 315	14	50.0	21	18	US-10-667-271-1560	Sequence 1560, Ap
c 243	15	53.6	15	10	US-09-817-879-4590	Sequence 4590, Ap	c 316	14	50.0	21	18	US-10-667-271-1569	Sequence 1569, Ap
c 244	15	53.6	15	10	US-09-817-879-4591	Sequence 4591, Ap	c 317	14	50.0	21	18	US-10-667-271-1572	Sequence 1572, Ap
c 245	15	53.6	15	10	US-09-817-879-4697	Sequence 4697, Ap	c 318	14	50.0	21	18	US-10-667-271-1581	Sequence 1581, Ap
c 246	15	53.6	15	10	US-09-817-879-4698	Sequence 4698, Ap	c 319	14	50.0	25	17	US-10-717-597-3732	Sequence 3732, Ap
c 247	15	53.6	15	10	US-09-817-879-4711	Sequence 4711, Ap	c 320	14	50.0	26	9	US-09-877-526A-8	Sequence 8, Appl
c 248	15	53.6	15	10	US-09-817-879-4712	Sequence 4712, Ap	c 321	14	50.0	26	10	US-09-992-160-8	Sequence 8, Appl
c 249	15	53.6	15	10	US-09-817-879-4728	Sequence 4728, Ap	c 322	14	50.0	26	14	US-10-056-761-8	Sequence 8, Appl
c 250	15	53.6	15	10	US-09-817-879-4729	Sequence 4729, Ap	c 323	14	50.0	26	16	US-10-422-050-8	Sequence 8, Appl
c 251	15	53.6	15	10	US-09-817-879-4753	Sequence 4753, Ap	c 324	14	50.0	30	9	US-09-037-657-48	Sequence 48, Appl
c 252	15	53.6	15	17	US-10-669-841-7183	Sequence 7183, Ap	c 325	14	50.0	30	9	US-09-037-657-52	Sequence 52, Appl
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c 254	15	53.6	15	17	US-10-669-841-7290	Sequence 7290, Ap	c 327	14	50.0	38	10	US-09-827-395A-1267	Sequence 1267, Ap
c 255	15	53.6	15	17	US-10-669-841-7291	Sequence 7291, Ap	c 328	14	50.0	38	10	US-09-827-395A-1364	Sequence 1364, Ap
c 256	15	53.6	15	17	US-10-669-841-7304	Sequence 7304, Ap	c 329	14	50.0	38	15	US-10-430-882-1267	Sequence 1267, Ap
c 257	15	53.6	15	17	US-10-669-841-7305	Sequence 7305, Ap	c 330	14	50.0	38	15	US-10-430-882-1364	Sequence 1364, Ap
c 258	15	53.6	15	17	US-10-669-841-7321	Sequence 7321, Ap	c 331	14	50.0	41	16	US-10-035-833A-529	Sequence 529, App
c 259	15	53.6	15	17	US-10-669-841-7322	Sequence 7322, Ap	c 332	14	50.0	41	16	US-10-035-833A-6096	Sequence 6096, Ap
c 260	15	53.6	15	17	US-10-669-841-7346	Sequence 7346, Ap	c 333	14	50.0	43	10	US-09-946-374-320	Sequence 320, App
c 261	15	53.6	16	10	US-09-825-805-18	Sequence 18, Appl	c 334	14	50.0	43	10	US-10-006-856A-320	Sequence 320, App
c 262	15	53.6	17	10	US-09-740-332-4489	Sequence 4489, Ap	c 335	14	50.0	43	14	US-10-006-818A-320	Sequence 320, App
c 263	15	53.6	17	10	US-09-740-332-4493	Sequence 4493, Ap	c 336	14	50.0	43	14	US-10-006-845A-320	Sequence 320, App
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c 265	15	53.6	17	10	US-09-817-879-4493	Sequence 4493, Ap	c 338	14	50.0	43	14	US-10-015-499A-320	Sequence 320, App
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c 275	15	53.6	19	15	US-10-309-438-37	Sequence 37, Appl	c 348	14	50.0	43	14	US-10-011-671A-320	Sequence 320, App
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c 280	15	53.6	19	18	US-10-667-271-717	Sequence 717, Appl	c 353	14	50.0	43	15	US-10-017-610A-320	Sequence 320, App
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c 286	15	53.6	46	15	US-10-339-674-2427	Sequence 2427, Ap	c 359	14	50.0	43	15	US-10-006-041A-320	Sequence 320, App
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c 292	14.4	51.4	25	15	US-10-098-263B-65485	Sequence 65485, A	c 365	14	50.0	43	15	US-10-015-953A-320	Sequence 320, App
c 293	14.4	51.4	25	17	US-10-717-597-811	Sequence 811, Appl	c 366	14	50.0	43	15	US-10-017-306A-320	Sequence 320, App
c 294	14.4	51.4	31	14	US-10-072-036-32	Sequence 32, Appl	c 367	14	50.0	43	15	US-10-017-867A-320	Sequence 320, App
c 295	14.2	50.7	20	15	US-10-218-969-37	Sequence 37, Appl	c 368	14	50.0	43	15	US-10-012-064A-320	Sequence 320, App
c 296	14.2	50.7	25	14	US-10-215-112-1725	Sequence 1725, Ap	c 369	14	50.0	43	15	US-10-013-909A-320	Sequence 320, App
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C 386	14	50.0	43	15	US-10-015-385A-320	Sequence 320, App	C 459	13	46.4	13	17	US-10-669-841-7314	Sequence 7314, App
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C 408	13.6	48.6	25	15	US-10-098-263B-41535	Sequence 41535, A	C 481	13	46.4	20	15	US-10-174-771-90	Sequence 90, Appl
C 409	13.6	48.6	38	10	US-09-827-395A-1566	Sequence 1566, App	C 482	13	46.4	20	15	US-10-215-112-8977	Sequence 8977, App
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C 438	13	46.4	13	10	US-09-740-332-4706	Sequence 4706, App	C 511	13	46.4	48	15	US-10-339-674-3145	Sequence 3145, App
C 439	13	46.4	13	10	US-09-740-332-4721	Sequence 4721, App	C 512	13	46.4	48	15	US-10-339-674-3145	Sequence 3145, App
C 440	13	46.4	13	10	US-09-740-332-4722	Sequence 4722, App	C 513	13	46.4	48	15	US-10-339-674-3145	Sequence 3145, App
C 441	13	46.4	13	10	US-09-740-332-4742	Sequence 4742, App	C 514	13	46.4	48	15	US-10-339-674-3145	Sequence 3145, App
C 442	13	46.4	13	10	US-09-817-879-4614	Sequence 4614, App	C 515	13	46.4	48	15	US-10-339-674-3145	Sequence 3145, App
C 443	13	46.4	13	10	US-09-817-879-4614	Sequence 4614, App	C 516	13	46.4	48	15	US-10-339-674-3145	Sequence 3145, App
C 444	13	46.4	13	10	US-09-817-879-4632	Sequence 4632, App	C 517	13	46.4	48	15	US-10-339-674-3145	Sequence 3145, App
C 445	13	46.4	13	10	US-09-817-879-4693	Sequence 4693, App	C 518	12.8	45.7	21	10	US-09-935-338-195	Sequence 195, App
C 446	13	46.4	13	10	US-09-817-879-4694	Sequence 4694, App	C 519	12.8	45.7	21	10	US-09-935-338-231	Sequence 231, App
C 447	13	46.4	13	10	US-09-817-879-4695	Sequence 4695, App	C 520	12.8	45.7	25	15	US-10-098-263B-22720	Sequence 22720, A
C 448	13	46.4	13	10	US-09-817-879-4705	Sequence 4705, App	C 521	12.8	45.7	25	15	US-10-098-263B-65486	Sequence 65486, A
C 449	13	46.4	13	10	US-09-817-879-4706	Sequence 4706, App	C 522	12.8	45.7	25	15	US-10-098-263B-127861	Sequence 127861, A
C 450	13	46.4	13	10	US-09-817-879-4721	Sequence 4721, App	C 523	12.8	45.7	25	15	US-10-098-263B-127862	Sequence 127862, A

524	12.8	45.7	31	13	US-10-109-971-2	Sequence 2, Appli	Sequence 2, Appli	12.4	44.3	38	16	US-10-138-674-13952	Sequence 13952, A
525	12.8	45.7	31	13	US-10-109-971-8	Sequence 8, Appli	Sequence 8, Appli	12.4	44.3	38	17	US-10-287-949A-9483	Sequence 9483, Ap
526	12.8	45.7	37	16	US-10-308-128-182	Sequence 182, App	Sequence 182, App	12.4	44.3	38	17	US-10-287-949A-11231	Sequence 11231, A
527	12.8	45.7	47	16	US-10-349-143-2844	Sequence 2844, Ap	Sequence 2844, Ap	12.4	44.3	38	17	US-10-287-949A-13952	Sequence 13952, A
528	12.8	45.7	50	10	US-09-885-731B-13	Sequence 13, Appl	Sequence 13, Appl	12.4	44.3	38	17	US-10-712-672-13909	Sequence 13909, Ap
529	12.8	45.7	50	10	US-09-885-731B-14	Sequence 14, Appl	Sequence 14, Appl	12.4	44.3	38	17	US-10-669-841-7493	Sequence 7493, Ap
530	12.8	45.7	50	10	US-09-885-731B-15	Sequence 15, Appl	Sequence 15, Appl	12.4	44.3	39	16	US-10-453-827-533	Sequence 533, App
531	12.8	45.7	50	13	US-10-103-002-12	Sequence 12, Appl	Sequence 12, Appl	12.4	44.3	41	16	US-10-252-155-257	Sequence 257, App
532	12.8	45.7	50	13	US-10-103-002-13	Sequence 13, Appl	Sequence 13, Appl	12.4	44.3	45	14	US-09-771-287-53	Sequence 53, Appl
533	12.8	45.7	50	16	US-10-131-827-426	Sequence 426, App	Sequence 426, App	12.4	44.3	45	14	US-10-007-132-53	Sequence 53, Appl
534	12.8	45.7	50	16	US-10-131-827-5975	Sequence 5975, Ap	Sequence 5975, Ap	12.4	44.3	45	15	US-10-006-343-53	Sequence 53, Appl
535	12.8	45.7	50	16	US-10-131-827-7622	Sequence 7622, Ap	Sequence 7622, Ap	12.4	44.3	47	16	US-10-349-143-777	Sequence 777, App
536	12.8	45.7	50	16	US-10-131-827-7936	Sequence 7936, Ap	Sequence 7936, Ap	12.4	44.3	47	16	US-10-349-143-3819	Sequence 3819, Ap
537	12.6	45.0	20	18	US-10-776-013-92	Sequence 92, Appl	Sequence 92, Appl	12.4	44.3	50	16	US-10-131-827-6012	Sequence 6012, Ap
538	12.6	45.0	22	16	US-10-210-281-170	Sequence 170, App	Sequence 170, App	12.2	43.6	17	9	US-09-864-785-2032	Sequence 2032, Ap
539	12.6	45.0	24	10	US-09-940-185-3512	Sequence 3512, Ap	Sequence 3512, Ap	12.2	43.6	20	15	US-10-243-468-25	Sequence 25, Appl
540	12.6	45.0	25	14	US-10-215-112-1851	Sequence 1851, Ap	Sequence 1851, Ap	12.2	43.6	20	15	US-10-380-931-97	Sequence 97, Appl
541	12.6	45.0	25	15	US-10-098-263B-29633	Sequence 29633, A	Sequence 29633, A	12.2	43.6	20	15	US-10-159-266-54	Sequence 54, Appl
542	12.6	45.0	25	15	US-10-098-263B-29634	Sequence 29634, A	Sequence 29634, A	12.2	43.6	20	15	US-10-159-266-128	Sequence 128, App
543	12.6	45.0	25	15	US-10-441-442-1	Sequence 1, Appli	Sequence 1, Appli	12.2	43.6	22	9	US-09-927-668-27	Sequence 27, Appl
544	12.6	45.0	30	9	US-09-929-924-30	Sequence 30, Appl	Sequence 30, Appl	12.2	43.6	24	16	US-10-269-021B-1	Sequence 1, Appli
545	12.6	45.0	30	15	US-10-366-044-44	Sequence 44, Appl	Sequence 44, Appl	12.2	43.6	25	15	US-10-098-263B-71553	Sequence 71553, A
546	12.6	45.0	30	16	US-10-682-553-44	Sequence 44, Appl	Sequence 44, Appl	12.2	43.6	25	15	US-10-098-263B-78772	Sequence 78772, A
547	12.6	45.0	32	15	US-10-207-655-411	Sequence 411, App	Sequence 411, App	12.2	43.6	25	15	US-10-098-263B-115934	Sequence 115934, A
548	12.6	45.0	32	15	US-10-339-674-1012	Sequence 1012, Ap	Sequence 1012, Ap	12.2	43.6	25	15	US-10-098-263B-127441	Sequence 127441, A
549	12.6	45.0	34	15	US-10-339-674-1852	Sequence 1852, Ap	Sequence 1852, Ap	12.2	43.6	25	17	US-10-775-169-4958	Sequence 4958, Ap
550	12.6	45.0	34	15	US-10-339-674-1853	Sequence 1853, Ap	Sequence 1853, Ap	12.2	43.6	26	15	US-10-360-849A-67	Sequence 67, Appl
551	12.6	45.0	35	10	US-09-736-116-56	Sequence 56, Appl	Sequence 56, Appl	12.2	43.6	40	18	US-10-469-851-222	Sequence 222, App
552	12.6	45.0	36	9	US-09-234-874A-60	Sequence 60, Appl	Sequence 60, Appl	12.2	43.6	41	14	US-10-043-573-109	Sequence 109, App
553	12.6	45.0	36	10	US-09-234-873A-60	Sequence 60, Appl	Sequence 60, Appl	12.2	43.6	41	14	US-10-038-723-42	Sequence 42, Appl
554	12.6	45.0	36	15	US-10-076-604-60	Sequence 60, Appl	Sequence 60, Appl	12.2	43.6	41	14	US-09-848-754A-8879	Sequence 8879, Ap
555	12.6	45.0	38	10	US-09-780-533A-3971	Sequence 3971, Ap	Sequence 3971, Ap	12.2	43.6	48	10	US-09-930-423-4374	Sequence 4374, Ap
556	12.6	45.0	38	10	US-09-776-474-1735	Sequence 1735, Ap	Sequence 1735, Ap	12.2	43.6	48	10	US-09-745-237A-4374	Sequence 4374, Ap
557	12.6	45.0	38	16	US-10-138-674-10145	Sequence 10145, A	Sequence 10145, A	12.2	43.6	48	15	US-10-230-006-2432	Sequence 2432, Ap
558	12.6	45.0	38	16	US-10-138-674-10145	Sequence 10145, A	Sequence 10145, A	12.2	43.6	48	15	US-10-131-827-5092	Sequence 5092, Ap
559	12.6	45.0	38	17	US-10-287-949A-10145	Sequence 10145, A	Sequence 10145, A	12.2	43.6	50	16	US-10-131-827-6091	Sequence 6091, Ap
560	12.6	45.0	38	17	US-10-287-949A-13003	Sequence 13003, A	Sequence 13003, A	12	42.9	13	10	US-09-740-332-4631	Sequence 4631, Ap
561	12.6	45.0	40	17	US-10-339-674-1854	Sequence 1854, Ap	Sequence 1854, Ap	12	42.9	13	10	US-09-740-332-4631	Sequence 4631, Ap
562	12.6	45.0	41	16	US-10-035-833A-3082	Sequence 3082, Ap	Sequence 3082, Ap	12	42.9	13	10	US-09-740-332-4741	Sequence 4741, Ap
563	12.6	45.0	41	16	US-10-035-833A-3082	Sequence 3082, Ap	Sequence 3082, Ap	12	42.9	13	10	US-09-817-879-4615	Sequence 4615, Ap
564	12.6	45.0	41	16	US-09-961-077-7	Sequence 7, Appli	Sequence 7, Appli	12	42.9	13	10	US-09-817-879-4631	Sequence 4631, Ap
565	12.6	45.0	42	10	US-10-339-674-1011	Sequence 1011, Ap	Sequence 1011, Ap	12	42.9	13	10	US-09-817-879-4741	Sequence 4741, Ap
566	12.6	45.0	43	15	US-10-339-674-395	Sequence 395, App	Sequence 395, App	12	42.9	13	10	US-10-669-841-7208	Sequence 7208, Ap
567	12.6	45.0	44	15	US-10-339-674-396	Sequence 396, App	Sequence 396, App	12	42.9	13	17	US-10-669-841-7224	Sequence 7224, Ap
568	12.6	45.0	44	15	US-10-339-674-397	Sequence 397, App	Sequence 397, App	12	42.9	13	17	US-10-669-841-7234	Sequence 7234, Ap
569	12.6	45.0	44	15	US-10-339-674-397	Sequence 397, App	Sequence 397, App	12	42.9	13	17	US-10-669-841-7334	Sequence 7334, Ap
570	12.6	45.0	44	15	US-10-339-674-398	Sequence 398, App	Sequence 398, App	12	42.9	14	16	US-10-332-626-2	Sequence 2, Appli
571	12.6	45.0	45	9	US-09-925-922-15	Sequence 15, Appl	Sequence 15, Appl	12	42.9	15	9	US-09-504-231A-1541	Sequence 1541, Ap
572	12.6	45.0	45	15	US-10-339-674-65	Sequence 65, Appl	Sequence 65, Appl	12	42.9	15	9	US-09-274-533D-1541	Sequence 1541, Ap
573	12.6	45.0	46	15	US-10-339-674-65	Sequence 65, Appl	Sequence 65, Appl	12	42.9	15	9	US-09-740-332-4494	Sequence 4494, Ap
574	12.6	45.0	46	15	US-10-339-674-63	Sequence 63, Appl	Sequence 63, Appl	12	42.9	17	10	US-09-817-879-4494	Sequence 4494, Ap
575	12.6	45.0	46	15	US-10-339-674-63	Sequence 63, Appl	Sequence 63, Appl	12	42.9	17	10	US-09-817-879-4494	Sequence 7087, Ap
576	12.6	45.0	46	15	US-10-339-674-64	Sequence 64, Appl	Sequence 64, Appl	12	42.9	17	17	US-10-669-841-7087	Sequence 11, Appl
577	12.6	45.0	50	16	US-10-131-827-1659	Sequence 1659, Ap	Sequence 1659, Ap	12	42.9	19	18	US-10-667-271-11	Sequence 11, Appl
578	12.6	45.0	50	16	US-10-131-827-3714	Sequence 3714, Ap	Sequence 3714, Ap	12	42.9	19	18	US-10-667-271-50	Sequence 50, Appl
579	12.4	44.3	18	15	US-10-322-138-39	Sequence 39, Appl	Sequence 39, Appl	12	42.9	19	18	US-10-667-271-707	Sequence 707, App
580	12.4	44.3	25	14	US-10-215-112-4165	Sequence 4165, Ap	Sequence 4165, Ap	12	42.9	19	18	US-10-667-271-746	Sequence 746, App
581	12.4	44.3	25	14	US-10-215-112-13965	Sequence 13965, A	Sequence 13965, A	12	42.9	20	15	US-10-159-266-55	Sequence 55, Appl
582	12.4	44.3	25	15	US-10-098-263B-1850	Sequence 1850, Ap	Sequence 1850, Ap	12	42.9	20	15	US-10-159-266-129	Sequence 129, App
583	12.4	44.3	25	15	US-10-098-263B-45266	Sequence 45266, A	Sequence 45266, A	12	42.9	20	16	US-10-361-725A-26	Sequence 26, Appl
584	12.4	44.3	25	17	US-10-098-263B-54862	Sequence 54862, A	Sequence 54862, A	12	42.9	20	17	US-10-688-706-1356	Sequence 1356, Ap
585	12.4	44.3	25	17	US-10-098-263B-54862	Sequence 54862, A	Sequence 54862, A	12	42.9	20	17	US-10-619-739-179	Sequence 179, App
586	12.4	44.3	38	10	US-09-780-533A-3878	Sequence 3878, Ap	Sequence 3878, Ap	12	42.9	21	16	US-09-940-185-2236	Sequence 2236, Ap
587	12.4	44.3	38	10	US-09-848-754A-4077	Sequence 4077, Ap	Sequence 4077, Ap	12	42.9	24	15	US-10-388-848-18	Sequence 18, Appl
588	12.4	44.3	38	10	US-09-930-423-2287	Sequence 2287, Ap	Sequence 2287, Ap	12	42.9	24	15	US-09-754-853A-743	Sequence 743, App
589	12.4	44.3	38	10	US-09-930-423-2505	Sequence 2505, Ap	Sequence 2505, Ap	12	42.9	25	14	US-10-215-112-5155	Sequence 5155, Ap
590	12.4	44.3	38	10	US-09-792-818-1264	Sequence 1264, Ap	Sequence 1264, Ap	12	42.9	25	14	US-10-215-112-5999	Sequence 9999, Ap
591	12.4	44.3	38	10	US-09-792-818-1298	Sequence 1298, Ap	Sequence 1298, Ap	12	42.9	25	15	US-10-098-263B-22554	Sequence 22554, A
592	12.4	44.3	38	10	US-09-745-237A-2287	Sequence 2287, Ap	Sequence 2287, Ap	12	42.9	25	15	US-10-098-263B-41536	Sequence 41536, A
593	12.4	44.3	38	10	US-09-745-237A-2505	Sequence 2505, Ap	Sequence 2505, Ap	12	42.9	25	15	US-10-098-263B-44720	Sequence 44720, A
594	12.4	44.3	38	16	US-10-342-502-2602	Sequence 2602, Ap	Sequence 2602, Ap	12	42.9	25	15	US-10-098-263B-58505	Sequence 58505, A
595	12.4	44.3	38	16	US-10-342-502-2602	Sequence 2602, Ap	Sequence 2602, Ap	12	42.9	25	15	US-10-098-263B-72959	Sequence 72959, A
596	12.4	44.3	38	16	US-10-138-674-9483	Sequence 9483, A	Sequence 9483, A	12	42.9	25	15	US-10-098-263B-99323	Sequence 99323, A
597	12.4	44.3	38	16	US-10-138-674-11231	Sequence 11231, A	Sequence 11231, A	12	42.9	25	15	US-10-098-263B-99323	Sequence 99323, A

c 670	12	42.9	25	18	US-10-427-696-196	Sequence 196, App	743	12	42.9	50	9	US-09-990-436-251	Sequence 251, App
671	12	42.9	28	16	US-10-069-040-14	Sequence 14, Appl	744	12	42.9	50	9	US-09-993-687-251	Sequence 251, App
672	12	42.9	29	17	US-10-670-863-13	Sequence 13, Appl	745	12	42.9	50	10	US-09-989-734-251	Sequence 251, App
c 673	12	42.9	30	9	US-09-901-484A-170	Sequence 170, App	746	12	42.9	50	10	US-09-997-653-251	Sequence 251, App
c 674	12	42.9	30	9	US-09-853-526-170	Sequence 170, App	747	12	42.9	50	10	US-09-989-724-251	Sequence 251, App
675	12	42.9	30	14	US-10-131-591A-69	Sequence 69, Appl	748	12	42.9	50	10	US-09-989-728-251	Sequence 251, App
676	12	42.9	30	15	US-10-251-385-161	Sequence 161, App	749	12	42.9	50	10	US-09-990-441-251	Sequence 251, App
c 677	12	42.9	30	17	US-10-676-248B-160	Sequence 160, App	750	12	42.9	50	10	US-09-993-667-251	Sequence 251, App
c 678	12	42.9	30	18	US-10-811-248-46	Sequence 46, Appl	751	12	42.9	50	10	US-09-997-428-251	Sequence 251, App
679	12	42.9	31	9	US-09-801-274-649	Sequence 649, App	752	12	42.9	50	10	US-09-997-666-251	Sequence 251, App
680	12	42.9	31	10	US-09-826-509-66	Sequence 66, Appl	753	12	42.9	50	10	US-09-990-438-251	Sequence 251, App
c 681	12	42.9	33	15	US-10-153-401-60	Sequence 60, Appl	754	12	42.9	50	10	US-09-990-563-251	Sequence 251, App
c 682	12	42.9	34	16	US-10-343-289-3	Sequence 3, Appli	755	12	42.9	50	10	US-09-990-711-251	Sequence 251, App
683	12	42.9	36	9	US-09-504-231A-1792	Sequence 1792, Ap	756	12	42.9	50	10	US-09-989-726-251	Sequence 251, App
684	12	42.9	36	9	US-09-504-231A-1874	Sequence 1874, Ap	757	12	42.9	50	10	US-09-998-156-251	Sequence 251, App
685	12	42.9	36	9	US-09-504-231A-2388	Sequence 2388, Ap	758	12	42.9	50	10	US-09-990-437-251	Sequence 251, App
686	12	42.9	36	9	US-09-274-553D-1792	Sequence 1792, Ap	759	12	42.9	50	10	US-09-991-157-251	Sequence 251, App
687	12	42.9	36	9	US-09-274-553D-1874	Sequence 1874, Ap	760	12	42.9	50	10	US-09-997-514-251	Sequence 251, App
688	12	42.9	36	9	US-09-274-553D-2388	Sequence 2388, Ap	761	12	42.9	50	10	US-09-997-573-251	Sequence 251, App
689	12	42.9	37	14	US-10-124-880-53	Sequence 53, Appl	762	12	42.9	50	10	US-09-991-172-251	Sequence 251, App
690	12	42.9	38	9	US-09-864-785-929	Sequence 929, App	763	12	42.9	50	10	US-09-990-726-251	Sequence 251, App
691	12	42.9	38	9	US-09-864-785-1121	Sequence 1121, Ap	764	12	42.9	50	10	US-09-997-559-251	Sequence 251, App
692	12	42.9	38	10	US-09-780-533A-2777	Sequence 2777, Ap	765	12	42.9	50	10	US-09-997-601-251	Sequence 251, App
693	12	42.9	38	10	US-09-780-533A-3003	Sequence 3003, Ap	766	12	42.9	50	10	US-09-990-443-251	Sequence 251, App
694	12	42.9	38	10	US-09-780-533A-3940	Sequence 3940, Ap	767	12	42.9	50	10	US-09-991-854-251	Sequence 251, App
695	12	42.9	38	10	US-09-927-046-2417	Sequence 2417, Ap	768	12	42.9	50	10	US-09-997-628-251	Sequence 251, App
696	12	42.9	38	10	US-09-877-478-3729	Sequence 3729, Ap	769	12	42.9	50	10	US-09-997-683-251	Sequence 251, App
697	12	42.9	38	10	US-09-848-754A-5406	Sequence 5406, Ap	770	12	42.9	50	10	US-09-989-729A-251	Sequence 251, App
698	12	42.9	38	10	US-09-780-164-1588	Sequence 1588, Ap	771	12	42.9	50	10	US-09-997-349-251	Sequence 251, App
699	12	42.9	38	16	US-10-342-902-3729	Sequence 3729, Ap	772	12	42.9	50	10	US-09-997-440-251	Sequence 251, App
700	12	42.9	38	16	US-10-138-674-11764	Sequence 11764, A	773	12	42.9	50	10	US-09-990-440-251	Sequence 251, App
701	12	42.9	38	17	US-10-287-949A-11764	Sequence 11764, A	774	12	42.9	50	10	US-09-997-857-251	Sequence 251, App
702	12	42.9	38	17	US-10-712-672-2804	Sequence 2804, Ap	775	12	42.9	50	10	US-09-993-469-251	Sequence 251, App
703	12	42.9	38	17	US-10-712-672-3219	Sequence 3219, Ap	776	12	42.9	50	10	US-09-997-542-251	Sequence 251, App
704	12	42.9	38	17	US-10-712-672-3609	Sequence 3609, Ap	777	12	42.9	50	10	US-09-997-748-251	Sequence 251, App
705	12	42.9	38	17	US-10-712-672-3709	Sequence 3709, Ap	778	12	42.9	50	10	US-09-990-439-251	Sequence 251, App
706	12	42.9	38	17	US-10-669-841-8620	Sequence 8620, Ap	779	12	42.9	50	10	US-09-989-328-251	Sequence 251, App
c 707	12	42.9	39	10	US-09-846-903-36	Sequence 36, Appl	780	12	42.9	50	10	US-09-993-583-251	Sequence 251, App
c 708	12	42.9	39	17	US-10-660-208-36	Sequence 36, Appl	781	12	42.9	50	10	US-09-941-992-251	Sequence 251, App
709	12	42.9	40	18	US-10-469-851-208	Sequence 208, App	782	12	42.9	50	10	US-09-997-333-251	Sequence 251, App
c 710	12	42.9	41	16	US-10-035-833A-1145	Sequence 1145, Ap	783	12	42.9	50	10	US-09-992-521-251	Sequence 251, App
c 711	12	42.9	41	16	US-10-035-833A-1146	Sequence 1146, Ap	784	12	42.9	50	10	US-09-997-384-251	Sequence 251, App
c 712	12	42.9	41	16	US-10-035-833A-1367	Sequence 1367, Ap	785	12	42.9	50	10	US-09-998-041-251	Sequence 251, App
c 713	12	42.9	41	16	US-10-035-833A-3493	Sequence 3493, Ap	786	12	42.9	50	10	US-09-997-585-251	Sequence 251, App
c 714	12	42.9	41	16	US-10-035-833A-3494	Sequence 3494, Ap	787	12	42.9	50	10	US-09-997-614-251	Sequence 251, App
c 715	12	42.9	41	16	US-10-035-833A-4159	Sequence 4159, Ap	788	12	42.9	50	10	US-09-989-862-251	Sequence 251, App
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c 717	12	42.9	44	15	US-10-339-674-3354	Sequence 3354, Ap	790	12	42.9	50	10	US-09-989-725-251	Sequence 251, App
c 718	12	42.9	45	16	US-10-361-208-160	Sequence 160, App	791	12	42.9	50	10	US-09-991-150-251	Sequence 251, App
c 719	12	42.9	46	15	US-10-361-208-161	Sequence 161, App	792	12	42.9	50	10	US-09-997-641-251	Sequence 251, App
720	12	42.9	46	15	US-10-137-473-23	Sequence 23, Appl	793	12	42.9	50	10	US-09-989-733-251	Sequence 251, App
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c 723	12	42.9	47	16	US-10-349-143-281	Sequence 281, App	796	12	42.9	50	16	US-10-131-827-724	Sequence 724, App
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731	12	42.9	50	9	US-09-991-073-251	Sequence 251, App	804	11.8	42.1	18	16	US-10-108-260A-5426	Sequence 4, Appli
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739	12	42.9	50	9	US-09-989-293A-251	Sequence 251, App	812	11.8	42.1	21	15	US-10-210-556-175	Sequence 774, App
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c 963 11.6 41.4 32 15 US-10-339-674-1042 Sequence 1042, Ap
c 964 11.6 41.4 33 10 US-09-826-509-80 Sequence 80, Appl
c 965 11.6 41.4 34 15 US-10-339-674-3241 Sequence 3241, Ap
c 966 11.6 41.4 35 15 US-10-339-674-3240 Sequence 3240, Ap
c 967 11.6 41.4 36 9 US-09-504-231A-1765 Sequence 1765, Ap
c 968 11.6 41.4 36 9 US-09-274-553D-1765 Sequence 1765, Ap
c 969 11.6 41.4 36 15 US-10-084-814-16 Sequence 16, Appl
c 970 11.6 41.4 36 15 US-10-261-159-3 Sequence 3, Appl
c 971 11.6 41.4 36 16 US-10-462-128-16 Sequence 16, Appl
c 972 11.6 41.4 36 17 US-10-712-672-4407 Sequence 4407, Ap
c 973 11.6 41.4 36 17 US-10-712-672-4495 Sequence 4495, Ap
c 974 11.6 41.4 37 10 US-09-846-430A-2 Sequence 2, Appl
c 975 11.6 41.4 37 14 US-10-085-906-270 Sequence 270, App
c 976 11.6 41.4 38 10 US-09-927-046-2456 Sequence 2456, Ap
c 977 11.6 41.4 38 10 US-09-927-046-3010 Sequence 3010, Ap
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c 983 11.6 41.4 38 10 US-09-776-474-1477 Sequence 1477, Ap
c 984 11.6 41.4 38 10 US-09-930-423-2143 Sequence 2143, Ap
c 985 11.6 41.4 38 10 US-09-745-237A-2143 Sequence 2143, Ap
c 986 11.6 41.4 38 15 US-10-261-159-6 Sequence 6, Appl
c 987 11.6 41.4 38 15 US-10-261-159-9 Sequence 9, Appl
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c 990 11.6 41.4 38 15 US-10-261-159-18 Sequence 18, Appl
c 991 11.6 41.4 38 15 US-10-230-006-1087 Sequence 1087, Ap
c 992 11.6 41.4 38 15 US-10-230-006-1102 Sequence 1102, Ap
c 993 11.6 41.4 38 15 US-10-230-006-1147 Sequence 1147, Ap
c 994 11.6 41.4 38 16 US-10-342-902-2830 Sequence 2830, Ap
c 995 11.6 41.4 38 16 US-10-342-902-3538 Sequence 3538, Ap
c 996 11.6 41.4 38 17 US-10-712-672-2947 Sequence 2947, Ap
c 997 11.6 41.4 38 17 US-10-712-672-3843 Sequence 3843, Ap
c 998 11.6 41.4 38 17 US-10-712-672-7721 Sequence 7721, Ap
c 999 11.6 41.4 38 17 US-10-669-841-8429 Sequence 8429, Ap
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ALIGNMENTS

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RESULT 1
US-10-087-631B-7
; Sequence 7, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: sequence
US-10-087-631B-7
Query Match 100.0%; Score 28; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCAAGCACCCCTATCAGGCAGTACCACAA 28
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DB 1 GCAAGCACCCCTATCAGGCAGTACCACAA 28

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RESULT 2
US-10-419-022-7
; Sequence 7, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; TITLE OF INVENTION: CONTROL
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ST778 HCV-specific primer
; OTHER INFORMATION: sequence
US-10-419-022-7
Query Match 100.0%; Score 28; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCAAGCACCCCTATCAGGCAGTACCACAA 28

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RESULT 3
US-10-147-679A-16
; Sequence 16, Application US/10147679A
; Publication No. US2003024366A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Riedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; TITLE OF INVENTION: and uses thereof
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide (HCV reverse)
; NAME/KEY: modified_base
; LOCATION: (28)
; OTHER INFORMATION: derivatization with a p-(t-butyl)benzyl-residue
US-10-147-679A-16
Query Match 100.0%; Score 28; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCAAGCACCCCTATCAGGCAGTACCACAA 28
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DB 1 GCAAGCACCCCTATCAGGCAGTACCACAA 28

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RESULT 4

US-10-225-501-11/c
; Sequence 11, Application US/10225501
; Publication No. US20030059443A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Molecular Interaction Sites Of Hepatitis C Virus RNA And Methods
; FILE REFERENCE: IBIS0428
; CURRENT APPLICATION NUMBER: US/10/225,501
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/314,236
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-225-501-11

Query Match 89.3%; Score 25; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCACCCTATCAGGCAGTACCA 25
Db 25 GCAGCACCCTATCAGGCAGTACCA 1
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RESULT 5

US-10-667-271-1398/c
; Sequence 1398, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1398
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq

; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq

US-10-667-271-1398

Query Match 82.1%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCCCTATCAGGCAGTACCACA 28
Db 23 CACCCCTATCAGGCAGTACCACA 1
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RESULT 6

US-10-667-271-1404/c
; Sequence 1404, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq

US-10-667-271-1404

Query Match 82.1%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCACCCCTATCAGGCAGTACCACA 27
Db 23 GCACCCCTATCAGGCAGTACCACA 1
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RESULT 7

US-10-667-271-1405/c
; Sequence 1405, Application US/10667271

Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (WBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1406
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq
US-10-667-271-1406

Query Match 82.1%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGCACCCCTATCAGGCAGTACCA 25
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Db 23 AGCACCCCTATCAGGCAGTACCA 1

RESULT 9
US-10-667-271-1407/c
Sequence 1407, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (WBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1407

Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (WBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1405
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq
US-10-667-271-1405

Query Match 82.1%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCACCCCTATCAGGCAGTACCA 26
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Db 23 AGCACCCCTATCAGGCAGTACCA 1

RESULT 8
US-10-667-271-1406/c
Sequence 1406, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (WBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26

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; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-1407

Query Match      82.1%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGCACCTATCAGGCAGTACC 24
Db 23 CAAGCACCTATCAGGCAGTACC 1

RESULT 10
US-10-182-126-6
; Sequence 6, Application US/10182126
; Publication No. US20030175691A1
; GENERAL INFORMATION:
; APPLICANT: ELAISSARI, Abdelhamid
; APPLICANT: MANDRAND, Bernard
; APPLICANT: DELAIR, Thierry
; APPLICANT: SPENCER, Doran
; APPLICANT: ARKIS, Ahmend
; TITLE OF INVENTION: METHOD FOR ISOLATING PROTEINS OR PROTEIN AND NUCLEIC ACID ASSOCIA
; TITLE OF INVENTION: PARTICLE AND PROTEIN COMPLEXES, REAGENTS AND USES.
; FILE REFERENCE: 113339
; CURRENT APPLICATION NUMBER: US/10/182,126
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/FR01/00205
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: FR 00.00862
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-182-126-6

Query Match      82.1%; Score 23; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTAC 23
Db 5 GCAAGCACCTATCAGGCAGTAC 27

RESULT 11
US-10-182-126-8
; Sequence 8, Application US/10182126
; Publication No. US20030175691A1
; GENERAL INFORMATION:
; APPLICANT: ELAISSARI, Abdelhamid
; APPLICANT: MANDRAND, Bernard
; APPLICANT: DELAIR, Thierry
; APPLICANT: SPENCER, Doran
; APPLICANT: ARKIS, Ahmend
; TITLE OF INVENTION: METHOD FOR ISOLATING PROTEINS OR PROTEIN AND NUCLEIC ACID ASSOCIA
; TITLE OF INVENTION: PARTICLE AND PROTEIN COMPLEXES, REAGENTS AND USES.
; FILE REFERENCE: 113339
; CURRENT APPLICATION NUMBER: US/10/182,126
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/FR01/00205
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: FR 00.00862
; PRIOR FILING DATE: 2000-01-21
```

```
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-182-126-8

Query Match      82.1%; Score 23; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTAC 23
Db 5 GCAAGCACCTATCAGGCAGTAC 27

RESULT 12
US-10-667-271-1399/c
; Sequence 1399, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrisey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1399
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-1399

Query Match      78.6%; Score 22; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCTATCAGGCAGTACCACAA 28
Db 23 ACCCTATCAGGCAGTACCACAA 2
```

```
RESULT 13
US-10-667-271-1408/c
; Sequence 1408, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/359,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1408
; TYPE: RNA
; LENGTH: 23
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA sense re
US-10-667-271-1408

Query Match 78.6%; Score 22; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 14
US-09-877-526A-10/c
; Sequence 10, Application US/09877526A
; Patent No. US20020102568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid Ca
; FILE REFERENCE: MBHB00-816-C (700/0002)
; CURRENT APPLICATION NUMBER: US/09/877,526A

Query Match 78.6%; Score 22; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 15
US-09-992-160-10/c
; Sequence 10, Application US/09992160
; Publication No. US20030008295A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Nucleic Acid Sensor Molecules
; FILE REFERENCE: MBHB00-816-D (700/004)
; CURRENT APPLICATION NUMBER: US/09/992,160
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic target signaling
US-09-992-160-10

Query Match 78.6%; Score 22; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 16
US-10-056-761-10/c
; Sequence 10, Application US/10056761
; Publication No. US20030065155A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
```

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; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic target signaling
US-09-877-526A-10

Query Match 78.6%; Score 22; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 15
US-09-992-160-10/c
; Sequence 10, Application US/09992160
; Publication No. US20030008295A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Nucleic Acid Sensor Molecules
; FILE REFERENCE: MBHB00-816-D (700/004)
; CURRENT APPLICATION NUMBER: US/09/992,160
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic target signaling
US-09-992-160-10

Query Match 78.6%; Score 22; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 16
US-10-056-761-10/c
; Sequence 10, Application US/10056761
; Publication No. US20030065155A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
```


; TITLE OF INVENTION: Nucleic Acid Sensor Molecules

; FILE REFERENCE: MBH00-816-E (700/005)

; CURRENT APPLICATION NUMBER: US/10/056,761

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 10

; LENGTH: 27

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Target Signaling

US-10-056-761-10

Query Match

Best Local Similarity 78.6%; Score 22; DB 14; Length 27;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22

Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 17

US-10-422-050-10/c

; Sequence 10, Application US/10422050

; Publication No. US20040009510A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Seiwert, Scott

; APPLICANT: Zinnen, Shawn

; APPLICANT: Vaish, Narendra

; APPLICANT: Jadhav, Vasant

; APPLICANT: Kossen, Karl

; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules

; FILE REFERENCE: 700/013 (MEHB 00-816-M)

; CURRENT APPLICATION NUMBER: US/10/422,050

; PRIOR FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: PCT/US 02/35529

; PRIOR FILING DATE: 2002-11-05

; PRIOR APPLICATION NUMBER: US 10/286,492

; PRIOR FILING DATE: 2002-11-01

; PRIOR APPLICATION NUMBER: US 10/283,858

; PRIOR FILING DATE: 2002-10-30

; PRIOR APPLICATION NUMBER: US 10/056,761

; PRIOR FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 09/992,160

; PRIOR FILING DATE: 2002-11-05

; PRIOR APPLICATION NUMBER: US 09/877,526

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 09/800,594

; PRIOR FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: US 60/187,128

; PRIOR FILING DATE: 2000-03-06

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 27

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Target Signaling

US-10-422-050-10

Query Match

Best Local Similarity 78.6%; Score 22; DB 16; Length 27;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22

Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 18

US-09-464-426A-4

; Sequence 4, Application US/09464426A

; Publication No. US20020119122A1

; GENERAL INFORMATION:

; APPLICANT: Scalgis, Carlos O., Albrecht, Janice K., and Glue, Paul W.

; TITLE OF INVENTION: Ribavirin- Pegylated Interferon-Alfa

; INDICATION: HCV Combination Therapy

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schering-Plough Corporation

; STREET: 2000 Galloping Hill Road

; CITY: Kenilworth

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07033

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: 7.5.3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/464,426A

; FILING DATE: 16-Dec-1999

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Hoffman, Thomas D.

; REGISTRATION NUMBER: 28,221

; REFERENCE/DOCKET NUMBER: IN0964Q

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-298-5037

; TELEFAX: 908-298-5388

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (Oligonucleotide)

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-464-426A-4

Query Match 75.0%; Score 21; DB 9; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGCAGTACCACAA 28

Db 1 CCCTATCAGCAGTACCACAA 21

RESULT 19

US-09-981-215-4

; Sequence 4, Application US/09981215

; Patent No. US2002012703A1

; GENERAL INFORMATION:

; APPLICANT: Albrecht, Janice K.

; TITLE OF INVENTION: Ribavirin-Pegylated Interferon Alfa

; INDICATION: HCV Combination Therapy

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schering-Plough Corporation

; STREET: 2000 Galloping Hill Road

; CITY: Kenilworth

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07033

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: 7.5.3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/981,215

; FILING DATE: 16-Oct-2001

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoffman, Thomas D.
REGISTRATION NUMBER: 28,221
REFERENCE/DOCKET NUMBER: IN01344
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-5037
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-981-215-4

Query Match 75.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCCTATCAGCAGTACCACAA 28
|||||
DB 1 CCCTATCAGCAGTACCACAA 21

RESULT 20
US-10-444-853A-194/c
; Sequence 194, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194

LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-194
Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CCCTATCAGCAGTACCACAA 28
|||||
DB 21 CCCTATCAGCAGTACCACAA 1
RESULT 21
US-10-444-853A-195/c
; Sequence 195, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-195

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCTATCAGGCAGTACCACA 27
 Db 21 ACCCTATCAGGCAGTACCACA 1

RESULT 22

US-10-444-853A-196/c

; Sequence 196, Application US/10444853A

; Publication No. US20040192626A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Haerberli, Peter

; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid

; APPLICANT: Macejak, Dennis

; APPLICANT: Zinnen, Shawn

; APPLICANT: Pavco, Pamela

; APPLICANT: Morrissey, David

; APPLICANT: Fosnaugh, Kathy

; APPLICANT: Mokler, Victor

; APPLICANT: Jamison, Sharon

; APPLICANT: Vaish, Nerendra

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using

; FILE REFERENCE: 400/114 (MBHB03-465)

; CURRENT APPLICATION NUMBER: US/10/444, 853A

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: US 10/417,012

; PRIOR FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: PCT/US03/05346

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT/US03/05028

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 196

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region

US-10-444-853A-196

Query Match

Best Local Similarity 75.0%; Score 21; DB 18; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

6 CACCCCTATCAGGCAGTACCAC 26

|||||

Db 21 CACCCCTATCAGGCAGTACCAC 1

RESULT 23

US-10-444-853A-203

; Sequence 203, Application US/10444853A

; Publication No. US20040192626A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Haerberli, Peter

; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid

; APPLICANT: Macejak, Dennis

; APPLICANT: Zinnen, Shawn

; APPLICANT: Pavco, Pamela

; APPLICANT: Morrissey, David

; APPLICANT: Fosnaugh, Kathy

; APPLICANT: Mokler, Victor

; APPLICANT: Jamison, Sharon

; APPLICANT: Vaish, Nerendra

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using

; FILE REFERENCE: 400/114 (MBHB03-465)

; CURRENT APPLICATION NUMBER: US/10/444, 853A

; CURRENT FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: US 10/417,012

; PRIOR FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: PCT/US03/05346

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT/US03/05028

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 203

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-444-853A-203

Query Match

Best Local Similarity 75.0%; Score 21; DB 18; Length 21;

Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY

8 CCCTATCAGGCAGTACCACAA 28

|||||

Db 1 CCCUACAGGCAGUACCACAA 21

RESULT 24

US-10-667-271-1451/c

; Sequence 1451, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBHB02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

US-10-667-271-1452/c

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTATCAGCAGTACCACA 27
DB 21 ACCTATCAGCAGTACCACA 1

RESULT 26

US-10-667-271-1453/c

Sequence 1453, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1453
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1452

US-10-667-271-1452/c

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCCTATCAGCAGTACCACAA 28
DB 21 CCCTATCAGCAGTACCACAA 1

RESULT 25

US-10-667-271-1452/c

Sequence 1452, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1451
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1451

```
RESULT 27
US-10-667-271-1460
; Sequence 1460, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1460
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1460

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
| | | | | | | | | | | | | | | | | | | | |
Db 1 CCCUACAGGCAGUACCACAA 21

RESULT 28
US-10-667-271-1400/c
; Sequence 1400, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1460
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1460

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
| | | | | | | | | | | | | | | | | | | | |
Db 1 CCCUACAGGCAGUACCACAA 21

RESULT 29
US-10-667-271-1409/c
; Sequence 1409, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1400
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
```

```

; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1409
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA sense re
US-10-667-271-1409

Query Match          75.0%; Score 21; DB 18; Length 23;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
DB 21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 30
US-09-880-945-2/c
; Sequence 2, Application US/09880945
; Patent No. US20020037868A1
; GENERAL INFORMATION:
; APPLICANT: BUDKOWSKA, Agata
; APPLICANT: MAILLARD, Patrick
; APPLICANT: BRONNERT, Christian
; APPLICANT: GOUNON, Pierre
; APPLICANT: NITKIEWICZ, Jadwiga
; APPLICANT: GRAINIC, Radu
; TITLE OF INVENTION: METHOD OF DETECTING HEPATITIS C
; FILE REFERENCE: 210017USOCIP
; CURRENT APPLICATION NUMBER: US/09/880,945
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US09/549,685
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US60/129,319
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-880-945-2

Query Match          75.0%; Score 21; DB 9; Length 24;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
DB 21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 31
US-09-549-685A-2/c
; Sequence 2, Application US/09549685A
; Publication No. US20030022155A1
; GENERAL INFORMATION:
; APPLICANT: BUDKOWSKA, AGATA
; APPLICANT: MAILLARD, PATRICK
; APPLICANT: NITKIEWICZ, JADWIGA
; APPLICANT: CRAINIC, RADU
; TITLE OF INVENTION: METHOD FOR DETECTING HEPATITIS C VIRUS WITH HYBRIDOMAS
; FILE REFERENCE: 0660-0175-0
; CURRENT APPLICATION NUMBER: US/09/549,685A
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,319

```

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; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
US-09-549-685A-2

Query Match          75.0%; Score 21; DB 10; Length 24;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
DB 21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 32
US-10-120-013-8
; Sequence 8, Application US/10120013
; Publication No. US20020192689A1
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; DuBois, David
; Brown, David
; Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/120,013
; FILING DATE: 10-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMB1:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-120-013-8

Query Match          75.0%; Score 21; DB 13; Length 24;

```

```
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 33
US-10-011-855-2
; Sequence 2, Application US/10011855
; Publication No. US20030104582A1
; GENERAL INFORMATION:
; APPLICANT: BAUMANN, RUSSELL
; APPLICANT: HAMDAN, HASNAH
; APPLICANT: LEWINSKI, MICHAEL
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS FOR DETECTING HEPATITIS C
; FILE REFERENCE: 034827/0702
; CURRENT APPLICATION NUMBER: US/10/011,855
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-10-011-855-2

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 34
US-10-037-990-2
; Sequence 2, Application US/10037990
; Publication No. US20030124654A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Vijay
; APPLICANT: Kondiboyina, Venkat Ramana
; TITLE OF INVENTION: Method and Device for the Rapid Clinical Diagnosis of Hepatitis C
; FILE REFERENCE: Infection in Biological Samples
; FILE REFERENCE: RELIA P-106
; CURRENT APPLICATION NUMBER: US/10/037,990
; CURRENT FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-037-990-2

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 35
US-10-230-381-34/c
; Sequence 34, Application US/10230381
```

```
; Publication No. US20030152591A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New hepatitis C virus genotype 13, and its use as prophylactic,
; FILE REFERENCE: INHX-124-EP
; CURRENT APPLICATION NUMBER: US/10/230,381
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: HCP# 666
US-10-230-381-34

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 21 GCAAGCACCTTATCAGGCAGT 1

RESULT 36
US-10-007-389-5
; Sequence 5, Application US/10007389
; Publication No. US20030165855A1
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-007-389-5

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 37
US-10-322-138-2
; Sequence 2, Application US/10322138
; Publication No. US2003017565A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Christoph
; APPLICANT: Haberhausen, Gerd
; APPLICANT: Bartl, Knut
; APPLICANT: Orum, Henrik
```

```
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS
; FILE REFERENCE: 4817/OQ
; CURRENT APPLICATION NUMBER: US/10/322,138
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/530,746B
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amplification primer
US-10-322-138-2

Query Match          75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAAGCACCCCTATCAGGCAGT 21
        |||||
Db       4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 38
US-10-396-964-51/c
; Sequence 51, Application US/10396964
; Publication No. US20030198946A1
; GENERAL INFORMATION:
; APPLICANT: Simmonds, Peter
; APPLICANT: Chan, Shiu-Wan
; APPLICANT: Yap, Peng L.
; TITLE OF INVENTION: Hepatitis-C Virus Testing
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: NO. US20030198946A1th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/396,964
; FILING DATE: 23-MARCH-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,116B
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02143
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
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; DESCRIPTION: oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis-C virus
US-10-396-964-51

Query Match          75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAAGCACCCCTATCAGGCAGT 21
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Db       21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 39
US-10-147-679A-6
; Sequence 6, Application US/10147679A
; Publication No. US20030224366A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Riedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; FILE OF INVENTION: and uses thereof
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide primer (HCV reverse)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-147-679A-6

Query Match          75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAAGCACCCCTATCAGGCAGT 21
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Db       4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 40
US-10-655-508-5
; Sequence 5, Application US/10655508
; Publication No. US20040063155A1
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE OF INVENTION: components using a protease from a Bacillus strain
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/655,508
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/10/007,389
; PRIOR FILING DATE: CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-655-508-5
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Query Match      75.0%; Score 21; DB 16; Length 24;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  GCAAGCACCTTATCAGGCAGT 21
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Db      4  GCAAGCACCTTATCAGGCAGT 24
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Search completed: November 24, 2004, 03:42:51
Job time : 139.396 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1342.43 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-7
Perfect score: 28
Sequence: 1 gcaagcaccctatcagcgatgacacaa 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gssi.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	13.8	49.3	38	8	A2437906 1M0226A08
C 3	13.8	49.3	45	8	A2402707 1M0170E08
C 4	13.8	49.3	50	7	CK136536 MM2_2_1_C
C 5	13.8	49.3	50	8	BH903991 SALK_1037
C 6	13.6	48.6	42	9	AU981240 Danilo rer
C 7	13.4	47.9	47	1	AV965348 AV965348
C 8	13.2	47.1	28	1	AA932343 oo60c02.s
C 9	13.2	47.1	32	8	A2434394 1M0220F13
C 10	13.2	47.1	40	8	A2775335 2M0007G07
C 11	13.2	47.1	49	1	AI445901 tj6eh01.x
C 12	13.2	47.1	49	1	AI965799 sc7ee01.y
C 13	13	46.4	32	9	CL210926 A027F07 G
C 14	13	46.4	40	9	AG192612 Pan trogl
C 15	13	46.4	41	8	A2768376 1M0568P14
C 16	13	46.4	41	9	CG887124 RRS785_Ba
C 17	12.8	45.7	30	5	BK625891 BX25891
C 18	12.8	45.7	37	1	AI077338 oy65902.x
C 19	12.8	45.7	37	1	AI917811 wb53c07.x
C 20	12.8	45.7	38	9	CL679725 PRI0126G
C 21	12.8	45.7	40	8	CC183071 XG571_Bay
C 22	12.8	45.7	42	8	A2329441 1M0053M07
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C 24	12.8	45.7	47	8	A2797405 2M0053D08

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CR397867	Arabidops
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C 99	11.6	41.4	43	9	TA388D01P	AL498777 T. brucei	172	11.2	40.0	46	9	HSKC04F12	X88481 H. sapiens D
C 100	11.6	41.4	45	8	BH911078	BH911078 SALK_0649	C 173	11.2	40.0	47	8	AZ488215	AZ488215 1M0318D20
C 101	11.6	41.4	46	6	CF334549	CF334549 JMT--03-O	C 174	11.2	40.0	47	8	AZ618994	AZ618994 1M0451C11
C 102	11.6	41.4	46	8	AZ324779	AZ324779 1M046D22	C 175	11.2	40.0	47	8	AZ769994	AZ769994 1M0571A14
C 103	11.6	41.4	46	8	AQ254727	AQ254727 EP(3)3520	C 176	11.2	40.0	47	8	BH851581	BH851581 SALK_0732
C 104	11.6	41.4	47	8	AZ584664	AZ584664 1M038A22	C 177	11.2	40.0	48	2	BF507210	BF507210 3659P-23
C 105	11.6	41.4	49	8	AZ497375	AZ497375 1M0334N1	C 178	11.2	40.0	48	2	AW497611	AW497611 RARGGSB34
C 106	11.6	41.4	49	8	AZ950523	AZ950523 2M0214G12	C 179	11.2	40.0	49	2	AY356299	AY356299 AY356299
C 107	11.6	41.4	50	1	AU103419	AU103419 AU103419	C 180	11.2	40.0	49	2	BE778801	BE778801 601463874
C 108	11.6	41.4	50	1	AU105582	AU105582 AU105582	C 181	11.2	40.0	49	2	AZ812510	AZ812510 2M0079A17
C 109	11.6	41.4	50	1	AU107620	AU107620 AU107620	C 182	11.2	40.0	50	1	AU1539113	AU1539113 CP78811.X
C 110	11.6	41.4	50	4	BH75539	BH75539 YW14H12.S1	C 183	11.2	40.0	50	1	AU103947	AU103947 AU103947
C 111	11.6	41.4	50	7	CG710737	CG710737 1119018F0	C 184	11.2	40.0	50	1	AU104141	AU104141 AU104141
C 112	11.6	41.4	50	9	AZ436588	AZ436588 1M0224H20	C 185	11.2	40.0	50	1	AU104173	AU104173 AU104173
C 113	11.4	40.7	24	8	AZ436588	N81476 TGESTZY47H0	C 186	11.2	40.0	50	1	AU106817	AU106817 AU106817
C 114	11.4	40.7	28	7	N81476	AZ592432 1M0403C19	C 187	11.2	40.0	50	1	AU107948	AU107948 AU107948
C 115	11.4	40.7	31	8	AZ592432	BH863404 SALK_0938	C 188	11.2	40.0	50	1	AU107953	AU107953 AU107953
C 116	11.4	40.7	35	8	BH863404	BH863405 SALK_0938	C 189	11.2	40.0	50	1	AU107959	AU107959 AU107959
C 117	11.4	40.7	35	8	BH863405	R37960 YC99G06.S1	C 190	11.2	40.0	50	1	AU107960	AU107960 AU107960
C 118	11.4	40.7	36	7	R37960	BF507311 8949P-20	C 191	11.2	40.0	50	1	AU107961	AU107961 AU107961
C 119	11.4	40.7	38	2	BF507311	AZ603310 1M0422N12	C 192	11.2	40.0	50	8	BH644632	BH644632 1008053H0
C 120	11.4	40.7	39	8	AZ603310	AZ992328 2M0276N21	C 193	11.2	40.0	50	9	CR035505	CR035505 Forward s
C 121	11.4	40.7	41	8	AZ992328	AZ770047 1M0571B19	C 194	11.2	40.0	50	9	CR210504	CR210504 Reverse s
C 122	11.4	40.7	42	8	AZ770047	AJ550295 AJ550295	C 195	11.2	40.0	50	9	CL437542	CL437542 PST5824-N
C 123	11.4	40.7	43	1	AJ550295	AA008276 mg9608.r	C 196	11.2	40.0	50	8	AZ815189	AZ815189 2M0083116
C 124	11.4	40.7	46	1	AA008276	C00602 HUMGS000814	C 197	11.2	40.0	50	8	AZ774487	AZ774487 2M0004D01
C 125	11.4	40.7	46	6	C00602	BZ353134 SALK_1198	C 198	11.2	40.0	50	8	TA174H12P	TA174H12P 2M0202E01
C 126	11.4	40.7	46	9	BZ353134	AG189289 Pan trogl	C 199	11.2	40.0	50	8	CF328601	CF328601 T. brucei
C 127	11.4	40.7	46	9	AG189289	AV970199 AV970199	C 200	11.2	40.0	50	8	AL416615	AL416615 NACL--03-
C 128	11.4	40.7	47	1	AV970199	H39908 y054b03.r1	C 201	11.2	40.0	50	8	AZ661810	AZ661810 1M0540M06
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C 131	11.4	40.7	49	1	AI743359	AZ639320 1M0499E15	C 204	11.2	40.0	50	8	AA112707	AA112707 zn70h11.s
C 132	11.4	40.7	49	8	AZ639320	AU104921 AU104921	C 205	11.2	40.0	50	8	AI437342	AI437342 fb30d01.x
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C 135	11.4	40.7	50	1	AU107067	AU107892 AU107892	C 208	11.2	40.0	50	8	AL048715	AL048715 DFPZP566G
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C 141	11.4	40.7	50	9	EX985119	AL458883 T. brucei	C 214	11.2	40.0	50	8	H62327	H62327 Yr15f04.r1
C 142	11.4	40.7	50	9	TA101G05P	AL458883 T. brucei	C 215	11.2	40.0	50	8	EZ379922	EZ379922 SALK_1142
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C 144	11.2	40.0	31	1	AA670361	AA670361 ad16607.s	C 217	11.2	40.0	50	8	AZ537206	AZ537206 AST-2P027
C 145	11.2	40.0	31	8	AZ670361	AZ348137 1M0084O12	C 218	11.2	40.0	50	8	BH641954	BH641954 1M08051F1
C 146	11.2	40.0	31	8	AZ348137	AZ823090 2M0096122	C 219	11.2	40.0	50	8	AZ509372	AZ509372 1M0352J17
C 147	11.2	40.0	32	8	AZ823090	AZ784432 2M0027E05	C 220	11.2	40.0	50	8	AZ833541	AZ833541 2M0115N08
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C 151	11.2	40.0	34	8	CC053711	AZ628011 1M0476K12	C 224	11.2	40.0	50	8	AA1389458	AA1389458 mp25e02.r
C 152	11.2	40.0	36	8	AA628011	AA625816 zv87a04.s	C 225	11.2	40.0	50	8	W07483	W07483 za96d11.r1
C 153	11.2	40.0	37	1	AA625816	CC053707 SALK_0469	C 226	11.2	40.0	50	8	AZ768227	AZ768227 1M0568C08
C 154	11.2	40.0	37	8	CC053707	AL497988 T. brucei	C 227	11.2	40.0	50	8	AZ795793	AZ795793 2M0051007
C 155	11.2	40.0	37	9	TA338E12Q	BJ082050 BJ082050	C 228	11.2	40.0	50	8	BH909849	BH909849 SALK_0562
C 156	11.2	40.0	39	4	BJ082050	AZ428906 1M0212C14	C 229	11.2	40.0	50	8	CC886323	CC886323 SALK_1484
C 157	11.2	40.0	39	8	AZ428906	AI766423 wh49H03.x	C 230	11.2	40.0	50	8	AZ801261	AZ801261 2M0059H08
C 158	11.2	40.0	40	1	AI766423	AJ600768 Arabidops	C 231	11.2	40.0	50	8	BI094799	BI094799 EP(2)-CD34N
C 159	11.2	40.0	40	9	AJ600768	AG203784 Pan trogl	C 232	11.2	40.0	50	8	AZ300919	AZ300919 EP(2)0882
C 160	11.2	40.0	40	9	AG203784	BE872091 601448183	C 233	11.2	40.0	50	8	AZ759426	AZ759426 1M0551113
C 161	11.2	40.0	41	2	BE872091	AZ335532 1M0065H05	C 234	11.2	40.0	50	8	AZ774612	AZ774612 2M0004O24
C 162	11.2	40.0	41	8	AZ335532	AZ873114 2M0196B15	C 235	11.2	40.0	50	8	AZ786390	AZ786390 2M0031E19
C 163	11.2	40.0	41	8	AZ873114	BE892628 601433437	C 236	11.2	40.0	50	8	AL464659	AL464659 T. brucei
C 164	11.2	40.0	42	1	BE892628	AI047023 uh57e09.r	C 237	11.2	40.0	50	8	AZ333191	AZ333191 1M0062F09
C 165	11.2	40.0	43	1	AI047023	AQ025179 EP(3)1110	C 238	11.2	40.0	50	8	BZ591175	BZ591175 3590_1.82
C 166	11.2	40.0	43	8	AQ025179	AJ599570 Arabidops	C 239	11.2	40.0	50	8	AJ600891	AJ600891 Arabidops
C 167	11.2	40.0	43	9	AJ599570	CG740003 S1LB06a25	C 240	11.2	40.0	50	8	CG807819	CG807819 1118087C0
C 168	11.2	40.0	44	7	CG740003	CG709849 1119015B0	C 241	11.2	40.0	50	8	AU102447	AU102447 AU102447
C 169	11.2	40.0	44	9	CG709849	CG709873 1119015C0	C 242	11.2	40.0	50	1		
C 170	11.2	40.0	44	9	CG709873		C 243	11.2	40.0	50	1		

C 244	11	39.3	50	1	AUI03013	AUI03013	317	10.8	38.6	50	1	AUI05458	AUI05458
C 245	11	39.3	50	1	AUI03014	AUI03014	318	10.8	38.6	50	1	AUI05460	AUI05460
C 246	11	39.3	50	1	AUI04142	AUI04142	319	10.8	38.6	50	1	AUI05461	AUI05461
C 247	11	39.3	50	1	AUI06298	AUI06298	320	10.8	38.6	50	1	AUI05462	AUI05462
C 248	11	39.3	50	1	AUI07101	AUI07101	321	10.8	38.6	50	1	AUI05464	AUI05464
C 249	11	39.3	50	8	A2875367	2M0189024	322	10.8	38.6	50	1	AUI05467	AUI05467
C 250	11	39.3	50	8	A2875367	2M0189024	323	10.8	38.6	50	1	AUI05468	AUI05468
C 251	11	39.3	50	8	B2664361	SALK_0706	324	10.8	38.6	50	1	AUI05469	AUI05469
C 252	11	39.3	50	9	BX293332	Arabidops	325	10.8	38.6	50	1	AUI05470	AUI05470
C 253	11	39.3	50	9	CL518432	SAB9F09 F	C 326	10.8	38.6	50	1	AUI07175	AUI07175
C 254	10.8	38.6	21	8	A2460367	1M0265J10	C 327	10.8	38.6	50	1	AUI07265	AUI07265
C 255	10.8	38.6	23	8	A2316364	1M0420P1f	C 328	10.8	38.6	50	1	AUI07266	AUI07266
C 256	10.8	38.6	27	8	A2303426	1M0003A09	C 329	10.8	38.6	50	1	AUI07267	AUI07267
C 257	10.8	38.6	28	7	T72278	Yc65H03.s1	C 330	10.8	38.6	50	1	AUI07268	AUI07268
C 258	10.8	38.6	28	8	A2432111	1M0217E05	C 331	10.8	38.6	50	1	AUI07269	AUI07269
C 259	10.8	38.6	29	8	BH846412	SALK_0078	C 332	10.8	38.6	50	1	AUI07270	AUI07270
C 260	10.8	38.6	29	9	CL661015	PR10138c	C 333	10.8	38.6	50	1	AUI07271	AUI07271
C 261	10.8	38.6	30	8	A2601864	1M0420P1f	C 334	10.8	38.6	50	1	AUI07272	AUI07272
C 262	10.8	38.6	32	9	CL524584	DAA9C01 F	C 335	10.8	38.6	50	1	AUI07273	AUI07273
C 263	10.8	38.6	33	8	A2641117	1M0503A06	C 336	10.8	38.6	50	1	AUI07274	AUI07274
C 264	10.8	38.6	34	1	A1796749	wal4d11.x	C 337	10.8	38.6	50	1	AUI07275	AUI07275
C 265	10.8	38.6	34	8	A2422317	1M0200007	C 338	10.8	38.6	50	1	AUI07276	AUI07276
C 266	10.8	38.6	35	2	BE909856	601496143	C 339	10.8	38.6	50	4	B3036965	B3036965
C 267	10.8	38.6	35	7	N73542	z850B02.s1	C 340	10.8	38.6	50	7	N70569	N70569
C 268	10.8	38.6	37	1	AA492333	ng81C07.s	C 341	10.8	38.6	50	9	BX662452	BX662452
C 269	10.8	38.6	37	2	AW245295	2820036.3	C 342	10.8	38.6	50	9	EX895538	EX895538
C 270	10.8	38.6	37	8	A2506198	1M0347C12	C 343	10.8	38.6	50	9	CR134688	Forward s
C 271	10.8	38.6	38	8	A2998182	2M0285D01	C 344	10.6	37.9	21	8	CR888380	SALK_1517
C 272	10.8	38.6	39	1	AV836734	AV836734	C 345	10.6	37.9	24	4	AZ805948	2M0067R12
C 273	10.8	38.6	39	7	B1087730	602852286	C 346	10.6	37.9	29	8	BH853496	BH853496
C 274	10.8	38.6	39	7	U44319	ENU44319 As	C 347	10.6	37.9	30	8	AQ026392	1(3)82976
C 275	10.8	38.6	39	9	TA306D11P		C 348	10.6	37.9	33	9	BX662497	Arabidops
C 276	10.8	38.6	40	8	BZ589649	3590_1.71	C 349	10.6	37.9	33	8	AZ784633	2M0027J23
C 277	10.8	38.6	41	6	CF298687	7LEAF--02	C 350	10.6	37.9	33	8	AZ482042	1M0306C20
C 278	10.8	38.6	41	6	CF300723	7LEAF--05	C 351	10.6	37.9	33	9	N67043	z850e12.s1
C 279	10.8	38.6	41	8	A2327077	1M0050C16	C 352	10.6	37.9	34	1	BX662497	Arabidops
C 280	10.8	38.6	41	8	A2645689	1M0511H16	C 353	10.6	37.9	34	1	AA798808	vn43d09.r
C 281	10.8	38.6	41	8	A2767690	1M0567003	C 354	10.6	37.9	34	1	A1790112	ue64902.r
C 282	10.8	38.6	42	6	CS8084	CS8084_Yuji	C 355	10.6	37.9	34	1	AA237815	mx29a05.r
C 283	10.8	38.6	42	8	A2492152	1M0326B09	C 356	10.6	37.9	34	8	AZ491530	1M0325H09
C 284	10.8	38.6	42	9	AG190850	Pan trogl	C 357	10.6	37.9	36	7	CF973738	PSU Joeca
C 285	10.8	38.6	43	1	A1004121	ot54a09.s	C 358	10.6	37.9	36	8	AZ308346	1M0011C14
C 286	10.8	38.6	43	1	A1795121	sb77a11.y	C 359	10.6	37.9	36	8	BZ383557	SALK_1341
C 287	10.8	38.6	43	1	AJ649066	AJ649066	C 360	10.6	37.9	37	8	AZ381090	1M0137J20
C 288	10.8	38.6	43	9	CL436351	FL27795-N	C 361	10.6	37.9	37	8	BZ383548	SALK_1340
C 289	10.8	38.6	44	6	CF298909	7LEAF--02	C 362	10.6	37.9	38	1	AJ648502	AJ648502
C 290	10.8	38.6	44	8	A2823752	2M0098A04	C 363	10.6	37.9	38	6	CL1982	HUMGS000400
C 291	10.8	38.6	44	9	A28242197	Lotus cor	C 364	10.6	37.9	38	9	CR400428	Arabidops
C 292	10.8	38.6	45	1	AV960508	AV960508	C 365	10.6	37.9	38	9	CL528419	ASV10F01
C 293	10.8	38.6	45	8	A2310900	1M0026N04	C 366	10.6	37.9	39	4	B1559436	603252932
C 294	10.8	38.6	45	8	A2796408	2M0052E12	C 367	10.6	37.9	39	4	B1838507	603083494
C 295	10.8	38.6	46	1	A1019594	uag1a06.r	C 368	10.6	37.9	39	6	CF113888	Shultzomi
C 296	10.8	38.6	46	1	A1144303	qb59h11.x	C 369	10.6	37.9	39	6	CF290826	14ROOT--0
C 297	10.8	38.6	46	1	AA145519	ms06f11.r	C 370	10.6	37.9	39	8	AZ663490	1M0543G11
C 298	10.8	38.6	46	8	A2498067	1M0335J12	C 371	10.6	37.9	39	1	AJ598250	Arabidops
C 299	10.8	38.6	46	8	AZ781445	2M0019N18	C 372	10.6	37.9	40	1	AA746897	nx69a09.s
C 300	10.8	38.6	46	8	BH171419	SALK_0042	C 373	10.6	37.9	40	1	AA937425	oxj9b08.s
C 301	10.8	38.6	46	8	BH611947	BH611947	C 374	10.6	37.9	40	1	A1318679	ta49g08.x
C 302	10.8	38.6	46	9	DR85D1T	Lotus rer	C 375	10.6	37.9	40	7	H79514	YU49g02.s1
C 303	10.8	38.6	47	8	A2308567	1M0016F07	C 376	10.6	37.9	40	8	AZ346802	1M0082011
C 304	10.8	38.6	47	8	BZ768669	SALK_1405	C 377	10.6	37.9	41	8	AZ436596	1M0224122
C 305	10.8	38.6	47	9	AL940725	Arabidops	C 378	10.6	37.9	41	9	EX203165	Danilo rer
C 306	10.8	38.6	48	7	U44313	ENU44313 As	C 379	10.6	37.9	42	8	AZ383427	1M0141N02
C 307	10.8	38.6	48	7	W10946	ms46b10.r1	C 380	10.6	37.9	43	1	AL669008	AL669008
C 308	10.8	38.6	48	8	AZ784814	2M0028M02	C 381	10.6	37.9	43	1	AA613679	no38b05.s
C 309	10.8	38.6	48	8	AZ805973	2M0067M10	C 382	10.6	37.9	44	8	AZ760412	1M0554110
C 310	10.8	38.6	48	8	BZ766237	SALK_1369	C 383	10.6	37.9	44	9	TA308F05Q	AL489136 T. brucei
C 311	10.8	38.6	49	1	AA995234	ou17a05.s	C 384	10.6	37.9	44	9	CG721761	111906BHO
C 312	10.8	38.6	49	7	CN752480	ApHL3LD-I	C 385	10.6	37.9	44	9	CG722451	1119072A1
C 313	10.8	38.6	50	1	AUI02362	AUI02362	C 386	10.6	37.9	45	1	AA276118	vc36d12.r
C 314	10.8	38.6	50	1	AUI02695	AUI02695	C 387	10.6	37.9	45	6	CF054916	CF054916
C 315	10.8	38.6	50	1	AUI02702	AUI02702	C 388	10.6	37.9	46	1	AA722219	zh21a09.s
C 316	10.8	38.6	50	1	AUI03416	AUI03416	C 389	10.6	37.9	46	1	AI545027	Fb75907.x

C 390	10.6	37.9	46	4	BI829941	BI829941	6030800075
C 391	10.6	37.9	46	8	AZ759592	AZ759592	1M0552D23
C 392	10.6	37.9	46	8	AZ792431	AZ792431	2M0043E21
C 393	10.6	37.9	46	8	AZ821566	AZ821566	2M00094F21
C 394	10.6	37.9	46	8	BX831992	BX831992	2M0112L06
C 395	10.6	37.9	46	9	AZ231478	Danio rer	BX231478
C 396	10.6	37.9	46	9	CG722939	CG722939	1119074B0
C 397	10.6	37.9	47	1	AS570265	AS570265	nf39F06.s
C 398	10.6	37.9	47	9	CG716081	CG716081	1119044E0
C 399	10.6	37.9	47	9	CL665793	CL665793	PR10144_A
C 400	10.6	37.9	48	1	AA602253	AA602253	np13d01.s
C 401	10.6	37.9	48	8	AZ496155	AZ496155	1M0332K15
C 402	10.6	37.9	48	8	BZ290752	BZ290752	SALK 0912
C 403	10.6	37.9	49	1	AA936278	AA936278	AJ75e07.s
C 404	10.6	37.9	49	1	AJ746758	AJ746758	AJ746758
C 405	10.6	37.9	49	4	BG099459	BG099459	na944e02.
C 406	10.6	37.9	49	4	BI113311	BI113311	602900277
C 407	10.6	37.9	49	4	BI873153	BI873153	603397612
C 408	10.6	37.9	49	6	CAB45431	CAB45431	hab99911.
C 409	10.6	37.9	49	7	H14049	H14049	vm35h05.r1
C 410	10.6	37.9	49	9	CG799286	CG799286	1118001F0
C 411	10.6	37.9	50	1	AU102669	AU102669	AU102669
C 412	10.6	37.9	50	1	AU102768	AU102768	AU102768
C 413	10.6	37.9	50	1	AU102773	AU102773	AU102773
C 414	10.6	37.9	50	1	AU102788	AU102788	AU102788
C 415	10.6	37.9	50	1	AU102792	AU102792	AU102792
C 416	10.6	37.9	50	1	AU103069	AU103069	AU103069
C 417	10.6	37.9	50	1	AU103147	AU103147	AU103147
C 418	10.6	37.9	50	1	AU104386	AU104386	AU104386
C 419	10.6	37.9	50	1	AU104854	AU104854	AU104854
C 420	10.6	37.9	50	1	AU107087	AU107087	AU107087
C 421	10.6	37.9	50	1	AA589316	AA589316	vm36402.z
C 422	10.6	37.9	50	7	D20656	D20656	HUMG501632
C 423	10.6	37.9	50	8	CA456525	CA456525	SALK 0989
C 424	10.6	37.9	50	8	AZ379036	AZ379036	1M0134L02
C 425	10.4	37.1	22	1	AI269362	AI269362	qj74g03.x
C 426	10.4	37.1	22	9	TA134810Q	TA134810Q	AI466318
C 427	10.4	37.1	22	9	TA70811Q	TA70811Q	T. brucei
C 428	10.4	37.1	24	6	CF329168	CF329168	AI458140
C 429	10.4	37.1	25	9	TA133B01P	TA133B01P	T. brucei
C 430	10.4	37.1	26	8	AZ435264	AZ435264	AI463977
C 431	10.4	37.1	26	9	TA129A07P	TA129A07P	AI4598234
C 432	10.4	37.1	29	8	AZ598234	AZ598234	1M0412023
C 433	10.4	37.1	30	9	AZ598234	AZ598234	Arabidops
C 434	10.4	37.1	31	1	AJ97593242	AJ97593242	Arabidops
C 435	10.4	37.1	31	1	AJ977899	AJ977899	oq62b09.s
C 436	10.4	37.1	31	9	CG707724	CG707724	11190003E1
C 437	10.4	37.1	31	9	CG707746	CG707746	11190003F0
C 438	10.4	37.1	31	9	CL682876	CL682876	PR10135b
C 439	10.4	37.1	32	1	AJ790259	AJ790259	AJ790259
C 440	10.4	37.1	32	8	AZ513928	AZ513928	1M0360G

463	10.4	37.1	40	1	AI580193
464	10.4	37.1	40	2	BE900485
465	10.4	37.1	40	4	BI087982
466	10.4	37.1	40	7	D44765
467	10.4	37.1	40	8	AZ579120
468	10.4	37.1	40	8	AZ581085
469	10.4	37.1	40	8	AZ974232
470	10.4	37.1	40	8	BZ381549
471	10.4	37.1	41	4	BG395476
472	10.4	37.1	41	6	CA965602
473	10.4	37.1	42	2	BE395464
474	10.4	37.1	42	8	CC457759
475	10.4	37.1	42	9	CL528325
476	10.4	37.1	43	1	AJ666336
477	10.4	37.1	43	4	BG707367
478	10.4	37.1	43	8	BH810200
479	10.4	37.1	43	8	BH910812
480	10.4	37.1	43	8	CC054159
481	10.4	37.1	44	8	AZ451728
482	10.4	37.1	44	9	CR361095
483	10.4	37.1	45	2	BE393504
484	10.4	37.1	45	8	AZ435105
485	10.4	37.1	45	8	AZ599531
486	10.4	37.1	45	8	CC037777
487	10.4	37.1	45	9	EX287762
488	10.4	37.1	45	9	CNS070VN
489	10.4	37.1	46	2	BE884491
490	10.4	37.1	46	4	BM393789
491	10.4	37.1	46	4	AZ496495
492	10.4	37.1	46	8	AZ946495
493	10.4	37.1	46	9	AJ588687
494	10.4	37.1	46	9	AJ950183
495	10.4	37.1	46	9	CL528347
496	10.4	37.1	47	9	BE652088
497	10.4	37.1	47	7	CF060824
498	10.4	37.1	47	9	AL942689
499	10.4	37.1	47	9	AL942689
500	10.4	37.1	48	9	CC886067
501	10.4	37.1	48	9	C1832686
502	10.4	37.1	49	1	AZ250141
503	10.4	37.1	49	1	AZ250141
504	10.4	37.1	49	5	BQ796164
505	10.4	37.1	49	8	AZ780575
506	10.4	37.1	49	9	CR356331
507	10.4	37.1	49	9	CR394781
508	10.4	37.1	49	9	HSNC17B04
509	10.4	37.1	50	1	AUI02323
510	10.4	37.1	50	1	AUI07621
511	10.4	37.1	50	1	AUI07622
512	10.4	37.1	50	1	AUI07623
513	10.4	37.1	50	1	AUI07890
514	10.4	37.1	50	1	AUI07936
515	10.4	37.1	50	2	AW271141
516	10.4	37.1	50	2	AW302109
517	10.4	37.1	50	5	AX621473
518	10.4	37.1	50	5	AZ435198
519	10.4	37.1	50	8	AZ626779
520	10.2	36.4	22	8	TA220811P
521	10.2	36.4	22	8	AZ623379
522	10.2	36.4	23	8	TA269C11Q
523	10.2	36.4	23	8	AZ813287
524	10.2	36.4	24	8	AZ797981
525	10.2	36.4	25	8	AG190823
526	10.2	36.4	26	1	AU255927
527	10.2	36.4	26	8	BH998885
528	10.2	36.4	27	6	CF310421
529	10.2	36.4	27	8	AZ331472
530	10.2	36.4	28	8	AZ473218
531	10.2	36.4	28	8	AL610699
532	10.2	36.4	28	9	CL662194
533	10.2	36.4	29	8	AZ623273
534	10.2	36.4	29	8	BZ764664
535	10.2	36.4	29	8	BE764664

536	10.2	36.4	30	9	AG204931	Pan trogl	609	10.2	36.4	49	1	AI185705	AI185705 qe6h06.x
c 537	10.2	36.4	31	8	AG794691	2M0048N04	c 610	10.2	36.4	49	1	AJ649956	AJ649956 AJ649956
538	10.2	36.4	32	9	CG720047	1L1906D00	611	10.2	36.4	49	1	AA410762	AA410762 zt35ell.r
c 539	10.2	36.4	33	8	AG287802	2M0140P14	c 612	10.2	36.4	49	2	BF203474	BF203474 601865731
c 540	10.2	36.4	34	1	AA889919	aj87g07.s	613	10.2	36.4	49	4	BG099520	BG099520 nag53c01
541	10.2	36.4	34	1	AI367422	qW18h03.x	c 614	10.2	36.4	49	7	D18209	D18209 MUSGS00479
c 542	10.2	36.4	34	4	BH396017	5009-0-15	c 615	10.2	36.4	49	7	HI4959	HI4959 ym19c11.s
c 543	10.2	36.4	34	6	CA587274	LBE10p42	c 616	10.2	36.4	49	7	H28255	H28255 y16e03.r1
c 544	10.2	36.4	34	8	AZ761910	1M0556C05	c 617	10.2	36.4	49	7	T56757	T56757 ya71d06.r1
c 545	10.2	36.4	34	8	AZ804148	2M0064G23	618	10.2	36.4	49	8	AZ578707	AZ578707 26C12 Sho
546	10.2	36.4	35	8	AZ48253	1M0245013	619	10.2	36.4	49	8	AZ615333	AZ615333 1M0444D09
547	10.2	36.4	35	9	DME545696	Drocephil	c 620	10.2	36.4	49	9	BX120175	BX120175 Danilo rer
c 548	10.2	36.4	36	9	CC888822	SALK_1524	c 621	10.2	36.4	50	1	AJ652427	AJ652427 AJ652427
c 549	10.2	36.4	37	1	AI790648	u103a07.x	c 622	10.2	36.4	50	1	AUI02661	AUI02661 AUI02661
c 550	10.2	36.4	37	8	AZ444497	1M0239A16	623	10.2	36.4	50	1	AUI02956	AUI02956 AUI02956
c 551	10.2	36.4	37	8	AZ789783	2M0037H19	c 624	10.2	36.4	50	1	AUI03410	AUI03410 AUI03410
c 552	10.2	36.4	37	8	AZ972111	2M0245A22	c 625	10.2	36.4	50	1	AUI03415	AUI03415 AUI03415
553	10.2	36.4	37	8	CC053865	CC053865 SALK_0494	c 626	10.2	36.4	50	1	AUI03418	AUI03418 AUI03418
c 554	10.2	36.4	37	9	DR43028	AL977257 Danilo rer	c 627	10.2	36.4	50	1	AUI05156	AUI05156 AUI05156
c 555	10.2	36.4	38	1	AB088499	AB088499	c 628	10.2	36.4	50	1	AUI05553	AUI05553 AUI05553
556	10.2	36.4	38	4	BG912318	602806861	c 629	10.2	36.4	50	1	AUI05839	AUI05839 AUI05839
c 557	10.2	36.4	38	4	AZ811787	2M0078N06	630	10.2	36.4	50	1	AUI07908	AUI07908 AUI07908
c 558	10.2	36.4	39	2	BE874819	601488760	631	10.2	36.4	50	1	AUI07909	AUI07909 AUI07909
c 559	10.2	36.4	40	1	AA160572	zq46d11.x	632	10.2	36.4	50	1	AUI07910	AUI07910 AUI07910
560	10.2	36.4	40	2	BF026645	BF026645 601672360	633	10.2	36.4	50	1	AUI07937	AUI07937 AUI07937
561	10.2	36.4	40	7	T18543	hbc2020 Hum	c 634	10.2	36.4	50	2	AW424126	AW424126 sh61c07.y
c 562	10.2	36.4	40	9	AL753199	AL753199 Arabidops	c 635	10.2	36.4	50	8	AZ765968	AZ765968 1M0563M12
c 563	10.2	36.4	40	9	TA253H01Q	TA253H01Q	c 636	10.2	36.4	50	8	AZ862310	AZ862310 2M0169022
c 564	10.2	36.4	41	8	AZ612511	AL483109 T. brucei	c 637	10.2	36.4	50	9	BX123067	BX123067 Danilo rer
c 565	10.2	36.4	41	1	AA976917	CG869712	638	10.2	36.4	50	9	CR236244	CR236244 Forward s
c 566	10.2	36.4	41	1	AI568481	AI568481 tn39g09.x	c 639	10.2	36.4	50	9	AG194315	AG194315 Pan trogl
567	10.2	36.4	41	8	AF039768	AF039768	c 640	10.2	36.4	50	6	CD531370	CD531370 10103 Ara
c 568	10.2	36.4	41	8	AZ612511	AZ612511 1M0439006	c 641	10.2	36.4	50	21	TA45803Q	TA45803Q T. brucei
569	10.2	36.4	42	7	R84748	R84748 vt68h09.r1	642	10.2	36.4	50	9	BG896918	BG896918 HOA59-1-B
c 570	10.2	36.4	42	8	AZ815699	AZ815699 2M0084C13	643	10.2	36.4	50	9	AJ587708	AJ587708 Arabidops
c 571	10.2	36.4	42	9	BX157082	BX157082 Danilo rer	644	10.2	36.4	50	9	AZ599552	AZ599552 AU259952
572	10.2	36.4	42	9	AB082313	AB082313 Drocephil	c 645	10.2	36.4	50	8	AZ307549	AZ307549 1M0009024
c 573	10.2	36.4	42	9	AG203402	AG203402 Pan trogl	c 646	10.2	36.4	50	8	AZ318715	AZ318715 1M0038D08
574	10.2	36.4	43	1	AA020994	AA020994 ua98e01.r	647	10.2	36.4	50	26	AA974354	AA974354 cq14f03.s
c 575	10.2	36.4	43	9	CG779709	CG779709 123033E0	648	10.2	36.4	50	8	AI218854	AI218854 qg75g06.x
c 576	10.2	36.4	43	9	CL212287	CL212287 G037D05.G	649	10.2	36.4	50	8	AZ647786	AZ647786 1M0514P23
577	10.2	36.4	44	7	H39421	H39421 DR115 IFNG	c 650	10.2	36.4	50	8	AZ661529	AZ661529 1M0540U01
c 578	10.2	36.4	44	7	H97472	H97472 yw1b07.b1	c 651	10.2	36.4	50	8	BH901129	BH901129 SALK_0731
c 579	10.2	36.4	44	7	T68451	T68451 yc42f02.b1	c 652	10.2	36.4	50	8	BZ769424	BZ769424 SALK_1421
c 580	10.2	36.4	44	8	BH811570	BH811570 SALK_0591	653	10.2	36.4	50	31	AI256721	AI256721 AU256721
c 581	10.2	36.4	44	8	BZ663210	BZ663210 SALK_0268	654	10.2	36.4	50	31	AZ789801	AZ789801 2M0037L19
c 582	10.2	36.4	44	9	TA83E04Q	TA83E04Q	c 655	10.2	36.4	50	31	BX893918	BX893918 Arabidops
c 583	10.2	36.4	45	8	BH862028	BH862028 603390903	c 656	10.2	36.4	50	31	BE316607	BE316607 601903146
c 584	10.2	36.4	45	8	BH848020	BH848020 SALK_0673	c 657	10.2	36.4	50	32	BE277972	BE277972 601179981
585	10.2	36.4	46	1	AA027616	AA027616 m108c08.r	658	10.2	36.4	50	32	T92842	T92842 ye27a08.r1
c 586	10.2	36.4	46	1	AA062105	AA062105 mj84d05.r	c 659	10.2	36.4	50	32	T92842	T92842 ye27a08.r1
587	10.2	36.4	46	1	AA906763	AA906763 oi16a08.s	660	10.2	36.4	50	32	BE277972	BE277972 601179981
c 588	10.2	36.4	46	1	AI021500	AI021500 ub12f02.r	661	10.2	36.4	50	32	BE277972	BE277972 601179981
c 589	10.2	36.4	46	1	AI182421	AI182421 uc24h04.r	c 662	10.2	36.4	50	32	T92842	T92842 ye27a08.r1
c 590	10.2	36.4	46	2	BE778884	BE778884 601465146	663	10.2	36.4	50	32	T92842	T92842 ye27a08.r1
c 591	10.2	36.4	46	8	BH848546	BH848546 SALK_0685	664	10.2	36.4	50	32	T92842	T92842 ye27a08.r1
c 592	10.2	36.4	47	9	BX658078	BX658078 Arabidops	665	10.2	36.4	50	32	TA326F02Q	TA326F02Q T. brucei
c 593	10.2	36.4	48	1	AA651618	AA651618 ns65g11.s	666	10.2	36.4	50	33	AZ242456	AZ242456 1M0203C09
594	10.2	36.4	48	4	BJ034532	BJ034532 BJ034532	667	10.2	36.4	50	33	AZ514079	AZ514079 1M0360F07
c 595	10.2	36.4	48	4	BM285362	BM285362 EST00003	668	10.2	36.4	50	33	AZ834737	AZ834737 2M0117006
c 596	10.2	36.4	48	4	BM493234	BM493234 EST000017	669	10.2	36.4	50	33	CC889158	CC889158 SALK_1528
c 597	10.2	36.4	48	5	BQ094078	BQ094078 040802_37	c 670	10.2	36.4	50	33	AG199552	AG199552 Pan trogl
598	10.2	36.4	48	5	BQ094080	BQ094080 040802_39	671	10.2	36.4	50	33	AG199552	AG199552 Pan trogl
c 599	10.2	36.4	48	5	BQ094081	BQ094081 040802_40	c 672	10.2	36.4	50	34	AA954884	AA954884 op20e10.s
600	10.2	36.4	48	5	BQ094082	BQ094082 040802_41	c 673	10.2	36.4	50	34	AI142664	AI142664 ok38h07.s
c 601	10.2	36.4	48	5	BQ094086	BQ094086 040802_45	674	10.2	36.4	50	34	BJ040736	BJ040736 BJ040736
602	10.2	36.4	48	5	BQ094088	BQ094088 040802_47	c 675	10.2	36.4	50	34	BX659099	BX659099 Arabidops
603	10.2	36.4	48	5	BQ094090	BQ094090 Danilo rer	c 676	10.2	36.4	50	34	TA196C06P	TA196C06P T. brucei
604	10.2	36.4	48	9	CL517714	CL517714 SAA6A01.F	c 677	10.2	36.4	50	35	AL044927	AL044927 DKFPz434N
c 605	10.2	36.4	48	9	CL528747	CL528747 ASV7F07.F	678	10.2	36.4	50	35	BH812616	BH812616 SALK_0621
606	10.2	36.4	49	1	AA870263	AA870263 vq13g11.r	c 679	10.2	36.4	50	36	BG765238	BG765238 602738656
c 607	10.2	36.4	49	1	AA990502	AA990502 ua62g06.s	680	10.2	36.4	50	36	BX654718	BX654718 Arabidops
c 608	10.2	36.4	49	1	AI052522	AI052522 oz27f05.x	c 681	10.2	36.4	50	36	CL684480	CL684480 PRI0139c_

682	10	35.7	37	1	AA706652	AA706652 ag90g06.i	c 755	10	35.7	49	1	AA717442	AA717442 vvl9406.i
683	10	35.7	37	1	A1047840	A1047840 u64a04.x	756	10	35.7	49	1	A1098407	A1098407 uc05d10.i
684	10	35.7	37	1	A1119228	A1119228 ue24a02.y	c 757	10	35.7	49	1	A1185705	A1185705 qe60h06.x
685	10	35.7	37	1	A119228	A119228 ue24a02.y	758	10	35.7	49	1	A1326039	A1326039 mr-66c09.x
686	10	35.7	38	9	A2463776	A2463776 1M0272P15	759	10	35.7	49	1	A1385645	A1385645 mq74c04.x
687	10	35.7	38	9	AG195969	AG195969 Pan trogl	c 760	10	35.7	49	1	A1719563	A1719563 as54a09.x
688	10	35.7	39	8	A2346424	A2346424 1M0081N12	761	10	35.7	49	1	A1883392	A1883392 as54a09.x
689	10	35.7	39	8	A2379756	A2379756 1M0135C12	c 762	10	35.7	49	4	BG058867	BG058867 nag43f03.
690	10	35.7	39	8	AZ797170	AZ797170 2M0053C18	763	10	35.7	49	4	BG153503	BG153503 nag43f03.
691	10	35.7	40	1	A1583366	A1583366 ts15906.x	764	10	35.7	49	6	CD533308	CD533308 31B7 Arab
692	10	35.7	40	1	A1609582	A1609582 tw28c02.x	c 765	10	35.7	49	7	CO780197	CO780197 BL0009A.A0
693	10	35.7	40	1	A1900047	A1900047 sb98b08.y	c 766	10	35.7	49	8	AZ816178	AZ816178 2M0084K18
694	10	35.7	40	1	A1959989	A1959989 sc36b11.x	c 767	10	35.7	49	8	BH802944	BH802944 1008097F1
695	10	35.7	40	1	AJ7281519	AJ7281519 4A3A-P5D7	c 768	10	35.7	49	9	CG729392	CG729392 111911G0
696	10	35.7	40	1	AV851018	AV851018 AV851018	769	10	35.7	50	1	AA798983	AA798983 vv95f06.i
697	10	35.7	40	1	CO793322	CO793322 NT017C.A0	c 770	10	35.7	50	1	AJ793098	AJ793098 AJ793098
698	10	35.7	40	8	AZ479725	AZ479725 1M0300002	c 771	10	35.7	50	1	AU103432	AU103432 AU103432
699	10	35.7	40	8	AZ490766	AZ490766 1M0323N19	c 772	10	35.7	50	1	AU103962	AU103962 AU103962
700	10	35.7	40	8	AZ810561	AZ810561 2M0076110	c 773	10	35.7	50	1	AU104241	AU104241 AU104241
701	10	35.7	40	8	BH847602	BH847602 SALK_0548	774	10	35.7	50	1	AU105497	AU105497 AU105497
702	10	35.7	40	8	BH850455	BH850455 SALK_0713	c 775	10	35.7	50	1	AU105673	AU105673 AU105673
703	10	35.7	40	8	BH850948	BH850948 SALK_0932	c 776	10	35.7	50	1	AU105680	AU105680 AU105680
704	10	35.7	40	9	BX572583	BX572583 Arabidops	c 777	10	35.7	50	1	AU105715	AU105715 AU105715
705	10	35.7	40	9	TA89E03P	TA89E03P T. brucei	c 778	10	35.7	50	1	AU105869	AU105869 AU105869
706	10	35.7	41	2	BF569468	BF569468 602185954	c 779	10	35.7	50	1	AU106784	AU106784 AU106784
707	10	35.7	41	6	CA851077	CA851077 D09H04.O0	780	10	35.7	50	1	AU107975	AU107975 AU107975
708	10	35.7	41	8	AZ951455	AZ951455 2M0215H22	781	10	35.7	50	4	BG099190	BG099190 nag48a07.
709	10	35.7	41	8	BH000491	BH000491 2M0288G22	782	10	35.7	50	4	BG153588	BG153588 nag51a07.
710	10	35.7	41	8	BZ383963	BZ383963 SALK_1348	783	10	35.7	50	4	BX733406	BX733406 BX733406
711	10	35.7	41	9	HSKC04C05	HSKC04C05 H.sapiens D	c 784	10	35.7	50	5	N75695	N75695 yw52a03.r1
712	10	35.7	41	9	TA317H07P	TA317H07P T. brucei	c 785	10	35.7	50	7	R70221	R70221 yj80f12.r1
713	10	35.7	42	6	CF300011	CF300011 7LEAF--04	786	10	35.7	50	8	AZ344473	AZ344473 1M0078F05
714	10	35.7	42	9	CL528487	CL528487 yv61b08.i	c 787	10	35.7	50	8	AZ406914	AZ406914 1M0176A24
715	10	35.7	43	1	AA920047	AA920047 yv61b08.i	788	10	35.7	50	8	AZ593037	AZ593037 1M0404B21
716	10	35.7	43	1	A1282013	A1282013 qg8c02.x	c 789	10	35.7	50	8	BH910236	BH910236 SALK_0585
717	10	35.7	43	1	A1969081	A1969081 wq71a01.x	790	10	35.7	50	8	BZ761715	BZ761715 SALK_0751
718	10	35.7	43	1	AV833356	AV833356 AV833356	c 791	10	35.7	50	9	CR220006	CR220006 Forward 8
719	10	35.7	43	5	BQ588067	BQ588067 F012337-0	792	10	35.7	50	9	CL437480	CL437480 PS75604-N
720	10	35.7	43	5	BQ593523	BQ593523 S015526-0	793	9.8	35.0	13	9	AZ486389	AZ486389 1M0314E21
721	10	35.7	43	6	CF319236	CF319236 HD--09-K1	c 794	9.8	35.0	19	8	AG201710	AG201710 Pan trogl
722	10	35.7	43	7	H62069	H62069 yu37h05.r1	795	9.8	35.0	20	9	AG201710	AG201710 Pan trogl
723	10	35.7	43	8	BH635056	BH635056 1008002C1	c 796	9.8	35.0	21	8	AZ476580	AZ476580 1M0295G04
724	10	35.7	43	8	BH907510	BH907510 SALK_0427	797	9.8	35.0	21	8	AZ75290	AZ75290 1M0128N01
725	10	35.7	43	9	AJ594917	AJ594917 Arabidops	c 798	9.8	35.0	21	8	AZ609424	AZ609424 1M0434016
726	10	35.7	43	9	AB082457	AB082457 Drosophil	c 799	9.8	35.0	21	8	AZ936357	AZ936357 2M0193F01
727	10	35.7	44	6	CF313317	CF313317 HD--01-G1	c 800	9.8	35.0	22	1	AB124816	AB124816 AB124816
728	10	35.7	44	9	CL437736	CL437736 PST6199-N	801	9.8	35.0	23	1	AB124816	AB124816 AB124816
729	10	35.7	45	8	AZ331523	AZ331523 1M0059F01	802	9.8	35.0	23	8	AZ361811	AZ361811 1M0106108
730	10	35.7	45	8	AZ589905	AZ589905 1M0393K12	c 803	9.8	35.0	23	8	AZ781193	AZ781193 1M0298N04
731	10	35.7	45	8	AZ943012	AZ943012 2M0203B02	c 804	9.8	35.0	23	8	AZ781499	AZ781499 2M0019N20
732	10	35.7	45	8	CC459052	CC459052 SALK_1238	c 805	9.8	35.0	23	8	AZ818003	AZ818003 2M0087116
733	10	35.7	46	1	AA902889	AA902889 OJ49G04.8	c 806	9.8	35.0	24	8	AZ818003	AZ818003 2M0087116
734	10	35.7	46	1	AA073235	AA073235 mm74f03.r	807	9.8	35.0	24	8	AZ824537	AZ824537 2M0099N08
735	10	35.7	46	1	A1740625	A1740625 wq23f04.x	c 808	9.8	35.0	25	8	AZ804257	AZ804257 AJ804257
736	10	35.7	46	4	AA292859	AA292859 z664f09.i	c 810	9.8	35.0	25	8	AJ804257	AJ804257 AJ804257
737	10	35.7	46	4	BI855184	BI855184 yd05d03.r1	c 811	9.8	35.0	26	1	AJ804257	AJ804257 AJ804257
738	10	35.7	46	7	T80386	T80386 yd05d03.r1	812	9.8	35.0	26	8	AJ804257	AJ804257 AJ804257
739	10	35.7	46	7	T80450	T80450 yd05d03.r1	c 813	9.8	35.0	26	8	AJ804257	AJ804257 AJ804257
740	10	35.7	46	8	AZ511075	AZ511075 1M0355N19	c 814	9.8	35.0	26	1	AJ804257	AJ804257 AJ804257
741	10	35.7	47	8	BJ084362	BJ084362 BJ084362	815	9.8	35.0	26	9	CG727937	CG727937 1119097C1
742	10	35.7	47	8	AZ818776	AZ818776 2M0099A24	c 816	9.8	35.0	26	9	CG727937	CG727937 1119097C1
743	10	35.7	47	8	AZ824937	AZ824937 2M0099A24	817	9.8	35.0	27	1	AJ666328	AJ666328 AJ666328
744	10	35.7	47	8	AZ863405	AZ863405 2M0171F05	c 818	9.8	35.0	27	1	AJ666328	AJ666328 AJ666328
745	10	35.7	47	9	AL766337	AL766337 Arabidops	819	9.8	35.0	27	8	AZ784619	AZ784619 2M0027L21
746	10	35.7	47	9	BX121019	BX121019 Danio rer	c 820	9.8	35.0	27	8	AZ784619	AZ784619 2M0027L21
747	10	35.7	47	9	CL569496	CL569496 AN0490.Sa	821	9.8	35.0	27	8	AZ784619	AZ784619 2M0027L21
748	10	35.7	48	4	BH083470	BH083470 BJ083470	c 822	9.8	35.0	27	8	AZ784619	AZ784619 2M0027L21
749	10	35.7	48	8	AZ613732	AZ613732 1M0442A17	823	9.8	35.0	28	1	A1435006	A1435006 th76g07.x
750	10	35.7	48	8	AJ595218	AJ595218 Arabidops	c 824	9.8	35.0	28	1	A1435006	A1435006 th76g07.x
751	10	35.7	48	8	AJ595218	AJ595218 Arabidops	825	9.8	35.0	28	8	AZ480444	AZ480444 1M0302A06
752	10	35.7	48	9	CG784372	CG784372 RRS387.Ba	c 826	9.8	35.0	28	8	AZ480444	AZ480444 1M0302A06
753	10	35.7	48	9	CL213195	CL213195 A031B01.G	827	9.8	35.0	28	8	AZ514563	AZ514563 1M0361N09
754	10	35.7	49	1	AA673527	AA673527 vn36f10.i	c 827	9.8	35.0	28	8	AZ774121	AZ774121 2M0003L07

C 828	9.8	35.0	29	8	BZ382171	BZ382171	SALK_1179	901	9.8	35.0	43	9	DME547032	AJ547032	Drosophil
C 829	9.8	35.0	30	8	AZ331753	AZ331753	1M059G19	C 902	9.8	35.0	44	6	C00309	C00309	HUMG000601
C 830	9.8	35.0	30	9	TA114A09Q	AL462923	T. brucei	C 903	9.8	35.0	44	6	CD530465	CD530465	06H11 Ara
C 831	9.8	35.0	30	9	TA122B10P	AL462631	T. brucei	C 904	9.8	35.0	44	8	AZ772309	1M0583P03	AZ772309
C 832	9.8	35.0	30	9	CU521134	CL521134	DAJ2H08 F	C 905	9.8	35.0	44	8	AZ862141	2M0169M04	AZ862141
C 833	9.8	35.0	31	1	A8666806	AA866806	vx90d03.r	C 906	9.8	35.0	44	8	BH864323	SALK_0957	BH864323
C 834	9.8	35.0	32	8	AZ7956042	AZ7956042	2M0051B13	C 907	9.8	35.0	44	8	BZ353313	SALK_1201	BZ353313
C 835	9.8	35.0	32	4	BG419594	BG419594	602451806	C 908	9.8	35.0	44	9	AL771575	Arabidops	AL771575
C 836	9.8	35.0	32	8	AZ467339	AZ467339	1M0278112	C 909	9.8	35.0	44	9	TA320A09Q	T. brucei	AL491821
C 837	9.8	35.0	32	8	AZ767973	AZ767973	2M0014N20	C 910	9.8	35.0	44	9	CL528676	ASV26H06	CL528676
C 838	9.8	35.0	32	9	DR10M11S	AL739302	Danio rer	C 911	9.8	35.0	44	9	AG215899	Drosophil	AG215899
C 839	9.8	35.0	32	9	TA822C07Q	AL459949	T. brucei	C 912	9.8	35.0	45	4	BI755939	603030159	BI755939
C 840	9.8	35.0	33	1	AU267504	AU267504	AU267504	C 913	9.8	35.0	45	8	CC249630	XI363 Bay	CC249630
C 841	9.8	35.0	33	8	AZ509017	AZ509017	1M0351G13	C 914	9.8	35.0	45	9	EX210693	Danio rer	EX210693
C 842	9.8	35.0	33	8	AZ6292J22	AZ6292J22	1M0482J22	C 915	9.8	35.0	45	9	CC884757	SALK_1352	CC884757
C 843	9.8	35.0	33	8	AZ461576	AZ461576	2M0139F07	C 916	9.8	35.0	46	1	AA639421	1M0583P03	AA639421
C 844	9.8	35.0	33	9	TA215H02P	AL479556	T. brucei	C 917	9.8	35.0	46	1	AA719000	zh22b04.s	AA719000
C 845	9.8	35.0	33	9	TA215H02P	AL479556	T. brucei	C 918	9.8	35.0	46	1	AA828900	od75h11.s	AA828900
C 846	9.8	35.0	34	1	AA939151	AA939151	mq07ell.s	C 919	9.8	35.0	46	1	AU014238	AU014238	AU014238
C 847	9.8	35.0	34	1	AA222577	AA222577	my13g01.r	C 920	9.8	35.0	46	4	BJ050218	BJ050218	BJ050218
C 848	9.8	35.0	34	8	AZ622092	AZ622092	1M0455H07	C 921	9.8	35.0	46	8	AQ025695	1(2)k0100	AQ025695
C 849	9.8	35.0	34	8	AZ824067	AZ824067	2M0098C01	C 922	9.8	35.0	46	8	AQ232570	1M0048H21	AQ232570
C 850	9.8	35.0	34	8	AZ957635	AZ957635	2M0224N04	C 923	9.8	35.0	46	8	AZ328369	1M0052B09	AZ328369
C 851	9.8	35.0	35	4	BX034483	BJ034483	BJ034483	C 924	9.8	35.0	46	8	BH858922	SALK_0775	BH858922
C 852	9.8	35.0	35	4	BW401165	BM401165	5009-0-83	C 925	9.8	35.0	46	8	BH892168	3526_1_20	BH892168
C 853	9.8	35.0	35	9	AL767832	AL767832	Arabidops	C 926	9.8	35.0	46	9	EX121139	Danio rer	EX121139
C 854	9.8	35.0	35	9	BX660083	BX660083	Arabidops	C 927	9.8	35.0	46	9	EX293301	Arabidops	EX293301
C 855	9.8	35.0	35	9	TA129B11P	AL463987	T. brucei	C 928	9.8	35.0	46	9	TA296G08Q	T. brucei	AL463987
C 856	9.8	35.0	36	1	AV833092	AV833092	AV833092	C 929	9.8	35.0	46	9	CG779295	1123032H0	CG779295
C 857	9.8	35.0	36	4	BX045071	BJ045071	BJ045071	C 930	9.8	35.0	46	9	CL212822	G023A04 G	CL212822
C 858	9.8	35.0	36	8	AZ760285	AZ760285	1M0553M19	C 931	9.8	35.0	47	1	AV741604	AV741604	AV741604
C 859	9.8	35.0	36	8	AZ818349	AZ818349	2M0088M17	C 932	9.8	35.0	47	1	AV956136	AV956136	AV956136
C 860	9.8	35.0	37	4	BG915991	BG915991	602815257	C 933	9.8	35.0	47	4	BG522577	24-43 Ste	BG522577
C 861	9.8	35.0	37	4	BG915991	BG915991	602815257	C 934	9.8	35.0	47	8	AZ493275	1M0327D24	AZ493275
C 862	9.8	35.0	37	9	CL528634	AZ775936	2M0009012	C 935	9.8	35.0	47	8	AZ588201	1M0396B22	AZ588201
C 863	9.8	35.0	38	2	B8570996	BE570996	601328884	C 936	9.8	35.0	47	8	BH620863	1007098C0	BH620863
C 864	9.8	35.0	38	7	CO781885	CO781885	BL013C_F0	C 937	9.8	35.0	47	8	BZ593018	SALK_0550	BZ593018
C 865	9.8	35.0	38	8	AZ346860	AZ346860	1M0082K15	C 938	9.8	35.0	47	8	CL156016	NPX242 Ba	CL156016
C 866	9.8	35.0	39	8	AZ402088	AZ402088	1M0169B16	C 939	9.8	35.0	48	4	BI753336	603026191	BI753336
C 867	9.8	35.0	39	8	AZ768302	AZ768302	1M0568B14	C 940	9.8	35.0	48	4	BI756103	603023994	BI756103
C 868	9.8	35.0	39	8	BZ665489	BZ665489	EY00232-5	C 941	9.8	35.0	48	7	H21537	Y132f09_e1	H21537
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C 870	9.8	35.0	40	1	AI023350	AI023350	ox04d10.s	C 943	9.8	35.0	48	8	AZ766335	1M0563P13	AZ766335
C 871	9.8	35.0	40	1	AI080507	AI080507	ox38f11.s	C 944	9.8	35.0	48	8	AZ768335	2M0028B05	AZ768335
C 872	9.8	35.0	40	1	AA086682	AA086682	mn91g09.r	C 945	9.8	35.0	48	8	AZ785009	1M0528B01	AZ785009
C 873	9.8	35.0	40	1	AT882509	AI882509	ub97a09.r	C 946	9.8	35.0	48	8	BZ660760	SALK_0242	BZ660760
C 874	9.8	35.0	40	1	AA544934	AA544934	vj70b09.r	C 947	9.8	35.0	48	8	BZ766924	SALK_1380	BZ766924
C 875	9.8	35.0	40	2	B8960473	B8960473	601853217	C 948	9.8	35.0	48	9	DME546992	Drosophil	DME546992
C 876	9.8	35.0	40	4	BM399990	BM399990	5009-0-64	C 949	9.8	35.0	49	1	AA028816	mn87d03.r	AA028816
C 877	9.8	35.0	40	8	AZ798767	AZ798767	2M0055D17	C 950	9.8	35.0	49	1	AA878633	7LEAF--08	AA878633
C 878	9.8	35.0	40	8	BZ767723	BZ767723	SALK_1392	C 951	9.8	35.0	49	1	AA922785	om62h01.s	AA922785
C 879	9.8	35.0	40	9	BX896855	BX896855	Arabidops	C 952	9.8	35.0	49	1	AA146415	mr66c08.r	AA146415
C 880	9.8	35.0	41	1	AJ680173	AJ680173	AJ680173	C 953	9.8	35.0	49	1	AI680543	tw82c11.x	AI680543
C 881	9.8	35.0	41	5	BX621835	BX621835	BX621835	C 954	9.8	35.0	49	2	B8615718	601279832	B8615718
C 882	9.8	35.0	41	8	AZ794084	AZ794084	2M0047N09	C 955	9.8	35.0	49	6	CF302478	7LEAF--08	CF302478
C 883	9.8	35.0	41	8	BH791218	BH791218	SALK_0589	C 956	9.8	35.0	49	8	AZ346989	1M0570H06	AZ346989
C 884	9.8	35.0	41	9	AL760282	AL760282	Arabidops	C 957	9.8	35.0	49	8	AZ769616	1M0570H06	AZ769616
C 885	9.8	35.0	41	9	BX292797	BX292797	Arabidops	C 958	9.8	35.0	49	8	AZ784737	2M0027L14	AZ784737
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C 887	9.8	35.0	42	1	AA095886	AA095886	16957.seq	C 960	9.8	35.0	49	8	BH791914	SALK_0619	BH791914
C 888	9.8	35.0	42	6	CF308435	CF308435	ABF--02-E	C 961	9.8	35.0	49	8	CC456020	SALK_0931	CC456020
C 889	9.8	35.0	42	9	BX222960	BX222960	Danio rer	C 962	9.8	35.0	49	9	TA366A08P	1M0570H06	TA366A08P
C 890	9.8	35.0	43	1	AA971669	AA971669	op85c10.s	C 963	9.8	35.0	49	9	CL520169	T. brucei	CL520169
C 891	9.8	35.0	43	1	AI098177	AI098177	ue31a07.x	C 964	9.8	35.0	49	9	AG202665	Pan trogl	AG202665
C 892	9.8	35.0	43	6	CA965921	CA965921	CcLL03a11	C 965	9.8	35.0	50	1	AU102352	AU102352	AU102352
C 893	9.8	35.0	43	6	CA969808	CA969808	CcLL06a24	C 966	9.8	35.0	50	1	AU102353	AU102353	AU102353
C 894	9.8	35.0	43	7	H94728	H94728	YH58c01.e1	C 967	9.8	35.0	50	1	AU102356	AU102356	AU102356
C 895	9.8	35.0	43	7	W87658	W87658	zh67e12.e1	C 968	9.8	35.0	50	1	AU102586	AU102586	AU102586
C 896	9.8	35.0	43	8	AZ393528	AZ393528	1M0156B10	C 969	9.8	35.0	50	1	AU102591	AU102591	AU102591
C 897	9.8	35.0	43	8	AZ467394	AZ467394	1M0278F16	C 970	9.8	35.0	50	1	AU102595	AU102595	AU102595
C 898	9.8	35.0	43	8	BH609433	BH609433	HIV18D12	C 971	9.8	35.0	50	1	AU102737	AU102737	AU102737
C 899	9.8	35.0	43	8	BZ352392	BZ352392	SALK_0789	C 972	9.8	35.0	50	1	AU102921	AU102921	AU102921
C 900	9.8	35.0	43	9	AJ591815	AJ591815	Arabidops	C 973	9.8	35.0	50	1	AU102954	AU102954	AU102954

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c 974 9.8 35.0 50 1 AUI03409 AUI03409
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ALIGNMENTS

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RESULT 1
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LOCUS 2M0096009F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0096009 F, genomic survey sequence.
ACCESSION AZ822723
VERSION AZ822723.1 GI:12992631
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: 0 column: 09
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"/
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match 50.7%; Score 14.2; DB 8; Length 28;

Best Local Similarity 70.4%; Pred. No. 9.7e+04;

Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CAAGCACCCTATCAGGCGAGTACCACAA 28

Db 28 CAAGCAGCCATCAAGTATACGAAA 2

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RESULT 2
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LOCUS 1M0226A08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0226A08 R, genomic survey sequence.
ACCESSION AZ437906
VERSION AZ437906.1 GI:10561919
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0226 row: A column: 08
Seq primer: CACACAGGAACAGCTATGACC
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.3%; Score 13.8; DB 8; Length 38;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 ATCAGGCGAGTACCACAA 28
|||||
Db 13 ATCAGGCGAGTACCACAA 29

RESULT 3

AZ402707
LOCUS AZ402707 45 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0170E08F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0170E08 F, genomic survey sequence.

ACCESSION AZ402707
VERSION AZ402707.1 GI:10517781
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 45)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0170 row: E column: 08
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

FEATURES

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/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.3%; Score 13.8; DB 8; Length 45;
Best Local Similarity 72.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 AGCACCTATCAGGACGTACCACAA 28
|||||
Db 7 AGCACCTATCAGGACGTACCACAA 31

RESULT 4

CK136536
LOCUS CK136536 50 bp mRNA linear EST 02-DEC-2003
DEFINITION MM2_2_1_C04 Sugar beet 10-week GH root cDNA Beta vulgaris cDNA 5', mRNA sequence.

ACCESSION CK136536
VERSION CK136536.1 GI:38628616
KEYWORDS EST.
SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta. 1 (bases 1 to 50)

REFERENCE

AUTHORS Klotz, K.L. and McGrath, J.M.
ESTs from 10-week old greenhouse grown sugar beet roots Unpublished (2003)

JOURNAL

COMMENT Contact: J. Mitchell McGrath
Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research Unit

Michigan State University
494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
Tel: 517 353 9262
Fax: (517)-337-6782
Email: mitchmc@msu.edu

Plate: MM2_2_1 row: C column: 04
Seq primer: 5'-GCATACATTATACGAGTTATCAG-3'.

FEATURES

source
1. .50
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="VDH66156"
/db_xref="taxon:161934"
/tissue_type="whole root"
/dev_stage="1- week old"
/lab_host="DH5-alpha"
/clone_lib="Sugar beet 10-week GH root cDNA"
/note="Organ: root; Vector: pDNR-LIB; Site 1: SfiI A; Site 2: SfiI B; cDNAs were derived from reverse transcription of mRNA samples from greenhouse grown whole roots frozen in liquid nitrogen, freeze-dried, and ground

to powder. RNA was extracted from the powder. The directional cDNA library was generated by Amplicon Express using the Clontech Creator SMART kit and transformed into DH5-alpha cells, with selection using chloramphenicol."

ORIGIN

Query Match 49.3%; Score 13.8; DB 7; Length 50;
Best Local Similarity 88.2%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 ATCAGCAGTACCACAA 28

Db 1 ATTAGGAAGTACCACAA 17

RESULT 5

BH903991 50 bp DNA linear GSS 04-SEP-2002
LOCUS SALK_103780.42.40.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_103780.42.40.x, genomic survey sequence.

ACCESSION BH903991 GI:22715434

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 50)

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of Atig55110.

Class: TDNA tagged.

FEATURES

source

1..50
Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clones="SALK_103780.42.40.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 49.3%; Score 13.8; DB 8; Length 50;

Best Local Similarity 72.0%; Pred. No. 1.6e+05;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 AGCACCTATCAGGCAGTACCACAA 28

Db 2 AACAACTTAGAAGAAGTACCACAA 26

RESULT 6

DR381135

LOCUS DR381135 42 bp DNA linear GSS 22-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-38113, genomic survey sequence.

ACCESSION AL981240

VERSION AL981240.1 GI:25181435

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 42)

AUTHORS

TITLE

JOURNAL

COMMENT

Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 38113. 38113 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

1..42
Location/Qualifiers

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="DKEY-38113"

/tissue_type="Testis"

/note="vector pindigobAC-536"

ORIGIN

Query Match 48.6%; Score 13.6; DB 9; Length 42;

Best Local Similarity 80.0%; Pred. No. 1.9e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 CCTATCAGGCAGTACCACAA 28

Db 4 CCGACGAGGACGACCAAAA 23

RESULT 7

AV965348/c

LOCUS

DEFINITION

AV965348 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad19p03 5', mRNA sequence.

ACCESSION AV965348

VERSION AV965348.1 GI:19455044

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 47)

AUTHORS

TITLE

JOURNAL

COMMENT

Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@scidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1..47

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="ciad19p03"

/tissue_type="whole animal"

/dev_stage="young adult"

/clone_lib="Nori Satoh unpublished cDNA library, young
adult"

Location/Qualifiers

1..47

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="ciad19p03"

/tissue_type="whole animal"

/dev_stage="young adult"

/clone_lib="Nori Satoh unpublished cDNA library, young
adult"

Location/Qualifiers

1..47

Query Match 47.9%; Score 13.4; DB 1; Length 47;
 Best Local Similarity 73.9%; Pred. No. 2.4e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 GCACCCATCAGGAGTACCACA 27
 |||||
 DB 41 GCACCAATCAGGCATATCCCA 19

RESULT 8
 AA932343

LOCUS
 DEFINITION AA932343 28 bp mRNA linear EST 07-JUL-1998
 O05002.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1570562 3' similar to SW:RLZA_HUMAN P46776 60S RIBOSOMAL PROTEIN L27A. ; mRNA sequence.

ACCESSION
 VERSION AA932343
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM
 Homo sapiens

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
 1 (bases 1 to 28)

TITLE
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL
 Unpublished (1997)

COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1517 Std Error: 0.00
 Seq primer: -40ml3 fwd ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1570562"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu5"
 /note="Organ: lung; Vector: pTY73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTY73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 47.1%; Score 13.2; DB 1; Length 28;
 Best Local Similarity 83.3%; Pred. No. 2.7e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CTATCAGCAGTACCACA 27
 |||||
 DB 9 CTATGAGCATTTACCACA 26

RESULT 9
 A2434394/c

LOCUS
 DEFINITION AZ434394 32 bp DNA linear GSS 03-OCT-2000
 iM0220F13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0220F13 R, genomic survey sequence.

ACCESSION
 VERSION AZ434394
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Mus musculus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
 1 (bases 1 to 32)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE
 Unpublished (2000)

JOURNAL
 Contact: Robert B. Weiss
 University of Utah Genome Center

COMMENT
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0220 row: F column: 13
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers
 1..32
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0220F13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 47.1%; Score 13.2; DB 8; Length 32;
 Best Local Similarity 69.2%; Pred. No. 2.8e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CAAGCACCCTATCAGGCAGTACCACA 27
 |||||
 DB 32 CCACCCCTTAATAGGCATACCACA 7

RESULT 10
 A2775335/c

LOCUS
DEFINITION AZ775335 40 bp DNA linear GSS 16-FEB-2001
2M0007G07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0007G07 R, genomic survey sequence.

ACCESSION
VERSION AZ775335
KEYWORDS GSS.
SOURCE AZ775335.1 GI:12901711
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Mus musculus
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0007 row: G column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.

FEATURES
source
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0007G07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GII4732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 47.1%; Score 13.2; DB 8; Length 40;
Best Local Similarity 83.3%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 11 TATCAGGCAGTACCACAA 28
||| ||||| ||||| |||||
Db 36 TACCAGGCAGTACCACAA 19

RESULT 11
AI445901

LOCUS
DEFINITION AI445901 49 bp mRNA linear EST 13-APR-1999
tj06h01.x1 NCI CGAP Gas4 Homo sapiens CDNA clone IMAGE:2140753 3'
similar to TR:P93237 P93237 PROLINE-RICH PROTEIN PRP2 PRECURSOR.
; contains MSRI.b3 MSRI repetitive element ;, mRNA sequence.

ACCESSION
VERSION AI445901
KEYWORDS EST.
SOURCE AI445901.1 GI:4291451
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Homo sapiens
1 (bases 1 to 49)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2140753"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

ORIGIN
Query Match 47.1%; Score 13.2; DB 1; Length 49;
Best Local Similarity 69.2%; Pred. No. 3e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 AAGCACCTATCAGGCAGTACCACAA 28
||| ||||| ||||| |||||
Db 9 AACCCACCAAGCCAGCGGGACCAAA 34

RESULT 12
AI965799

LOCUS
DEFINITION AI965799 49 bp mRNA linear EST 12-JUL-2004
sc76e01.y1 Gm-cl018 Glycine max CDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl018-817 5' similar to SW:UBIQ_LBITA P49635 UBIQUITIN. ;, mRNA
sequence.

ACCESSION
VERSION AI965799
KEYWORDS EST.
SOURCE AI965799.1 GI:5760372
ORGANISM Glycine max (soybean)

REFERENCE
AUTHORS Glycine max
1 (bases 1 to 49)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,

Wed Nov 24 08:46:09 2004

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 46.4%; Score 13; DB 8; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTAT 13
|||||
Db 25 GCAAGCACCCCTAT 13

RESULT 16

CG887124/c 41 bp mRNA linear GSS 16-JUN-2004
LOCUS RRS785 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA,
DEFINITION mRNA sequence.

ACCESSION CG887124.1 GI:38641534
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE 1 (bases 1 to 41)
AUTHORS BayGenomics.
TITLE http://baygenomics.ucsf.edu/
JOURNAL Unpublished (2001)
COMMENT Bay Area Functional Genomics Consortium (BayGenomics)
Contact: BayGenomics
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=RRS785
Class: Gene Trap.

FEATURES

Location/Qualifiers
1..41
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"

ORIGIN

Query Match 46.4%; Score 13; DB 9; Length 41;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CACCCTATCAGGACGATACCAC 26
|||||
Db 24 CACACACTCAGGACGACCCAC 4

RESULT 17

CG887124/c 30 bp mRNA linear EST 08-AUG-2003
LOCUS BX625891
DEFINITION BX625891 NAP1 Anopheles gambiae cDNA clone ANGNP1163B01T7, mRNA

R.Site 1 : EcoRI.
R.Site 2 : EcoRI.
Location/Qualifiers
1..40
/organism="pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-069E06.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 46.4%; Score 13; DB 9; Length 40;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CAAGCACCCCTATCAGGACGTA 22
|||||
Db 21 CAAGAAACTTACCAGCCAGTA 1

RESULT 15

AZ768376/c 41 bp DNA linear GSS 16-FEB-2001
LOCUS IM0568P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0568P14 F, genomic survey sequence.

ACCESSION AZ768376
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE 1 (bases 1 to 41)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0568 row: p column: 14
Seq primer: GGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
1..41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0568P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

FEATURES

Location/Qualifiers
1..41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0568P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were


```

source
1..37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2309389"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pTV3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 45.7%; Score 12.8; DB 1; Length 37;
Best Local Similarity 70.8%; Pred. No. 4.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24
Db 27 GGAGAACCTGTCTGCGCGCCCC 4

RESULT 20
LOCUS CL679725 38 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0126d_D08.2 - PRI0126d.BR (38) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL679725.1 GI:50186437
VERSION CL679725
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
Location/Qualifiers
1..38
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 45.7%; Score 12.8; DB 9; Length 38;
Best Local Similarity 70.8%; Pred. No. 4.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24

```

```

Db 15 GCACGGCTCCTATGCTGCAGCACC 38
|||||
|||||
|||||
|||||
|||||

RESULT 21
LOCUS CC183071/c 40 bp mRNA linear GSS 08-MAY-2003
DEFINITION X5571 BayGenomics Gene Trap Library pGTLLxf Mus musculus cDNA, mRNA
sequence.
ACCESSION CC183071
VERSION CC183071.1 GI:30426971
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BayGenomics.
REFERENCE 1 (bases 1 to 40)
AUTHORS http://baygenomics.ucsf.edu/
JOURNAL http://baygenomics.ucsf.edu/
COMMENT Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XG571
Class: Gene Trap.
FEATURES
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTLLxf"
/note="Vector: pGTLLxf"

ORIGIN
Query Match 45.7%; Score 12.8; DB 8; Length 40;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TCAGGCAGTACCACAA 28
Db 24 TCAGGCAGTACCACCA 9

RESULT 22
LOCUS AZ329441 42 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0053M07R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0053M07 R, genomic survey sequence.
ACCESSION AZ329441
VERSION AZ329441.1 GI:10390156
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 42)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: M column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.

FEATURES

Location/Qualifiers
1..42

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0053M07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 42;
Best Local Similarity 70.8%; Pred. No. 4.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGTACC 24
|||||
Db 2 GCAGGCGGCGAGCGAGCGGCGCC 25

RESULT 23

AZ663255
LOCUS
DEFINITION
IM0542K15R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0542K15 R, genomic survey sequence.

ACCESSION
AZ663255

VERSION
AZ663255.1 GI:11800401

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: K column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.

FEATURES

Location/Qualifiers
1..47

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0542K15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 47;
Best Local Similarity 70.8%; Pred. No. 4.5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 AGCACCTATCAGGCAGTACCACA 27
|||||
Db 23 AGGACCTATCATGGCTTACACA 46

RESULT 24

AZ797405/c
LOCUS
DEFINITION
2M0053D08R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0053D08 R, genomic survey sequence.

ACCESSION
AZ797405

VERSION
AZ797405.1 GI:12946449

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.

FEATURES
source

1. .47
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0053D08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 47;
Best Local Similarity 70.8%; Pred. No. 4.5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGAGTACC 24
Db 29 GGAAGCAGCCGAGAGAGTGTACC 6

RESULT 25
A2790187 49 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0038N03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0038N03 R, genomic survey sequence.

ACCESSION A2790187
VERSION A2790187.1 GI:12931784

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)

REFERENCE 1 (bases 1 to 49)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0038 row: N column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 49.

FEATURES
source

1. .49
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0038N03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 49;
Best Local Similarity 70.8%; Pred. No. 4.5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 AAGCACCCCTATCAGGAGTACCAC 26
Db 1 ATGCATCCATTGAGGAGTCTCCTC 24

RESULT 26

BI223057/c
LOCUS BI223057.1

DEFINITION 32 bp mRNA linear EST 11-JUL-2001
602942007F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5105088 5', mRNA sequence.

ACCESSION BI223057

VERSION BI223057.1 GI:14676501

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 32)

REFERENCE NIH-MGC http://mgs.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM11253 row: n column: 01

High quality sequence stop: 32.

FEATURES

Location/Qualifiers
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5105088"
/tissue type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."

ORIGIN

Query Match 45.0%; Score 12.6; DB 4; Length 32;
Best Local Similarity 78.9%; Pred. No. 5.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAGCACCCTATCAGGCA 19
Db 31 GCAGCAGCCTGTCTGCA 13

RESULT 27

AG200947/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-083D01.TJ, genomic survey sequence.

ACCESSION AG200947

VERSION AG200947.1 GI:45233122

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43

AUTHORS

Unpublished

TITLE

2 (bases 1 to 35)

REFERENCE

1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.kribb.re.kr, URL: <http://phs.grc.kribb.re.kr/>, Tel: 82-42-866-7181, Fax: 82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

Location/Qualifiers

1..35

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-083D01.TJ"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

FEATURES

source

ORIGIN

Query Match 45.0%; Score 12.6; DB 9; Length 35;

Best Local Similarity 66.7%; Pred. No. 5.2e+05;

Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCAGCACCCTATCAGGCA 27
Db 29 GCATGCAACCTATGGTGAATAAACA 3

RESULT 28

LOCUS

DEFINITION AG2760045 43 bp DNA linear GSS 16-FEB-2001
clone UUGC1M0553K20 F, genomic survey sequence.

ACCESSION

AG2760045

VERSION

AG2760045.1 GI:12867458

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0553 row: K column: 20

Seq primer: CGTGTAAACGACGGCAGT

Class: plasmid ends

High quality sequence stop: 43.

FEATURES

Location/Qualifiers

1..43

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0553K20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN		15	CCAACACCCCTCTCTGAAGAAATAAA	41
Query Match			49 bp	mRNA
Best Local Similarity		45.0%;	Score 12.6;	DB 8; Length 43;
Matches		18;	Conservative	0; Mismatches 9; Indels 0; Gaps 0;
QY		2	CAAGCACCCCTATCAGGCAGTACCACAA	28
DB		7	CAACACCCCTGAAGAGGTTACACAA	33
RESULT 29			44 bp	mRNA
LOCUS		AA529852		linear
DEFINITION		v113c07.r1 Barstead mouse proximal colon MPLRB6 Mus musculus cDNA		EST 22-JUL-1997
ACCESSION		AA529852		
VERSION		AA529852.1	GI:2272558	
KEYWORDS		EST.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE		1 (bases 1 to 44)		
AUTHORS		Marrs, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.		
TITLE		The WashU-HMI Mouse EST Project		
JOURNAL		Unpublished (1996)		
COMMENT		Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:533828 Trace considered overall poor quality Putative full length read vector to vector length is 101 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1. .44 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clones="IMAGE:921612" /dev_stage="7 day juvenile" /lab_host="DH10B" /clone_lib="Barstead mouse proximal colon MPLRB6" /note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(GT) primer [5' TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT TGTTCAGATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGATCTTGG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."		
ORIGIN				
Query Match		45.0%;	Score 12.6;	DB 1; Length 44;
Best Local Similarity		66.7%;	Pred. No. 5.4e+05;	
Matches		18;	Conservative	0; Mismatches 9; Indels 0; Gaps 0;
QY		2	CAAGCACCCCTATCAGGCAGTACCACAA	28
DB		7	CAACACCCCTGAAGAGGTTACACAA	33
RESULT 30			49 bp	mRNA
LOCUS		T53793		linear
DEFINITION		Yb83q02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:77810 3' similar to gb:M64982_cds2 FIBRINOGEN ALPHA CHAIN PRECURSOR (HUMAN), mRNA sequence.		
ACCESSION		T53793		
VERSION		T53793.1	GI:655654	
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		1 (bases 1 to 49)		
AUTHORS		Hallier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevasaki, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.		
TITLE		Generation and analysis of 280,000 human expressed sequence tags		
JOURNAL		Genome Res. 6 (9), 807-828 (1996)		
MEDLINE		97044478		
PUBMED		889549		
COMMENT		Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu Insert Size: 1556 High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LML. This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 1556 Std Error: 0.00 Seq primer: -2lml3 High quality sequence stop: 1. Location/Qualifiers 1. .49 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:497555" /db_xref="taxon:9606" /clone="IMAGE:77810" /sex="male" /dev_stage="49 years old" /lab_host="SOLR cells (kanamycin resistant)" /clone_lib="Stratagene liver (#937224)" /note="Organ: liver; Vector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"		
FEATURES		source		
ORIGIN				
Query Match		45.0%;	Score 12.6;	DB 7; Length 49;
Best Local Similarity		75.0%;	Pred. No. 5.5e+05;	
Matches		15;	Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY		4	AGCACCCCTATCAGGCAGTAC	23
DB		29	AGCTCINTATCTGGTAGTAC	48
RESULT 31			50 bp	DNA
LOCUS		BX143358		linear
GSS		28-JAN-2003		

DEFINITION Danio rerio genomic clone DKEY-109K22, genomic survey sequence.
ACCESSION BX143358
VERSION BX143358.1 GI:27974696
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 109K22. 109K22 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygens. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
source
1. .50
Location/Qualifiers
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-109K22"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

ORIGIN
Query Match 45.0%; Score 12.6; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 5.5e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2 CAAGCACCTATCAGGCAGTACCACAA 28
|||||
Db 22 CAAGCACCTACCTAGAAAGCGCAAAA 48
|||||

RESULT 32
LOCUS CR397867 50 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-530E06-025923, genomic survey sequence.
ACCESSION CR397867
VERSION CR397867.1 GI:46938595
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weissshaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12674060
REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weissshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

14682050
REFERENCE 4 (bases 1 to 50)
AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weissshaar, B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weissshaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone fca all. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
Location/Qualifiers
1. .50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-530E06-025923"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 45.0%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 5.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 9 CCTATCAGGCAGTACCACA 27
|||||
Db 22 CCCATAAGGCGCTAACACA 4
|||||

RESULT 33
LOCUS AZ402223 32 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0169L21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0169L21 F, genomic survey sequence.
ACCESSION AZ402223
VERSION AZ402223.1 GI:10517297
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0169 row: L column: 21
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 38.

FEATURES

source
1. 38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0170C23"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.3%; Score 12.4; DB 8; Length 38;
Best Local Similarity 92.9%; Pred. No. 6.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CCTATCAGCAGTA 22
|||||

DB 34 CCTATCAGGAGTA 21
|||||

RESULT 36

LOCUS

DEFINITION BJ063882 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL077k13 5', mRNA sequence.
ACCESSION BJ063882
KEYWORDS
SOURCE
ORGANISM Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Xenopus.
1. (bases 1 to 39)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
1. 44
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL059p19"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud library"

REFERENCE

AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

TITLE Expressed genes in X. laevis embryo

JOURNAL Unpublished (2001)

COMMENT Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

The information of this clone is available through the following URL.

http://xenopus.nibb.ac.jp.

Location/Qualifiers

1. 39

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL077k13"

/tissue_type="whole embryo"

/dev_stage="stage 25"

/clone_lib="NIBB Mochii normalized Xenopus tailbud library"

ORIGIN

Query Match 44.3%; Score 12.4; DB 4; Length 39;
Best Local Similarity 72.7%; Pred. No. 6.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 AGCACCTTATCAGCAGTACCA 25
|||||

DB 30 AGCACTCGTTCATACAGAACCA 9
|||||

RESULT 37

LOCUS BJ077137/c

DEFINITION BJ077137 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL059p19 3', mRNA sequence.
ACCESSION BJ077137
KEYWORDS
SOURCE
ORGANISM Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Xenopus.
1. (bases 1 to 44)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
1. 44
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL059p19"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud library"

ORIGIN

Query Match 44.3%; Score 12.4; DB 4; Length 44;
Best Local Similarity 69.6%; Pred. No. 6.7e+05;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 AGCACCTTATCAGCAGTACCA 26
|||||

DB 33 AGTATGGTATCAAGAGNACCAC 11
|||||

RESULT 38

LOCUS AZ621023/c

DEFINITION AZ621023 50 bp DNA linear GSS 13-DEC-2000
1M0454C04F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0454C04 F, genomic survey sequence.
ACCESSION AZ621023
VERSION AZ621023.1 GI:11743213

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0389 row: A column: 07
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.
FEATURES Location/Qualifiers
1..39
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0389A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 43.6%; Score 12.2; DB 8; Length 39;
Best Local Similarity 68.0%; Pred. No. 8.1e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 AAGCACCTTATCAGGCAGTACCACA 27
||| ||||| ||| |||||
DB 38 AAACACCTTGAAGGAGTTACCAGA 14

RESULT 40
AZ828302/c
LOCUS AZ828302
DEFINITION 2M0105011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105011 F, genomic survey sequence.
ACCESSION AZ828302
VERSION AZ828302.1 GI:12998210

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: 0 column: 11
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
FEATURES
High quality sequence stop: 42.
Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0105011"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 43.6%; Score 12.2; DB 8; Length 42;
Best Local Similarity 68.0%; Pred. No. 8.2e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCAAGCACCTCATCAGGACGTACCA 25
Db 42 GTAACCACTCATCTACTCTCCCA 18

Search completed: November 23, 2004, 22:24:28
Job time : 1371.43 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 468.195 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-8

Perfect score: 26
Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_ph.*
- 7: gb_pl.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_ro.*
- 11: gb_atg.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	6	BD181369
2	26	100.0	26	6	AX523949 Sequence
3	26	100.0	26	6	AX524847 Sequence
4	15.2	58.5	44	6	I38537 Sequence 5
5	14.6	56.2	41	6	AR053999 Sequence
6	14.6	56.2	41	6	AR146175 Sequence
7	14.4	55.4	40	6	BD263605 Novel str
8	14.4	55.4	40	6	AX343106 Sequence
9	14.2	54.6	30	6	AX454034 Sequence
10	14	53.8	48	14	MLMLTRB1
11	13.8	53.1	24	6	AX445171 Sequence
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13	13.6	52.3	40	6	BD190521 NOVEL ESS
14	13.6	52.3	40	6	AX038843 Sequence
15	13.4	51.5	24	6	CQ824393 Sequence
16	13.4	51.5	25	6	AR448717 Sequence
17	13.4	51.5	31	6	AR101054 Sequence
18	13.4	51.5	39	6	AR099751 Sequence
19	13.4	51.5	39	6	BD064614 Cloned gl

93	12.6	48.5	43	6	BD181430	BD181430 Method fo	166	12	45.2	27	6	BD1813640	BD1813640 Process f
94	12.6	48.5	43	6	BD091643	BD091643 Method fo	167	12	46.2	27	6	AX343658	AX343658 Sequence
95	12.6	48.5	48	6	I07867	I07867 Sequence 7	168	12	46.2	28	6	E32356	E32356 Plant havin
96	12.4	47.7	17	6	AX722703	AX722703 Sequence	169	12	46.2	30	6	Q0814749	Q0814749 Sequence
97	12.4	47.7	17	6	AX781699	AX781699 Sequence	170	12	46.2	32	6	AR217261	AR217261 Sequence
98	12.4	47.7	17	6	AX781700	AX781700 Sequence	171	12	46.2	32	6	BD000511	BD000511 Protein,
99	12.4	47.7	20	6	AX295269	AX295269 Sequence	172	12	46.2	33	6	Q0812759	Q0812759 Transgeni
100	12.4	47.7	24	6	AX164372	AX164372 Sequence	173	12	46.2	35	6	BD243702	BD243702 Sequence
101	12.4	47.7	24	6	AX290636	AX290636 Sequence	174	12	46.2	36	6	AR006796	AR006796 Sequence
102	12.4	47.7	24	6	AX291378	AX291378 Sequence	175	12	46.2	36	6	AR135404	AR135404 Sequence
103	12.4	47.7	27	6	E32354	E32354 Plant havin	176	12	46.2	36	6	I71308	I71308 Sequence 46
104	12.4	47.7	28	6	AX399202	AX399202 Sequence	177	12	46.2	38	6	AR000580	AR000580 Sequence
105	12.4	47.7	28	6	AX108668	AX108668 Sequence	178	12	46.2	38	6	BD267995	BD267995 Polynucle
106	12.4	47.7	33	6	I00040	I00040 Sequence 3	179	12	46.2	38	6	BD003632	BD003632 A polynuc
107	12.4	47.7	35	6	AR201623	AR201623 Sequence	180	12	46.2	38	6	BD057133	BD057133 Polynucle
108	12.4	47.7	35	6	AR491606	AR491606 Sequence	181	12	46.2	38	6	AX525430	AX525430 Sequence
109	12.4	47.7	37	6	AR411038	AR411038 Sequence	182	12	46.2	42	6	AX525431	AX525431 Sequence
110	12.4	47.7	40	6	AR364170	AR364170 Sequence	183	12	46.2	42	6	AR19038	AR19038 Sequence
111	12.4	47.7	41	6	AX515174	AX515174 Sequence	184	12	46.2	43	6	AR179154	AR179154 Sequence
112	12.4	47.7	41	6	AX517968	AX517968 Sequence	185	12	46.2	43	6	AX305167	AX305167 Sequence
113	12.4	47.7	42	6	AR104422	AR104422 Sequence	186	12	46.2	48	6	AX305167	AX305167 Sequence
114	12.4	47.7	42	6	BD262362	BD262362 Bacterici	187	12	46.2	48	6	AX612167	AX612167 Sequence
115	12.4	47.7	45	6	BD102842	BD102842 Beta-Lipo	188	12	46.2	48	6	AX612168	AX612168 Sequence
116	12.4	47.7	45	6	BD102842	BD102842 Beta-Lipo	189	12	46.2	48	6	AX612169	AX612169 Sequence
117	12.4	47.7	45	9	HS2242496	HS2242496 Homo sapi	190	12	46.2	50	1	FVBFOXIF	FVBFOXIF
118	12.4	47.7	50	6	Q0086630	Q0086630 Sequence	191	12	46.2	50	6	AR381690	AR381690 Sequence
119	12.4	47.7	50	6	Q0086631	Q0086631 Sequence	192	12	46.2	50	6	AX395202	AX395202 Sequence
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121	12.2	46.9	19	6	Q0757899	Q0757899 Sequence	194	11.8	45.4	17	6	AX822204	AX822204 Sequence
122	12.2	46.9	20	6	AX293269	AX293269 Sequence	195	11.8	45.4	18	6	AX825844	AX825844 Sequence
123	12.2	46.9	24	6	AR217186	AR217186 Sequence	196	11.8	45.4	22	6	AX231093	AX231093 Sequence
124	12.2	46.9	24	6	AX288636	AX288636 Sequence	197	11.8	45.4	22	6	AX231554	AX231554 Sequence
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126	12.2	46.9	30	6	AX600867	AX600867 Sequence	199	11.8	45.4	22	6	AX232214	AX232214 Sequence
127	12.2	46.9	30	6	AX642344	AX642344 Sequence	200	11.8	45.4	22	6	AX233339	AX233339 Sequence
128	12.2	46.9	31	6	AR411312	AR411312 Sequence	201	11.8	45.4	22	6	AX233348	AX233348 Sequence
129	12.2	46.9	33	6	Q0770998	Q0770998 Sequence	202	11.8	45.4	23	6	E09823	E09823 Antisense p
130	12.2	46.9	33	6	AR474321	AR474321 Sequence	203	11.8	45.4	23	6	BD249648	BD249648 Pi-ta gen
131	12.2	46.9	33	6	AR474335	AR474335 Sequence	204	11.8	45.4	24	6	AR254321	AR254321 Sequence
132	12.2	46.9	33	6	AR474342	AR474342 Sequence	205	11.8	45.4	24	6	AR277969	AR277969 Sequence
133	12.2	46.9	33	6	AX282625	AX282625 Sequence	206	11.8	45.4	24	6	AX081035	AX081035 Sequence
134	12.2	46.9	33	6	AX282639	AX282639 Sequence	207	11.8	45.4	24	6	AR020992	AR020992 Sequence
135	12.2	46.9	33	6	AX282646	AX282646 Sequence	208	11.8	45.4	25	6	AR209035	AR209035 Sequence
136	12.2	46.9	35	6	AX665221	AX665221 Sequence	209	11.8	45.4	25	6	AR482104	AR482104 Sequence
137	12.2	46.9	36	6	AR231285	AR231285 Sequence	210	11.8	45.4	25	6	AX782454	AX782454 Sequence
138	12.2	46.9	36	6	AR268971	AR268971 Sequence	211	11.8	45.4	25	6	AX930018	AX930018 Sequence
139	12.2	46.9	36	6	BD009830	BD009830 Compositi	212	11.8	45.4	25	6	BD132732	BD132732 Regulator
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141	12.2	46.9	43	6	BD217529	BD217529 Glucoamy1	214	11.8	45.4	27	6	AX105562	AX105562 Sequence 3
142	12.2	46.9	43	6	Q0770999	Q0770999 Sequence	215	11.8	45.4	30	6	AX6166	AX6166 Sequence 4
143	12.2	46.9	43	6	AR198409	AR198409 Sequence	216	11.8	45.4	30	6	AX361090	AX361090 Sequence
144	12.2	46.9	43	6	AR093110	AR093110 Sequence	217	11.8	45.4	30	6	AX361091	AX361091 Sequence
145	12.2	46.9	48	6	AX522764	AX522764 Sequence	218	11.8	45.4	30	6	AX31480	AX31480 Sequence
146	12.2	46.9	48	6	BD009934	BD009934 BH3 inter	219	11.8	45.4	31	6	AR195952	AR195952 Sequence
147	12	46.2	20	6	AR314113	AR314113 Sequence 9	220	11.8	45.4	31	6	AR9684	AR9684 Sequence 16
148	12	46.2	21	6	AX5350	AX5350 Sequence	221	11.8	45.4	32	6	AR002996	AR002996 Sequence
149	12	46.2	21	6	AR098956	AR098956 Sequence	222	11.8	45.4	32	6	AR151699	AR151699 Sequence
150	12	46.2	21	6	AR154843	AR154843 Sequence	223	11.8	45.4	32	6	AR209038	AR209038 Sequence
151	12	46.2	21	6	AR170540	AR170540 Sequence	224	11.8	45.4	32	6	AR336822	AR336822 Sequence
152	12	46.2	21	6	AR170704	AR170704 Sequence	225	11.8	45.4	32	6	AR482107	AR482107 Sequence
153	12	46.2	21	6	AR174772	AR174772 Sequence	226	11.8	45.4	32	6	BD132735	BD132735 Regulator
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155	12	46.2	21	6	I79796	I79796 Sequence 92	228	11.8	45.4	33	6	AR016829	AR016829 Sequence
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160	12	46.2	25	6	AX690087	AX690087 Sequence	233	11.8	45.4	34	6	AR067532	AR067532 Sequence
161	12	46.2	25	6	AX690088	AX690088 Sequence	234	11.8	45.4	34	6	I07358	I07358 Sequence 10
162	12	46.2	25	6	AX690089	AX690089 Sequence	235	11.8	45.4	34	6	I38484	I38484 Sequence 58
163	12	46.2	25	6	AX690090	AX690090 Sequence	236	11.8	45.4	34	6	I56959	I56959 Sequence 58
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165	12	46.2	26	6	Q0818874	Q0818874 Sequence	238	11.8	45.4	34	6		

C 239	11.8	45.4	34	6	I75152	I75152 Sequence 58	312	11.6	44.6	20	6	AR312363	AR312363 Sequence
C 240	11.8	45.4	34	6	AR409700	AR409700 Sequence	C 313	11.6	44.6	20	6	AR382864	AR382864 Sequence
C 241	11.8	45.4	36	6	I35618	I35618 Sequence 4	C 314	11.6	44.6	20	6	AX294379	AX294379 Sequence
C 242	11.8	45.4	37	6	AR2991	AR2991 Sequence 1	C 315	11.6	44.6	20	6	BD012499	BD012499 Guanosine
C 243	11.8	45.4	37	6	AR2993	AR2993 Sequence 3	C 316	11.6	44.6	23	6	AX172363	AX172363 Sequence
C 244	11.8	45.4	37	6	AR175560	AR175560 Sequence	C 317	11.6	44.6	23	6	AX394772	AX394772 Sequence
C 245	11.8	45.4	37	6	AR175562	AR175562 Sequence	C 318	11.6	44.6	24	6	AR229825	AR229825 Sequence
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C 247	11.8	45.4	37	6	AX207717	AX207717 Sequence	C 320	11.6	44.6	25	6	BD245283	BD245283 Developme
C 248	11.8	45.4	37	6	BD106502	BD106502 Method fo	C 321	11.6	44.6	25	6	BD245360	BD245360 Developme
C 249	11.8	45.4	37	6	BD106504	BD106504 Method fo	C 322	11.6	44.6	25	6	AX690084	AX690084 Sequence
C 250	11.8	45.4	38	6	AR018828	AR018828 Sequence	C 323	11.6	44.6	25	6	AX690085	AX690085 Sequence
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C 253	11.8	45.4	38	6	AR038464	AR038464 Sequence	C 326	11.6	44.6	27	6	CQ788626	CQ788626 Sequence
C 254	11.8	45.4	38	6	AR064606	AR064606 Sequence	C 327	11.6	44.6	27	6	I08539	I08539 Sequence 1
C 255	11.8	45.4	38	6	AR067531	AR067531 Sequence	C 328	11.6	44.6	28	6	AX404949	AX404949 Sequence
C 256	11.8	45.4	38	6	I07357	I07357 Sequence 9	C 329	11.6	44.6	28	6	BD006148	BD006148 Methods a
C 257	11.8	45.4	38	6	I38483	I38483 Sequence 57	C 330	11.6	44.6	29	6	A99074	A99074 Sequence 82
C 258	11.8	45.4	38	6	I56958	I56958 Sequence 57	C 331	11.6	44.6	29	6	AR195389	AR195389 Sequence 9
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C 262	11.8	45.4	40	6	AR8998	AR8998 Sequence 6	C 335	11.6	44.6	31	6	E59841	E59841 Method for
C 263	11.8	45.4	40	6	AR195315	AR195315 Sequence	C 336	11.6	44.6	31	6	I52169	I52169 Sequence 12
C 264	11.8	45.4	40	6	AX514618	AX514618 Sequence	C 337	11.6	44.6	31	6	AR196031	AR196031 Sequence
C 265	11.8	45.4	40	6	AX520560	AX520560 Sequence	C 338	11.6	44.6	31	6	AR340186	AR340186 Sequence
C 266	11.8	45.4	40	6	AX539378	AX539378 Sequence	C 339	11.6	44.6	31	6	AR408584	AR408584 Sequence
C 267	11.8	45.4	41	6	AX515336	AX515336 Sequence	C 340	11.6	44.6	31	6	AX151283	AX151283 Sequence
C 268	11.8	45.4	41	6	AX517833	AX517833 Sequence	C 341	11.6	44.6	31	6	BD002480	BD002480 Gene comp
C 269	11.8	45.4	42	6	A09950	A09950 Nucleotide	C 342	11.6	44.6	31	6	BD002532	BD002532 Gene comp
C 270	11.8	45.4	44	6	E09822	E09822 Antisense p	C 343	11.6	44.6	32	6	AR016831	AR016831 Sequence
C 271	11.8	45.4	44	6	E27278	E27278 Method for	C 344	11.6	44.6	32	6	AR020857	AR020857 Sequence
C 272	11.8	45.4	44	6	AR411399	AR411399 Sequence	C 345	11.6	44.6	32	6	AR027180	AR027180 Sequence
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C 277	11.8	45.4	47	6	AR288427	AR288427 Sequence	C 350	11.6	44.6	32	6	I07360	I07360 Sequence 12
C 278	11.8	45.4	47	6	AR194985	AR194985 Sequence	C 351	11.6	44.6	32	6	I38486	I38486 Sequence 60
C 279	11.8	45.4	48	6	AX234365	AX234365 Sequence	C 352	11.6	44.6	32	6	I56961	I56961 Sequence 60
C 280	11.8	45.4	48	6	AX234385	AX234385 Sequence	C 353	11.6	44.6	32	6	I59827	I59827 Sequence 60
C 281	11.8	45.4	48	6	AX305153	AX305153 Sequence	C 354	11.6	44.6	32	6	I75154	I75154 Sequence 60
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C 286	11.8	45.4	48	6	AX305163	AX305163 Sequence	C 359	11.6	44.6	35	6	I52170	I52170 Sequence 13
C 287	11.8	45.4	48	6	AX305164	AX305164 Sequence	C 360	11.6	44.6	35	6	AR381716	AR381716 Sequence
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C 290	11.8	45.4	48	6	AX305170	AX305170 Sequence	C 363	11.6	44.6	35	6	AX590521	AX590521 Sequence
C 291	11.8	45.4	48	6	AX305175	AX305175 Sequence	C 364	11.6	44.6	35	6	AR209737	AR209737 Sequence
C 292	11.8	45.4	48	6	AX305178	AX305178 Sequence	C 365	11.6	44.6	36	6	AR209737	AR209737 Sequence
C 293	11.8	45.4	48	6	AX305179	AX305179 Sequence	C 366	11.6	44.6	36	6	AX794109	AX794109 Sequence
C 294	11.8	45.4	49	6	AR125772	AR125772 Sequence	C 367	11.6	44.6	37	6	E40796	E40796 Antihuman F
C 295	11.8	45.4	49	6	I47184	I47184 Sequence 11	C 368	11.6	44.6	37	6	AX581930	AX581930 Sequence
C 296	11.8	45.4	50	6	AR125770	AR125770 Sequence	C 369	11.6	44.6	39	6	E36951	E36951 Human telom
C 297	11.8	45.4	50	6	AR151515	AR151515 Sequence	C 370	11.6	44.6	39	6	E36953	E36953 Human telom
C 298	11.8	45.4	50	6	AR151516	AR151516 Sequence	C 371	11.6	44.6	39	6	E36957	E36957 Human telom
C 299	11.8	45.4	50	6	AR151517	AR151517 Sequence	C 372	11.6	44.6	39	6	AR243472	AR243472 Sequence
C 300	11.8	45.4	50	6	AR151518	AR151518 Sequence	C 373	11.6	44.6	39	6	AR243474	AR243474 Sequence
C 301	11.8	45.4	50	6	AR151519	AR151519 Sequence	C 374	11.6	44.6	39	6	AR243476	AR243476 Sequence
C 302	11.8	45.4	50	6	AR151520	AR151520 Sequence	C 375	11.6	44.6	39	6	AR243478	AR243478 Sequence
C 303	11.8	45.4	50	6	AR151521	AR151521 Sequence	C 376	11.6	44.6	39	6	AR390628	AR390628 Sequence
C 304	11.8	45.4	50	6	AR151522	AR151522 Sequence	C 377	11.6	44.6	39	6	AR390630	AR390630 Sequence
C 305	11.8	45.4	50	6	I42213	I42213 Sequence 26	C 378	11.6	44.6	39	6	AR390632	AR390632 Sequence
C 306	11.8	45.4	50	6	I47182	I47182 Sequence 11	C 379	11.6	44.6	39	6	AR390634	AR390634 Sequence
C 307	11.8	45.4	50	6	AX156795	AX156795 Sequence	C 380	11.6	44.6	39	6	AR393242	AR393242 Sequence
C 308	11.8	45.4	50	6	AX305160	AX305160 Sequence	C 381	11.6	44.6	39	6	AR393244	AR393244 Sequence
C 309	11.8	45.4	50	6	BD014158	BD014158 Probe for	C 382	11.6	44.6	39	6	AR393246	AR393246 Sequence
C 310	11.6	44.6	19	6	AR815569	AR815569 Antisense	C 383	11.6	44.6	39	6	AR393248	AR393248 Sequence
C 311	11.6	44.6	20	6	BD196073	BD196073 Antisense	C 384	11.6	44.6	39	6	AX810533	AX810533 Sequence

385	11.6	44.6	39	6	AX810535	AX810535 Sequence	458	11.4	43.8	33	6	BD011030	BD011030 HIV probe
386	11.6	44.6	39	6	AX810537	AX810537 Sequence	459	11.4	43.8	33	6	BD061585	BD061585 Peptide h
387	11.6	44.6	39	6	AX810539	AX810539 Sequence	460	11.4	43.8	34	6	AX1791	AX1791 Sequence 14
388	11.6	44.6	39	6	BD011202	BD011202 Human tel	461	11.4	43.8	34	6	CQ840153	CQ840153 Sequence
389	11.6	44.6	39	6	BD011204	BD011204 Human tel	462	11.4	43.8	34	6	AX353829	AX353829 Sequence
390	11.6	44.6	39	6	BD011206	BD011206 Human tel	463	11.4	43.8	34	6	AX358614	AX358614 Sequence
391	11.6	44.6	39	6	BD011208	BD011208 Human tel	464	11.4	43.8	35	6	AR099783	AR099783 Sequence
392	11.6	44.6	40	6	AX052782	AX052782 Sequence 10	465	11.4	43.8	35	6	AR159970	AR159970 Sequence
393	11.6	44.6	41	6	I06800	I06800 Sequence 10	466	11.4	43.8	35	6	AR210049	AR210049 Sequence
394	11.6	44.6	41	6	AX516903	AX516903 Sequence	467	11.4	43.8	35	6	AR392075	AR392075 Sequence
395	11.6	44.6	41	6	AX519414	AX519414 Sequence	468	11.4	43.8	35	6	AX028956	AX028956 Sequence
396	11.6	44.6	41	6	BD137163	BD137163 Autonomou	469	11.4	43.8	35	6	AX684159	AX684159 Sequence
397	11.6	44.6	42	6	AR490210	AR490210 Sequence	470	11.4	43.8	35	6	BD136770	BD136770 Human pla
398	11.6	44.6	42	6	AX018715	AX018715 Sequence	471	11.4	43.8	37	6	AR3835	AR3835 Sequence 4
399	11.6	44.6	44	6	AR104030	AR104030 Sequence	472	11.4	43.8	37	6	AR360582	AR360582 Sequence
400	11.6	44.6	44	6	AR104118	AR104118 Sequence	473	11.4	43.8	37	6	AX000221	AX000221 Sequence
401	11.6	44.6	44	6	AR104119	AR104119 Sequence	474	11.4	43.8	38	6	CQ821251	CQ821251 Sequence
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404	11.6	44.6	45	6	AX404956	AX404956 Sequence	477	11.4	43.8	40	6	BD240782	BD240782 Substanti
405	11.6	44.6	45	6	AX513776	AX513776 Sequence	478	11.4	43.8	40	6	CQ772558	CQ772558 Sequence
406	11.6	44.6	46	6	AR032405	AR032405 Sequence	479	11.4	43.8	41	6	I06806	I06806 Sequence 16
407	11.6	44.6	46	6	I29145	I29145 Sequence 17	480	11.4	43.8	41	6	AX514784	AX514784 Sequence
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409	11.6	44.6	46	6	AR209069	AR209069 Sequence	482	11.4	43.8	42	3	SCAFNCNII	J03789 S.americana
410	11.6	44.6	46	6	AX357202	AX357202 Sequence	483	11.4	43.8	43	6	E14886	E14886 DNA contain
411	11.6	44.6	47	6	CQ753988	CQ753988 Sequence	484	11.4	43.8	44	6	BD181482	BD181482 Poxvirus
412	11.6	44.6	47	6	AR290918	AR290918 Sequence	485	11.4	43.8	45	6	CQ772690	CQ772690 Sequence
413	11.6	44.6	48	3	DME300022	DME300022 Sequence 6	486	11.4	43.8	45	6	CQ772698	CQ772698 Sequence
414	11.6	44.6	50	6	CQ004570	CQ004570 Sequence	487	11.4	43.8	45	6	AX092135	AX092135 Sequence
415	11.6	44.6	50	6	AX510148	AX510148 Sequence	488	11.4	43.8	47	6	AX092135	AX092135 Sequence
416	11.6	44.6	50	6	AX781698	AX781698 Sequence	489	11.4	43.8	47	6	AX138315	AX138315 Sequence
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418	11.4	43.8	20	6	AX718426	AX718426 Sequence	491	11.4	43.8	49	6	AR166620	AR166620 Sequence
419	11.4	43.8	20	6	AX823896	AX823896 Sequence	492	11.4	43.8	49	6	E09371	E09371 DNA fragmen
420	11.4	43.8	21	6	BD228617	BD228617 Sequence	493	11.4	43.8	49	6	AR279828	AR279828 Sequence
421	11.4	43.8	21	6	E35039	E35039 Sequence 1	494	11.4	43.8	50	6	AR148168	AR148168 Sequence
422	11.4	43.8	21	6	I19720	I19720 Sequence 1	495	11.4	43.8	50	6	CQ006611	CQ006611 Sequence
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424	11.4	43.8	23	6	E09959	E09959 Primer for	497	11.2	43.1	17	6	AX688588	AX688588 Sequence
425	11.4	43.8	23	6	E14873	E14873 VZV-specifi	498	11.2	43.1	17	6	AX688588	AX688588 Sequence
426	11.4	43.8	23	6	AX0279190	AX0279190 Sequence	499	11.2	43.1	18	6	BD226573	BD226573 Antisense
427	11.4	43.8	23	6	AX021131	AX021131 Sequence	500	11.2	43.1	18	6	BD226573	BD226573 Antisense
428	11.4	43.8	23	6	BD082764	BD082764 Method fo	501	11.2	43.1	18	6	BD250478	BD250478 Identific
429	11.4	43.8	25	6	AX042816	AX042816 Sequence	502	11.2	43.1	19	6	E49440	E49440 Screening m
430	11.4	43.8	25	6	BD262681	BD262681 Informati	503	11.2	43.1	19	6	AX129020	AX129020 Sequence
431	11.4	43.8	26	6	AX038104	AX038104 Sequence	504	11.2	43.1	19	6	AX100076	AX100076 Sequence
432	11.4	43.8	26	6	AX127109	AX127109 Sequence	505	11.2	43.1	20	6	I24530	I24530 Sequence 10
433	11.4	43.8	26	6	BD165726	BD165726 Novel pol	506	11.2	43.1	20	6	I33872	I33872 Sequence 10
434	11.4	43.8	26	6	AX039574	AX039574 Sequence	507	11.2	43.1	20	6	I83696	I83696 Sequence 26
435	11.4	43.8	27	6	AX088623	AX088623 Sequence	508	11.2	43.1	20	6	AR312047	AR312047 Sequence
436	11.4	43.8	28	6	AX088624	AX088624 Sequence	509	11.2	43.1	20	6	AR315986	AR315986 Sequence
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438	11.4	43.8	28	6	BD223222	BD223222 Isolated	511	11.2	43.1	20	6	AX296011	AX296011 Sequence
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440	11.4	43.8	28	6	AX024607	AX024607 Sequence	513	11.2	43.1	21	6	BD251424	BD251424 Ion chann
441	11.4	43.8	29	6	AX089374	AX089374 Sequence	514	11.2	43.1	21	6	AX023788	AX023788 Sequence
442	11.4	43.8	29	6	AX212299	AX212299 Sequence	515	11.2	43.1	21	6	AR071135	AR071135 Sequence
443	11.4	43.8	30	6	AX093846	AX093846 Sequence	516	11.2	43.1	24	6	AX446835	AX446835 Sequence
444	11.4	43.8	30	6	AX397661	AX397661 Sequence	517	11.2	43.1	24	6	AX741444	AX741444 Sequence
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446	11.4	43.8	30	6	BD061403	BD061403 Peptide h	519	11.2	43.1	25	6	AX548340	AX548340 Sequence
447	11.4	43.8	30	6	BD096247	BD096247 Process f	520	11.2	43.1	25	6	AX610231	AX610231 Sequence
448	11.4	43.8	31	6	AR087440	AR087440 Sequence	521	11.2	43.1	25	6	AX610232	AX610232 Sequence
449	11.4	43.8	31	6	E33094	E33094 Tetrahydroc	522	11.2	43.1	26	6	A68453	A68453 Sequence 26
450	11.4	43.8	31	6	E55109	E55109 DNA encodin	523	11.2	43.1	27	6	A34133	A34133 Synthetic H
451	11.4	43.8	31	6	AR184333	AR184333 Sequence	524	11.2	43.1	27	6	AX35388	AX35388 Synthetic H
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453	11.4	43.8	32	6	BD181214	BD181214 Expressio	526	11.2	43.1	27	6	BD141082	BD141082 Transform
454	11.4	43.8	32	6	AX522092	AX522092 Sequence	527	11.2	43.1	27	6	BD141086	BD141086 Transform
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C 536	11.2	43.1	28	6	AR198064 Sequence	AR198064 Sequence	C 609	11.2	43.1	41	6	BD274163 Identific
C 537	11.2	43.1	28	6	AR214480 Sequence	AR214480 Sequence	C 610	11.2	43.1	41	6	BD274167 Identific
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C 547	11.2	43.1	28	6	AX704517 Sequence	AX704517 Sequence	C 620	11.2	43.1	43	6	I17032 Sequence 43
C 548	11.2	43.1	29	6	AR172331 Sequence	AR172331 Sequence	C 621	11.2	43.1	43	6	AX484541 Sequence
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C 550	11.2	43.1	29	6	AR361346 Sequence	AR361346 Sequence	C 623	11.2	43.1	44	9	HUMTCCVJ6
C 551	11.2	43.1	30	6	AX528934 Sequence	AX528934 Sequence	C 624	11.2	43.1	45	6	CQ767583 Sequence
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C 553	11.2	43.1	31	6	AR102872 Sequence	AR102872 Sequence	C 626	11.2	43.1	45	6	BD170184 Method of
C 554	11.2	43.1	31	6	AR129416 Sequence	AR129416 Sequence	C 627	11.2	43.1	45	6	AR072106 Sequence
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C 557	11.2	43.1	32	6	AR104380 Sequence	AR104380 Sequence	C 630	11.2	43.1	47	6	AR288330 Sequence
C 558	11.2	43.1	32	6	BD249054 Centrifug	BD249054 Centrifug	C 631	11.2	43.1	47	6	AR289708 Sequence
C 559	11.2	43.1	33	6	BD187139 Saponin d	BD187139 Saponin d	C 632	11.2	43.1	48	6	AX224370 Sequence
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C 564	11.2	43.1	34	6	AX001491 Sequence	AX001491 Sequence	C 637	11.2	43.1	50	6	AR403356 Sequence
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C 567	11.2	43.1	35	6	A64752 Sequence 12	A64752 Sequence 12	C 640	11.2	43.1	50	10	AF071693 Mus muscu
C 568	11.2	43.1	35	6	AR161649 Sequence	AR161649 Sequence	C 641	11	42.3	11	6	AX472204 Sequence
C 569	11.2	43.1	36	6	AR217661 Sequence	AR217661 Sequence	C 642	11	42.3	20	6	A58720 Sequence 39
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C 571	11.2	43.1	37	6	AX752552 Sequence	AX752552 Sequence	C 644	11	42.3	20	6	AR256412 Sequence
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C 577	11.2	43.1	38	6	AR043823 Sequence	AR043823 Sequence	C 650	11	42.3	21	6	AR138429 Sequence
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C 587	11.2	43.1	38	6	AR164133 Sequence	AR164133 Sequence	C 660	11	42.3	24	6	AR012296 Sequence
C 588	11.2	43.1	38	6	BD222639 Method of	BD222639 Method of	C 661	11	42.3	24	6	I14994 Sequence 80
C 589	11.2	43.1	38	6	BD234606 Thymidine	BD234606 Thymidine	C 662	11	42.3	24	6	I73714 Sequence 80
C 590	11.2	43.1	38	6	I05098 Sequence 2	I05098 Sequence 2	C 663	11	42.3	24	6	AX097392 Sequence
C 591	11.2	43.1	38	6	I32818 Sequence 14	I32818 Sequence 14	C 664	11	42.3	24	6	AX112094 Sequence
C 592	11.2	43.1	38	6	I32819 Sequence 15	I32819 Sequence 15	C 665	11	42.3	24	6	AX288381 Sequence
C 593	11.2	43.1	38	6	I59632 Sequence 14	I59632 Sequence 14	C 666	11	42.3	24	6	AX290064 Sequence
C 594	11.2	43.1	38	6	I59633 Sequence 15	I59633 Sequence 15	C 667	11	42.3	24	6	AX290281 Sequence
C 595	11.2	43.1	38	6	AR230202 Sequence	AR230202 Sequence	C 668	11	42.3	24	6	AX290964 Sequence
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C 599	11.2	43.1	39	6	A84044 Sequence 31	A84044 Sequence 31	C 672	11	42.3	24	6	AX446561 Sequence
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C 677	11	42.3	25	6	AR271709 Sequence	C 750	11	42.3	36	6	AR103024 Sequence
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C 681	11	42.3	26	6	AR203540 Sequence	C 754	11	42.3	36	6	AR160349 Sequence
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C 683	11	42.3	27	6	BD269107 Directed	C 756	11	42.3	36	6	I0865 Sequence 33
C 684	11	42.3	27	6	AR203923 Sequence	C 757	11	42.3	36	6	AX357941 Sequence
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C 687	11	42.3	27	6	AX511873 Sequence	C 760	11	42.3	36	9	HS278043
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C 699	11	42.3	29	6	BD235512	C 772	11	42.3	40	6	BD227214
C 700	11	42.3	29	6	AR243663	C 773	11	42.3	40	6	BD092068
C 701	11	42.3	30	6	E08861	C 774	11	42.3	40	6	BD103876
C 702	11	42.3	30	6	AR352983	C 775	11	42.3	41	6	AR061592
C 703	11	42.3	30	6	AR449100	C 776	11	42.3	41	6	AR061592
C 704	11	42.3	30	6	PFDFRGMENH	C 777	11	42.3	41	6	AR108491 Sequence
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C 706	11	42.3	31	6	AR026803	C 779	11	42.3	41	6	BD185539 A method
C 707	11	42.3	31	6	AR026803	C 780	11	42.3	41	6	BD188250 bHLH-PAS
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C 710	11	42.3	31	6	AR080578	C 783	11	42.3	41	6	I66934 Sequence 27
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ALIGNMENTS

BD181369 26 bp DNA linear PAT 15-MAY-2003
 A method for determination of a nucleic acid using a control.

BD181369
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

OS Artificial Sequence
 Patent: JP 2002335981-A 8 26-NOV-2002;
 F HOFFMANN LA ROCHE AG
 PN JP 2002335981-A/8
 PD 26-NOV-2002
 PF 04-MAR-2002 JP 2002057515
 PR 02-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
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QY 1 CGTCTTTTCGACATCGGTACTCTCAAT 26
 DB 1 CGTCTTTTCGACATCGGTACTCTCAAT 26

RESULT 2
 AX523949 26 bp DNA linear PAT 21-NOV-2002
 LOCUS
 DEFINITION
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 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES

AX523949
 Sequence 8 from Patent EP1236804.
 AX523949
 AX523949.1 GI:25168880
 synthetic construct
 synthetic construct
 artificial sequences.
 Jaeger, S.
 A method for determination of a nucleic acid using a control
 Patent: EP 1236804-A 8 04-SEP-2002;
 Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
 Location/Qualifiers
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RESULT 3
 AX524847 26 bp DNA linear PAT 21-NOV-2002
 LOCUS
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES

AX524847
 Sequence 8 from Patent EP1236805.
 AX524847
 AX524847.1 GI:25169941
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 synthetic construct
 artificial sequences.
 Jaeger, S.
 A method for the determination of a nucleic acid using a control
 Patent: EP 1236805-A 8 04-SEP-2002;
 Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
 Location/Qualifiers
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 /organism="synthetic construct"
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 DB 1 CGTCTTTTCGACATCGGTACTCTCAAT 26

RESULT 4
LOCUS I38537 44 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 5 from patent US 5614398.
ACCESSION I38537
VERSION I38537.1 GI:2084591
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS O'Brochta,D., Warren,W. and Atkinson,P.
TITLE Gene transfer system for insects
JOURNAL Patent: US 5614398-A 5 25-MAR-1997;
FEATURES Location/Qualifiers
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Query Match 58.5%; Score 15.2; DB 6; Length 44;
Best Local Similarity 85.0%; Pred. No. 9.9e+03;
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Qy 6 TTCGAGATCGGTACCTCAA 25
Db 26 TTCACAGTTCGGTACCTGAA 7

RESULT 5
LOCUS AR053999/c 41 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5834306.
ACCESSION AR053999
VERSION AR053999.1 GI:5978861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Webster,K.A. and Bishopric,N.H.
TITLE Tissue specific hypoxia regulated therapeutic constructs
JOURNAL Patent: US 5834306-A 4 10-NOV-1998;
FEATURES Location/Qualifiers
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Db 30 GTCCTTTCCCTATCGGTACCT 10

RESULT 6
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DEFINITION Sequence 4 from patent US 6218179.
ACCESSION AR146175
VERSION AR146175.1 GI:15109364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Webster,K.A., Bishopric,N.H., Murphy,B., Laderoute,K.R. and Green,C.J.
TITLE Tissue specific hypoxia regulated constructs
JOURNAL Patent: US 6218179-A 4 17-APR-2001;

FEATURES Location/Qualifiers
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Best Local Similarity 75.0%; Pred. No. 2.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 TCTTTCCGACATCGGTACCTCAAT 26
Db 37 TTTTCCAAAGATAGGTACTTCCAT 14

RESULT 7
LOCUS BD263605/c 40 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel streptococcus antigens.
ACCESSION BD263605
VERSION BD263605.1 GI:33073373
KEYWORDS JP 2002533123-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 40)
AUTHORS Hamel,J., Brodeur,B.R., Pineau,I., Martin,D., Rioux,C. and Charland,N.
TITLE Novel streptococcus antigens
JOURNAL Patent: JP 2002533123-A 22 08-OCT-2002;
COMMENT SHIRE BIOCHEM INC
PN JP 2002533123-A/22
PD 08-OCT-2002
PF 20-DEC-1999 JP 2000591190
PR 23-DEC-1998 US 60/113800
PI JOSSE HAMEL, BERNARD R BRODEUR, ISABELLE PINEAU, DENIS MARTIN, PI CLEMENT RIOUX,
PI NATHALIE CHARLAND
PC C12N15/09,A61K39/00,A61K39/39,A61P11/00,A61P25/00,
PC A61P27/16,
PC A61P31/04,C07K14/315,C07K19/00,C12N1/15,C12N1/19,C12N1/21, PC C12N5/10,
PC C12P21/02,C12N15/00,C12N5/00
CC PCR oligonucleotide primer
FH Key Location/Qualifiers
FT source 1..40
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..40
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 55.4%; Score 14.4; DB 6; Length 40;
Best Local Similarity 75.0%; Pred. No. 2.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 TCTTTCCGACATCGGTACCTCAAT 26
Db 37 TTTTCCAAAGATAGGTACTTCCAT 14

RESULT 8
LOCUS AX343106/c 40 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 37 from Patent WO0198334.
ACCESSION AX343106
VERSION AX343106.1 GI:18152286
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

unclassified.

REFERENCE
AUTHORS Hamel,J., Ouellet,C., Charland,N., Martin,D. and Brodeur,B.
TITLE Streptococcus antigens
JOURNAL Patent: WO 0198334-A 37 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
FEATURES
source 1. 40
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="HAMJ 281"

ORIGIN
Query Match 55.4%; Score 14.4; DB 6; Length 40;
Best Local Similarity 75.0%; Pred. No. 2.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TCTTTCGAGATCGGTACTTCCAT 26
Db 37 TTTTTCAGATAGGTACTTCCAT 14

RESULT 9
LOCUS AX454034/c 30 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 10 from Patent WO0198539.
ACCESSION AX454034
VERSION AX454034.1 GI:21713674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Mitsuhashi,M., Kambara,H., Matsunaga,H. and Kawamura,M.
TITLE Gene markers for lung cancer
JOURNAL Patent: WO 0198539-A 10 27-DEC-2001;
Hitachi Chemical Co., Ltd. (JP); HITACHI CHEMICAL RESEARCH CENTER,
INC. (US); Hitachi, Ltd. (JP)
FEATURES
source 1. 30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="7013 Primer P10."

ORIGIN
Query Match 54.6%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CGCAGATCGGTACTTCAAT 26
Db 30 CGCAGATGGGAACCTTAAT 12

RESULT 10
LOCUS MLMLTRB1 48 bp ss-RNA linear VRL 05-AUG-2004
DEFINITION M-MuLV unintegrated circular retroviral DNA, partial LTR.
ACCESSION M10582
VERSION M10582.1 GI:331953
KEYWORDS
SEGMENT 1 of 2
SOURCE Moloney murine leukemia virus
ORGANISM Moloney murine leukemia virus
VIRUSES; Retroid viruses; Retroviridae; Gammaretrovirus.
REFERENCE
AUTHORS 1 (bases 1 to 48)
Shoenmaker,C., Goff,S., Gilboa,E., Paskind,M., Mitra,S.W. and Baltimore,D.
TITLE Structure of cloned retroviral circular DNAs: implications for virus integration
JOURNAL Cold Spring Harb. Symp. Quant. Biol. 45 Pt 2, 711-717 (1981)

unclassified.

REFERENCE
AUTHORS Hamel,J., Ouellet,C., Charland,N., Martin,D. and Brodeur,B.
TITLE Streptococcus antigens
JOURNAL Patent: WO 0198334-A 37 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
FEATURES
source 1. 40
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="HAMJ 281"

ORIGIN
Query Match 53.8%; Score 14; DB 14; Length 48;
Best Local Similarity 77.3%; Pred. No. 4.4e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCTTTCGAGATCGGTACTTCC 23
Db 17 GTCTTTCACCTGATACGTTCTC 38

RESULT 11
LOCUS AX445171/c 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1626 from Patent WO0216649.
ACCESSION AX445171
VERSION AX445171.1 GI:21692449
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 1626 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
source 1. 24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

ORIGIN
Query Match 53.1%; Score 13.8; DB 6; Length 24;
Best Local Similarity 88.2%; Pred. No. 5.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CAGATCGGTACTTCAAT 26
Db 22 CAGATCGGTACTTCAAT 6

RESULT 12
LOCUS AR182869 34 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 41 from patent US 6339068.
ACCESSION AR182869
VERSION AR182869.1 GI:20226076
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 41 15-JAN-2002;
FEATURES
source 1. 34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 52.3%; Score 13.6; DB 6; Length 34;

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Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
Db 10 TCGCAGATCGATACCGAT 29

RESULT 13
LOCUS BD190521 40 bp DNA linear PAT 17-JUL-2003
DEFINITION NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS.
ACCESSION BD190521
VERSION BD190521.1 GI:33000260
KEYWORDS JP 2002541819-A/14.
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1 (bases 1 to 40)
AUTHORS Rabisinski,H., Brettu,H., Ehrat,K., Frykberg,C., Spaltmann,F. and
TITLE NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS
JOURNAL Patent: JP 2002541819-A 14 10-DEC-2002;
COMMENT OS Escherichia coli
PN JP 2002541819-A/14
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000611714
PR 10-APR-1999 DE 199 16 176.3
PI harald rabisinski,heike brettu,kersten ehrat,christoph PI
frykberg,
PI frank spaltmann,bernd berand
CC Primer YGBP2A
FH Key Location/Qualifiers
FEATURES
source
1..40
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"

ORIGIN
Query Match 52.3%; Score 13.6; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TTTCGACATCGGTACCTCA 24
Db 9 TTTAGTGGATCGGTACCTCA 28

RESULT 14
LOCUS AX038843 40 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 22 from Patent WO0061792.
ACCESSION AX038843
VERSION AX038843.1 GI:11228168
KEYWORDS Escherichia coli
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1
AUTHORS Labischinski,H., Wieland,B., Broetz,H., Ehler,K., Freiberg,C. and
TITLE NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS
JOURNAL Patent: WO 0061792-A 22 19-OCT-2000;
LABISCHINSKI HARALD (DE) ; WIELAND BERND (DE) ; BAYER AG (DE) ;
BROETZ HEIKE (DE) ; EHLERT KERSTIN (DE) ; FREIBERG CHRISTOPH (DE) ;
SPALTWANN FRANK (US)
FEATURES
source
1..40
/organism="Escherichia coli"

Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TTTCGACATCGGTACCTCA 24
Db 9 TTTAGTGGATCGGTACCTCA 28

RESULT 15
LOCUS CQ824393 24 bp DNA linear PAT 21-JUN-2004
DEFINITION Sequence 7 from Patent WO2004047866.
ACCESSION CQ824393
VERSION CQ824393.1 GI:49021418
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Margioris,A.N. and Gravanis,A.
TITLE Use of the crh (corticotropin releasing hormone) - ucn (urocortin)
JOURNAL system in the treatment of inflammatory diseases
Patent: WO 2004047866-A 7 10-JUN-2004;
Bionature E.A. Limited (Cy)
FEATURES
source
1..24
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide, PCR Primer"

ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 24;
Best Local Similarity 73.9%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCCTTCGACATCGGTACCTCA 24
Db 23 GTCCTTCGACAGAGAACTTCA 1

RESULT 16
LOCUS AR448717 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6673605.
ACCESSION AR448717
VERSION AR448717.1 GI:42677328
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Sawada,M.
TITLE Established cell line of microglia
JOURNAL Patent: US 6673605-A 3 06-JAN-2004;
FEATURES
source
1..25
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 25;
Best Local Similarity 73.9%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCCTTCGACATCGGTACCTCA 24
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Db      24  GTCCTCTGCAGAGAGAACTTCA 2
RESULT 17
LOCUS   AR101054                      31 bp  DNA  linear  PAT 14-FEB-2001
DEFINITION   Sequence 24 from patent US 6083694.
ACCESSION   AR101054
VERSION     AR101054.1  GI:12811852
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 31)
AUTHORS    Hardy, J. and Goate, A.M.
TITLE      Method for elucidation and detection of polymorphisms, splice
           variants, and proximal coding mutations using intronic sequences of
           the alzheimer's S182 gene
JOURNAL    Patent: US 6083694-A 24 04-JUL-2000;
FEATURES    Location/Qualifiers
             source
             1..31
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Query Match      51.5%; Score 13.4; DB 6; Length 31;
Best Local Similarity 93.3%; Pred. No. 9.2e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  3  TCTTTCGAGATCGGTACTCTCAA 25
      |||||
Db  7  TCTTTCCTTTTCAGAACTCTCAA 29

RESULT 18
LOCUS   AR099751/c                    39 bp  DNA  linear  PAT 14-FEB-2001
DEFINITION   Sequence 22 from patent US 6077949.
ACCESSION   AR099751
VERSION     AR099751.1  GI:12809517
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 39)
AUTHORS    Munroe, D.G., Gupta, A.K., Vyas, T.B., McCallum, K. and Fan, E.
TITLE      Cloned glucagon-like peptide 2 receptors
JOURNAL    Patent: US 6077949-A 22 20-JUN-2000;
FEATURES    Location/Qualifiers
             source
             1..39
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Query Match      51.5%; Score 13.4; DB 6; Length 39;
Best Local Similarity 93.3%; Pred. No. 9.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  11  AGATCGGTACTCTCAA 25
       |||||
Db  22  AGATCGGTACTCTCGA 8

RESULT 19
LOCUS   BD064614/c                    39 bp  DNA  linear  PAT 27-AUG-2002
DEFINITION   Cloned glucagon-like peptide-2 receptors.
ACCESSION   BD064614
VERSION     BD064614.1  GI:22610217
KEYWORDS    JP 2001507571-A/19.
SOURCE      synthetic construct
ORGANISM    synthetic construct
           artificial sequences.

REFERENCE   1 (bases 1 to 39)
AUTHORS    Munroe, D.G., Gupta, A.K., Vyas, T.B., McCallum, K. and Fan, E.
TITLE      Cloned glucagon-like peptide 2 receptors
JOURNAL    Patent: US 6077949-A 22 20-JUN-2000;
FEATURES    Location/Qualifiers
             source
             1..39
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Query Match      51.5%; Score 13.4; DB 6; Length 39;
Best Local Similarity 93.3%; Pred. No. 9.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  11  AGATCGGTACTCTCAA 25
       |||||
Db  22  AGATCGGTACTCTCGA 8

RESULT 20
LOCUS   AX305162                      48 bp  RNA  linear  PAT 11-DEC-2001
DEFINITION   Sequence 10 from Patent WO0188123.
ACCESSION   AX305162
VERSION     AX305162.1  GI:17644792
KEYWORDS    .
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM    James, W.S.
REFERENCE   1
AUTHORS    Ligands specific for an isoform of the prion protein
TITLE      Patent: WO 0188123-A 10 22-NOV-2001;
JOURNAL    Isis Innovation Limited (GB)
FEATURES    Location/Qualifiers
             source
             1..48
             /organism="synthetic construct"
             /mol_type="unassigned RNA"
             /db_xref="taxon:32630"
             /note="Aptamer"

ORIGIN
Query Match      51.5%; Score 13.4; DB 6; Length 48;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  4  CTTTCGACATCGGTACTCTCAAT 26
       |||||
Db  6  CTAGCGACATCGGTACTCTAT 28

RESULT 21
LOCUS   AY124654S3                    50 bp  DNA  linear  MAM 11-FEB-2003
DEFINITION   Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3
           and complete cds.
ACCESSION   AY124656
VERSION     AY124656.1  GI:28315892
KEYWORDS    .

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REFERENCE   1 (bases 1 to 39)
AUTHORS    Munroe, D.G., Gupta, A.K., Vyas, T.B., McCallum, K. and Fan, E.
TITLE      Cloned glucagon-like peptide-2 receptors
JOURNAL    Patent: JP 2001507571-A 19 12-JUN-2001;
           ALLELIX BIOPHARMACEUTICALS INC
COMMENT    PN  JP 2001507571-A/19
           PD  12-JUN-2001
           PF  15-DEC-1997 JP 1998526050
           PR  13-DEC-1996 US 08/767224, 24-JAN-1997 US 08/787721 PR
           24-APR-1997 US 08/845546
           PI  DONALD G MUNROE, ASHWANI K GUPTA, TEJAL B VYAS, KIRK MCCALLUM, PI
           ERMEI FAN
           PC  C12N15/12, C07K14/705, C12N5/10, C12N15/62, C07K16/28, C12Q1/68, PC
           GOIN33/50
           CC  Strandedness: Single;
           CC  Topology: Linear;
           FH  Key  Location/Qualifiers.
FEATURES    Location/Qualifiers
             source
             1..39
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

ORIGIN
Query Match      51.5%; Score 13.4; DB 6; Length 39;
Best Local Similarity 93.3%; Pred. No. 9.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  11  AGATCGGTACTCTCAA 25
       |||||
Db  22  AGATCGGTACTCTCGA 8

RESULT 20
LOCUS   AX305162                      48 bp  RNA  linear  PAT 11-DEC-2001
DEFINITION   Sequence 10 from Patent WO0188123.
ACCESSION   AX305162
VERSION     AX305162.1  GI:17644792
KEYWORDS    .
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM    James, W.S.
REFERENCE   1
AUTHORS    Ligands specific for an isoform of the prion protein
TITLE      Patent: WO 0188123-A 10 22-NOV-2001;
JOURNAL    Isis Innovation Limited (GB)
FEATURES    Location/Qualifiers
             source
             1..48
             /organism="synthetic construct"
             /mol_type="unassigned RNA"
             /db_xref="taxon:32630"
             /note="Aptamer"

ORIGIN
Query Match      51.5%; Score 13.4; DB 6; Length 48;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  4  CTTTCGACATCGGTACTCTCAAT 26
       |||||
Db  6  CTAGCGACATCGGTACTCTAT 28

RESULT 21
LOCUS   AY124654S3                    50 bp  DNA  linear  MAM 11-FEB-2003
DEFINITION   Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3
           and complete cds.
ACCESSION   AY124656
VERSION     AY124656.1  GI:28315892
KEYWORDS    .

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AUTHORS	Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
TITLE	Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL	Immunogenetics 54 (10), 725-733 (2003)
MEDLINE	22444330
PUBMED	12557059
REFERENCE	2 (bases 1 to 50)
AUTHORS	Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUN-2002) James A. Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
FEATURES	Location/Qualifiers
source	1..50
	/organism="Equus caballus"
	/mol_type="genomic DNA"
	/db_xref="taxon:9796"
	/chromosome="1"
gene	/note="breed: Clydesdale"
	order(AY124657.1:<1..67,AY124658.1:1..276,1.>50)
mRNA	/gene="b-2-m"
	join(AY124657.1:<1..67,AY124658.1:1..276,20.>50)
	/gene="b-2-m"
CDS	/product="beta-2-microglobulin precursor"
	join(AY124657.1:1..67,AY124658.1:1..276,20..33)
	/gene="b-2-m"
	/codon_start=1
	/product="beta-2-microglobulin precursor"
	/protein_id="AAW77009.1"
	/db_xref="GI:28315898"
	/translation="MARVALVLLGLSLTGLEAVRPVKQVYSRHPAENGKPNFLN CYVSGFPHPEIIDLKNGEKMKVDRLSFSKDWSFYLLVHTDFTPNGVDEYSRCRV HSTLKDLPIVKWRDL"
mat_peptide	join(AY124657.1:61..67,AY124658.1:1..276,20..30)
exon	/gene="b-2-m"
	/product="beta-2-microglobulin"
	20..>50
	/gene="b-2-m"
	/number=3
3'UTR	34..>50
	/gene="b-2-m"
ORIGIN	
Query Match	51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity	73.9%; Pred. No. 9.3e+04;
Matches	17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Dn	3 TCTTTGCGAGATCGGTACCTCAA 25 10 TTTTTCATAGATCGAGACTCTA 32
RESULT 23	
LOCUS	AY124660S3 50 bp DNA linear MAM 11-FEB-2003
DEFINITION	Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3 and complete cds.
ACCESSION	AY124662
VERSION	AY124662.1 GI:28315902
KEYWORDS	3 of 3
SEGMENT	Equus caballus (horse)
SOURCE	Equus caballus
ORGANISM	Equus caballus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus. 1 (bases 1 to 50)
AUTHORS	Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
TITLE	Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL	Immunogenetics 54 (10), 725-733 (2003)
MEDLINE	22444330
PUBMED	12557059
REFERENCE	2 (bases 1 to 50)
AUTHORS	Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUN-2002) James A. Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
FEATURES	Location/Qualifiers
source	1..50
	/organism="Equus caballus"
	/mol_type="genomic DNA"
	/db_xref="taxon:9796"
	/chromosome="1"
gene	/notes="breed: Arabian"
	order(AY124654.1:<1..67,AY124655.1:1..276,1.>50)
mRNA	/gene="b-2-m"
	join(AY124654.1:<1..67,AY124655.1:1..276,20.>50)
	/gene="b-2-m"
CDS	/product="beta-2-microglobulin precursor"
	join(AY124654.1:1..67,AY124655.1:1..276,20..33)
	/gene="b-2-m"
	/codon_start=1
	/product="beta-2-microglobulin precursor"
	/protein_id="AAW77009.1"
	/db_xref="GI:28315893"
	/translations="MARVALVLLGLSLTGLEAVRPVKQVYSRHPAENGKPNFLN CYVSGFPHPEIIDLKNGEKMKVDRLSFSKDWSFYLLVHTDFTPNGVDEYSRCRV HSTLKDLPIVKWRDL"
mat_peptide	join(AY124654.1:61..67,AY124655.1:1..276,20..30)
exon	/gene="b-2-m"
	/product="beta-2-microglobulin"
	20..>50
	/gene="b-2-m"
	/number=3
3'UTR	34..>50
	/gene="b-2-m"
ORIGIN	
Query Match	51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity	73.9%; Pred. No. 9.3e+04;
Matches	17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Dn	3 TCTTTGCGAGATCGGTACCTCAA 25 10 TTTTTCATAGATCGAGACTCTA 32
RESULT 22	
LOCUS	AY124657S3 50 bp DNA linear MAM 11-FEB-2003
DEFINITION	Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3 and complete cds.
ACCESSION	AY124659
VERSION	AY124659.1 GI:28315897
KEYWORDS	3 of 3
SEGMENT	Equus caballus (horse)
SOURCE	Equus caballus
ORGANISM	Equus caballus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus. 1 (bases 1 to 50)

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REFERENCE      2 (bases 1 to 50)
AUTHORS        Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
                Carpenter,S.L., and Antczak,D.F.
TITLE          Direct Submission
JOURNAL        Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
                College of Veterinary Medicine, Cornell University, Hungerford Hill
                Rd., Ithaca, NY 14850, USA
FEATURES       Location/Qualifiers
source         1..50
                /organism="Equus caballus"
                /mol_type="genomic DNA"
                /db_xref="taxon:9796"
                /chromosome="1"
                /note="breed: Miniature Horse"
gene          order(AV124660.1:<1..67,AV124661.1:1..276,1..>50)
                /gene="b-2-m"
mRNA          join(AV124660.1:<1..67,AV124661.1:1..276,20..>50)
                /gene="b-2-m"
CDS           join(AV124660.1:1..67,AV124661.1:1..276,20..33)
                /gene="b-2-m"
                /codon_start=1
                /product="beta-2-microglobulin precursor"
                /protein_id="AAM77011.1"
                /db_xref="GI:28315903"
                /translation="MARVVALVLLGLSLTGLEAVRPVKQVYGRHHPAENGKPNFLN
                CVVSGFHPPEIIDLKNGEKVKDRSDFSFKDWSFYLLVHTDFTPNGVDYSCRVO
                HSTLKDPLIVKWDRL"
mat_peptide   join(AV124660.1:61..67,AV124661.1:1..276,20..30)
                /gene="b-2-m"
exon          20..>50
                /gene="b-2-m"
                /number=3
3'UTR         34..>50
                /gene="b-2-m"
ORIGIN
Query Match      51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAA 25
    ||||| ||||| ||||| |||||
Db 10 TTTTTCATAGATCGAGACCTCTA 32

RESULT 24
AV124663S3      50 bp DNA linear MAM 11-FEB-2003
LOCUS           Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3
DEFINITION      and complete cds.
ACCESSION       AV124665
VERSION         AV124665.1 GI:28315907
KEYWORDS        3 of 3
SEGMENT         Equus caballus (horse)
SOURCE          Equus caballus
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE       1 (bases 1 to 50)
AUTHORS         Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
                Carpenter,S.L., and Antczak,D.F.
TITLE           Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL         Immunogenetics 54 (10), 725-733 (2003)
MEDLINE         22444330
PUBMED         12557059
REFERENCE       2 (bases 1 to 50)
AUTHORS         Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
                Carpenter,S.L., and Antczak,D.F.
TITLE           Direct Submission
JOURNAL         Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
                College of Veterinary Medicine, Cornell University, Hungerford Hill

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Rd., Ithaca, NY 14850, USA
FEATURES       Location/Qualifiers
source         1..50
                /organism="Equus caballus"
                /mol_type="genomic DNA"
                /db_xref="taxon:9796"
                /chromosome="1"
                /note="breed: Standardbred"
gene          order(AV124663.1:<1..67,AV124664.1:1..276,1..>50)
                /gene="b-2-m"
mRNA          join(AV124663.1:<1..67,AV124664.1:1..276,20..>50)
                /gene="b-2-m"
                /product="beta-2-microglobulin precursor"
CDS           join(AV124663.1:1..67,AV124664.1:1..276,20..33)
                /gene="b-2-m"
                /codon_start=1
                /product="beta-2-microglobulin precursor"
                /protein_id="AAM77012.1"
                /db_xref="GI:28315908"
                /translation="MARVVALVLLGLSLTGLEAVRPVKQVYGRHHPAENGKPNFLN
                CVVSGFHPPEIIDLKNGEKVKDRSDFSFKDWSFYLLVHTDFTPNGVDYSCRVO
                HSTLKDPLIVKWDRL"
mat_peptide   join(AV124663.1:61..67,AV124664.1:1..276,20..30)
                /gene="b-2-m"
exon          20..>50
                /gene="b-2-m"
                /number=3
3'UTR         34..>50
                /gene="b-2-m"
ORIGIN
Query Match      51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAA 25
    ||||| ||||| ||||| |||||
Db 10 TTTTTCATAGATCGAGACCTCTA 32

RESULT 25
AV124666S3      50 bp DNA linear MAM 11-FEB-2003
LOCUS           Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3
DEFINITION      and complete cds.
ACCESSION       AV124668
VERSION         AV124668.1 GI:28315912
KEYWORDS        3 of 3
SEGMENT         Equus caballus (horse)
SOURCE          Equus caballus
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE       1 (bases 1 to 50)
AUTHORS         Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
                Carpenter,S.L., and Antczak,D.F.
TITLE           Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL         Immunogenetics 54 (10), 725-733 (2003)
MEDLINE         22444330
PUBMED         12557059
REFERENCE       2 (bases 1 to 50)
AUTHORS         Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
                Carpenter,S.L., and Antczak,D.F.
TITLE           Direct Submission
JOURNAL         Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
                College of Veterinary Medicine, Cornell University, Hungerford Hill
                Rd., Ithaca, NY 14850, USA
FEATURES       Location/Qualifiers
source         1..50
                /organism="Equus caballus"
                /mol_type="genomic DNA"
                /db_xref="taxon:9796"

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/chromosome="1"
/note="breed: Thoroughbred"
order (AY124666.1:<1..67,AY124667.1:1..276,1..>50)
/gene="b-2-m"
join (AY124666.1:<1..67,AY124667.1:1..276,20..>50)
/gene="b-2-m"
product="beta-2-microglobulin precursor"
translation="MARVALVLGLSLTGLEAVPRVKQVYSRHPAENGKPNFLN
CYVSGFHPPEIIDLKNGEKMKVDRSDLSFKDMSFYLLVHTDFTNGVDEYSCRVO
HSTLKDPLIVKWRDL"
join (AY124666.1:1..61..67,AY124667.1:1..276,20..30)
/gene="b-2-m"
/codon_start=1
/product="beta-2-microglobulin precursor"
/protein_id="AA077013.1"
/db_xref="GI:28315913"
translation="MARVALVLGLSLTGLEAVPRVKQVYSRHPAENGKPNFLN
CYVSGFHPPEIIDLKNGEKMKVDRSDLSFKDMSFYLLVHTDFTNGVDEYSCRVO
HSTLKDPLIVKWRDL"
join (AY124666.1:1..61..67,AY124667.1:1..276,20..30)
/gene="b-2-m"
/product="beta-2-microglobulin"
20..>50
/gene="b-2-m"
/number=3
34..>50
/gene="b-2-m"

mat_peptide
join (AY124666.1:1..61..67,AY124667.1:1..276,20..30)
/gene="b-2-m"

exon
20..>50
/gene="b-2-m"
/number=3
34..>50
/gene="b-2-m"

3'UTR

ORIGIN
Query Match 51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCCTTCGAGATCGTACTCAA 25
| |||| |||| ||||
Db 10 TTTTCATAGATCGAGACTCTA 32

RESULT 26
AY124669S3
LOCUS
DEFINITION
Equis przewalskii beta-2-microglobulin precursor (b-2-m) gene, exon
3 and complete cds.
ACCESSION
AY124671.1 GI:28315917
VERSION
3 of 3
KEYWORDS
Equis przewalskii
SEGMENT
Equis przewalskii
SOURCE
Equis asinus (ass)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE
1 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
Characterization of the beta(2)-microglobulin gene of the horse
Immunogenetics 54 (10), 725-733 (2003)
22444330
PUBMED
12557059
2 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
Direct Submission
Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
College of Veterinary Medicine, Cornell University, Hungerford Hill
Rd., Ithaca, NY 14850, USA
Location/Qualifiers
1..50
/organism="Equis przewalskii"
/mol_type="genomic DNA"
/db_xref="taxon:9798"
/note="breed: Przewalski's Horse"
order (AY124669.1:<1..67,AY124670.1:1..276,1..>50)
/gene="b-2-m"
join (AY124669.1:<1..67,AY124670.1:1..276,20..>50)
/gene="b-2-m"
product="beta-2-microglobulin precursor"

gene
mRNA

FEATURES
source
1..50
/organism="Equis asinus"
/mol_type="genomic DNA"
/isolate="1"
/db_xref="taxon:9793"
order (AY124672.1:<1..67,AY124673.1:1..276,1..>50)
/gene="b-2-m"
join (AY124672.1:<1..67,AY124673.1:1..276,20..>50)
/gene="b-2-m"
/product="beta-2-microglobulin precursor"
join (AY124672.1:1..67,AY124673.1:1..276,20..33)
/gene="b-2-m"
/codon_start=1
/product="beta-2-microglobulin precursor"
/protein_id="AA077015.1"
/db_xref="GI:28315923"
translation="MARVALVLGLSLTGLEAVQRIKQVYSRHPAENGKPNFLN

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CDS
join (AY124669.1:1..67,AY124670.1:1..276,20..33)
/gene="b-2-m"
/codon_start=1
/product="beta-2-microglobulin precursor"
/protein_id="AA077014.1"
/db_xref="GI:28315918"
translation="MARVALVLGLSLTGLEAVPRVKQVYSRHPAENGKPNFLN
CYVSGFHPPEIIDLKNGEKMKVDRSDLSFKDMSFYLLVHTDFTNGVDEYSCRVO
HSTLKDPLIVKWRDL"
join (AY124669.1:1..61..67,AY124670.1:1..276,20..30)
/gene="b-2-m"
/product="beta-2-microglobulin"
20..>50
/gene="b-2-m"
/number=3
34..>50
/gene="b-2-m"

mat_peptide
join (AY124669.1:1..61..67,AY124670.1:1..276,20..30)
/gene="b-2-m"

exon
20..>50
/gene="b-2-m"
/number=3
34..>50
/gene="b-2-m"

3'UTR

ORIGIN
Query Match 51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCCTTCGAGATCGTACTCAA 25
| |||| |||| ||||
Db 10 TTTTCATAGATCGAGACTCTA 32

RESULT 27
AY124672S3
LOCUS
DEFINITION
Equis asinus isolate 1 beta-2-microglobulin precursor (b-2-m) gene,
exon 3 and complete cds.
ACCESSION
AY124674
VERSION
AY124674.1 GI:28315922
KEYWORDS
3 of 3
SEGMENT
Equis asinus (ass)
SOURCE
Equis asinus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE
1 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
Characterization of the beta(2)-microglobulin gene of the horse
Immunogenetics 54 (10), 725-733 (2003)
22444330
PUBMED
12557059
2 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
Direct Submission
Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
College of Veterinary Medicine, Cornell University, Hungerford Hill
Rd., Ithaca, NY 14850, USA
Location/Qualifiers
1..50
/organism="Equis asinus"
/mol_type="genomic DNA"
/isolate="1"
/db_xref="taxon:9793"
order (AY124672.1:<1..67,AY124673.1:1..276,1..>50)
/gene="b-2-m"
join (AY124672.1:<1..67,AY124673.1:1..276,20..>50)
/gene="b-2-m"
/product="beta-2-microglobulin precursor"
join (AY124672.1:1..67,AY124673.1:1..276,20..33)
/gene="b-2-m"
/codon_start=1
/product="beta-2-microglobulin precursor"
/protein_id="AA077015.1"
/db_xref="GI:28315923"
translation="MARVALVLGLSLTGLEAVQRIKQVYSRHPAENGKPNFLN

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	mat_peptide	CYVSGFHPPEIEIDLLKNGEKMKVDRLSFDLSQWSFYLLVHTDFTPNGVDEYSRCRV HSTLKEPLIVKWDRDL"
	exon	join(AV124672.1:61..67,AV124673.1:1..276,20..30) /gene="b-2-m" /product="beta-2-microglobulin" 20..>50 /gene="b-2-m" number=3 34..>50 /gene="b-2-m"
	3'UTR	
ORIGIN		
	Query Match	51.5%; Score 13.4; DB 4; Length 50;
	Best Local Similarity	73.9%; Pred. No. 9.3e+04;
	Matches	17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
	Dn	3 TCTTTCGCGAGATCGGTACTCAA 25 10 TTTTTCATAGATCGAGACCTCTA 32
RESULT 28		
AV124675S3		50 bp DNA linear MAM 11-FEB-2003
LOCUS		Equis asinus isolate 2 beta-2-microglobulin precursor (b-2-m) gene,
DEFINITION		exon 3 and complete cds.
ACCESSION		AV124677
VERSION		AV124677.1 GI:28315927
KEYWORDS		
SEGMENT		
SOURCE		3 of 3. Equis asinus (ass)
ORGANISM		Equis asinus
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactylia; Equidae; Equus.
AUTHORS		1 (bases 1 to 50) Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
TITLE		Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL		Immunogenetics 54 (10), 725-733 (2003)
MEDLINE		22444330
PUBMED		12557059
REFERENCE		2 (bases 1 to 50) Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
AUTHORS		Direct Submission
TITLE		Submitted (20-JUN-2002) James A. Baker Institute for Animal Health
JOURNAL		College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
FEATURES		Location/Qualifiers 1..50 /organism="Equus asinus" /mol_type="genomic DNA" /isolate="2" /db_xref="taxon:9793" order(AV124675.1:<1..67,AV124676.1:1..276,1..>50) /gene="b-2-m" join(AV124675.1:<1..67,AV124676.1:1..276,20..>50) /gene="b-2-m" /product="beta-2-microglobulin precursor" join(AV124675.1:1..67,AV124676.1:1..276,20..33) /gene="b-2-m" /codon_start=1 /product="beta-2-microglobulin precursor" /protein_id="AAW7016.1" /db_xref="GI:28315928" /translation="MARVALVLGLSLTGLEAVORIPKVQVSHPAENGKPNFI CYVSGFHPPEIEIDLLKNGEKMKVDRLSFDLSQWSFYLLVHTDFTPNGVDEYSRCRV HSTLKEPLIVKWDRDL"
	gene	
	mRNA	
	CDS	
	mat_peptide	join(AV124675.1:61..67,AV124676.1:1..276,20..30)
	exon	/gene="b-2-m" 20..>50 /product="beta-2-microglobulin" 20..>50 /gene="b-2-m"

[illegible]

KEYWORDS
SEGMENT 3 of 3
SOURCE Equus burchellii chapmani (Chapman's Zebra)
ORGANISM Equus burchellii chapmani
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE
AUTHORS 1 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL Immunogenetics 54 (10), 725-733 (2003)
MEDLINE 22444330
PUBMED 12557059

REFERENCE
AUTHORS 2 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
College of Veterinary Medicine, Cornell University, Hungerford Hill
Rd., Ithaca, NY 14850, USA
MEDLINE 22444330
PUBMED 12557059

REFERENCE
AUTHORS 2 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
College of Veterinary Medicine, Cornell University, Hungerford Hill
Rd., Ithaca, NY 14850, USA
MEDLINE 22444330
PUBMED 12557059

FEATURES
source
1. .50
/organism="Equus burchellii chapmani"
/mol_type="genomic DNA"
/sub_species="chapmani"
/db_xref="taxon:192603"
/notes="common: Chapman's Zebra"
order(AY124687.1<1. .67,AY124688.1:1. .276,1. .>50)
/gene="b-2-m"
/genes="b-2-m"
join(AY124687.1<1. .67,AY124688.1:1. .276,20. .>50)
/genes="b-2-m"
/product="beta-2-microglobulin precursor"
join(AY124687.1:1. .67,AY124688.1:1. .276,20. .33)
/gene="b-2-m"
/codon_start=1
/product="beta-2-microglobulin precursor"
/protein_id="AAM77020.1"
/db_xref="GI:28315948"
/translators="MARVALVLLGLSLTGLEAVORIPKQVYSEHPAENGKPNFLN
CYVSGFHPPEIIDLKNGEKMKVDRSDLSFSKOWSFYLLVHTDFTPNGVDYSYCRVQ
HSTLKEPLIVKWRDL"
mat_peptide join(AY124687.1:61. .67,AY124688.1:1. .276,20. .30)
/gene="b-2-m"
/product="beta-2-microglobulin"
20. .>50
/gene="b-2-m"
/number=3
34. .>50
/gene="b-2-m"
exon
3'UTR
ORIGIN
Query Match 51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 TCTTTCGAGATCGTACTCAA 25
Db 10 TTTTTCATAGATCGAGACTCTA 32
RESULT 33
AY124690S3 50 bp DNA linear MAM 11-FEB-2003
LOCUS Equus burchellii antiquorum beta-2-microglobulin precursor (b-2-m)
DEFINITION gene, exon 3 and complete cds.
ACCESSION AY124692
VERSION AY124692.1 GI:28315952
KEYWORDS
SEGMENT 3 of 3
SOURCE Equus burchellii antiquorum (Damara's Zebra)
ORGANISM Equus burchellii antiquorum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE
AUTHORS 1 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL Immunogenetics 54 (10), 725-733 (2003)
MEDLINE 22444330
PUBMED 12557059

REFERENCE
AUTHORS 2 (bases 1 to 50)
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
College of Veterinary Medicine, Cornell University, Hungerford Hill
Rd., Ithaca, NY 14850, USA
MEDLINE 22444330
PUBMED 12557059

FEATURES
source
1. .50
/organism="Equus burchellii antiquorum"
/mol_type="genomic DNA"
/sub_species="antiquorum"
/db_xref="taxon:200155"
/notes="common: Damara's Zebra"
order(AY124690.1<1. .67,AY124691.1:1. .276,1. .>50)
/gene="b-2-m"
/genes="b-2-m"
join(AY124690.1<1. .67,AY124691.1:1. .276,20. .>50)
/genes="b-2-m"
/product="beta-2-microglobulin precursor"
join(AY124690.1:1. .67,AY124691.1:1. .276,20. .33)
/gene="b-2-m"
/codon_start=1
/product="beta-2-microglobulin precursor"
/protein_id="AAM77021.1"
/db_xref="GI:28315953"
/translators="MARVALVLLGLSLTGLEAVORIPKQVYSEHPAENGKPNFLN
CYVSGFHPPEIIDLKNGEKMKVDRSDLSFSKOWSFYLLVHTDFTPNGVDYSYCRVQ
HSTLKEPLIVKWRDL"
mat_peptide join(AY124690.1:61. .67,AY124691.1:1. .276,20. .30)
/gene="b-2-m"
/product="beta-2-microglobulin"
20. .>50
/gene="b-2-m"
/number=3
34. .>50
/gene="b-2-m"
exon
3'UTR
ORIGIN
Query Match 51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 TCTTTCGAGATCGTACTCAA 25
Db 10 TTTTTCATAGATCGAGACTCTA 32
RESULT 34
AY124693S3 50 bp DNA linear MAM 11-FEB-2003
LOCUS Equus burchellii boehmi beta-2-microglobulin precursor (b-2-m)
DEFINITION gene, exon 3 and complete cds.
ACCESSION AY124695
VERSION AY124695.1 GI:28315957
KEYWORDS
SEGMENT 3 of 3
SOURCE Equus burchellii boehmi (Grant's Zebra)
ORGANISM Equus burchellii boehmi
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL Immunogenetics 54 (10), 725-733 (2003)
MEDLINE 22444330

PUBMED 12557059
 REFERENCE 2 (bases 1 to 50)
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
 FEATURES Location/Qualifiers
 source 1..50
 /organism="Equus burchellii boehmi"
 /mol_type="genomic DNA"
 /sub_species="boehmi"
 /db_xref="taxon:89250"
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 DEFINITION and complete cds.
 ACCESSION AY124698
 VERSION AY124698.1 GI:28315962
 KEYWORDS
 SEGMENT
 SOURCE
 ORGANISM
 Equus grevyi (Grevy's Zebra)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 1 (bases 1 to 50)
 Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
 Carpenter,S.L. and Antczak,D.F.
 TITLE Characterization of the beta(2)-microglobulin gene of the horse
 JOURNAL Immunogenetics 54 (10), 725-733 (2003)
 MEDLINE 22444330
 PUBMED 12557059
 REFERENCE 2 (bases 1 to 50)
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
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 Db 10 TTTTTCATAGATCGAGACCTCTA 32
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 DEFINITION exon 3 and complete cds.
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 VERSION AY124701.1 GI:28315967
 KEYWORDS
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 SOURCE
 ORGANISM
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 Equus zebra hartmannae
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 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 1 (bases 1 to 50)
 Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
 Carpenter,S.L. and Antczak,D.F.
 TITLE Characterization of the beta(2)-microglobulin gene of the horse
 JOURNAL Immunogenetics 54 (10), 725-733 (2003)
 MEDLINE 22444330
 PUBMED 12557059
 REFERENCE 2 (bases 1 to 50)
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
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College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
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 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 3 TCTTTCCGAGATCGGTACCTCAA 25
 Db 10 TTTTTCATAGATCGAGACCTCTA 32
 RESULT 36
 AY124699S3
 LOCUS Equus zebra hartmannae beta-2-microglobulin precursor (b-2-m) gene,
 DEFINITION exon 3 and complete cds.
 ACCESSION AY124701
 VERSION AY124701.1 GI:28315967
 KEYWORDS
 SEGMENT
 SOURCE
 ORGANISM
 Equus zebra hartmannae (Hartmann's Zebra)
 Equus zebra hartmannae
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 1 (bases 1 to 50)
 Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
 Carpenter,S.L. and Antczak,D.F.
 TITLE Characterization of the beta(2)-microglobulin gene of the horse
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 MEDLINE 22444330
 PUBMED 12557059
 REFERENCE 2 (bases 1 to 50)
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V., Carpenter,S.L. and Antczak,D.F.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA
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Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 10 TTTTTCATAGATCGAGACCTCTA 32

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LOCUS Method of constructing transgenic plant having improved amino acid
DEFINITION composition and yield.
ACCESSION BD189528.1 GI:32999267
VERSION WO 03000041-A/13.
KEYWORDS synthetic construct
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 30)
REFERENCE 1 (bases 1 to 30)
AUTHORS Kizaka,H. and Kida,T.
TITLE Method of constructing transgenic plant having improved amino acid
JOURNAL composition and yield
COMMENT Patent: WO 03000041-A 13 03-JAN-2003;
AJINOMOTO CO INC,HIROAKI KISAKA,TAKAO KIDA
OS Artificial Sequence
PN WO 03000041-A/13
PD 03-JAN-2003
PF 14-JUN-2001 WO 2001JP005077
PI HIROAKI KISAKA,TAKAO KIDA
PC A01H5/00,C12N15/53,C12N15/83
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CC sequence for chloroplast transit peptide
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Description of Artificial Sequence:PCR primer for amplifying CC
the coding

CC sequence for chloroplast transit peptide

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Location/Qualifiers

1..30

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LOCUS

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Method for making transgenic plants having improved amino acid

composition.

ACCESSION BD017636

VERSION BD017636.1 GI:22558812

KEYWORDS JP 2001238556-A/19.

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1 (bases 1 to 30)

AUTHORS Kisaka,H. and Kida,T.

TITLE Method for making transgenic plants having improved amino acid

composition

JOURNAL Patent: JP 2001238556-A 19 04-SEP-2001;

AJINOMOTO CO INC

COMMENT OS Artificial Sequence

PN JP 2001238556-A/19

PD 04-SEP-2001

PF 18-DEC-2000 JP 2000404322

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PC A01H5/00,C12N5/10,C12N9/06,C12N15/09,C12N15/00 CC

Description of artificial Sequence:PCR primer for producing CC

chloroplast

CC transit peptide-GDH coding sequence

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Job time : 471.195 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 139.543 Seconds
(without alignments)
978.085 Million cell updates/sec

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Perfect score: 26
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	15.4	59.2	25	9	ACI53778 Human mic
C 6	15.2	58.5	25	9	ACH57668 DNA targe
C 7	15.2	58.5	25	9	ACH57794 DNA targe
C 8	15.2	58.5	25	9	ACH54380 DNA targe
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C 11	14.6	56.2	41	2	AAT31022 Human end
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C 13	14.4	55.4	23	2	AAT88375 Primer fo
C 14	14.4	55.4	25	9	ACI161181 Human mic
C 15	14.4	55.4	25	9	ACH57248 DNA targe
C 16	14.4	55.4	40	3	AAA65754 Streptoco
C 17	14.4	55.4	40	6	ABK33676 S. pneumo
C 18	14.2	54.6	25	9	ACK29528 Human mic
C 19	14.2	54.6	25	9	ACH56079 DNA targe
C 20	14.2	54.6	30	6	AAT72282 7013 mark
C 21	14	53.8	25	9	ACI42451 Human mic

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c 97	12.8	49.2	30	10	ADF76152	Adf76152 Mutagenic	170	12.4	47.7	28	4	AXF86135	Aaf86135 PCR prime
c 98	12.8	49.2	34	4	AF81897	Aaf81897 Human thy	171	12.4	47.7	28	8	ABT14499	Abt14499 Cynomolog
c 99	12.8	49.2	38	2	AA111361	Aat11361 Class B t	c 172	12.4	47.7	31	2	AAQ34049	Aaq34049 Sequence
c 100	12.8	49.2	38	2	AA111361	Aat11361 Class B t	c 173	12.4	47.7	32	8	ACD56655	Acd56655 HBV enzym
c 101	12.8	49.2	38	2	AAV60084	Aav60084 Class B t	c 174	12.4	47.7	32	8	ACD56656	Acd56656 HBV enzym
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c 113	12.8	49.2	41	6	ABZ47382	Abz47382 Human ATP	c 186	12.4	47.7	42	12	ADL93867	Adl93867 Human FOX
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c 140	12.6	48.5	32	10	ABV99697	Abv99697 Escherich	c 213	12.2	46.9	35	10	ACF03415	Acf03415 Synthetic
c 141	12.6	48.5	32	12	ABA03912	Abao3912 Human pho	c 214	12.2	46.9	36	2	AAV40058	Aav40058 D3 cdna S
c 142	12.6	48.5	33	6	ABN88722	Abn88722 Dombrock	c 215	12.2	46.9	36	2	AAV40058	Aav40058 D3 cdna S
c 143	12.6	48.5	37	6	ACN19435	Acn19435 WNV Zinzy	c 216	12.2	46.9	36	2	AAT99555	Aat99555 Tissue pl
c 144	12.6	48.5	40	2	AAV72465	Aav72465 Human PRO	c 217	12.2	46.9	36	8	ABS55918	Abes55918 Tissue pl
c 145	12.6	48.5	43	3	AAH41456	Aah41456 HBV ampli	c 218	12.2	46.9	36	8	ABS55918	Abes55918 Tissue pl
c 146	12.6	48.5	43	4	AAH41822	Aah41822 Hepatitis	c 219	12.2	46.9	37	6	ACN30963	Acn30963 WNV minus
c 147	12.6	48.5	50	6	ABZ04517	Abz04517 Human leu	c 220	12.2	46.9	37	6	ACN31204	Acn31204 WNV minus
c 148	12.4	47.7	17	8	ACC63143	Acc63143 Murine ol	c 221	12.2	46.9	37	6	ACN30714	Acn30714 WNV minus
c 149	12.4	47.7	17	10	ADF62126	Adf62126 Human PCC	c 222	12.2	46.9	39	11	ADM39488	Adm39488 Recombina
c 150	12.4	47.7	17	10	ADF62127	Adf62127 Human PCC	c 223	12.2	46.9	41	2	AAQ21814	Aaq21814 PCR prime
c 151	12.4	47.7	20	6	AB195311	Abi95311 Capture o	c 224	12.2	46.9	41	3	AAQ21814	Aaq21814 PCR prime
c 152	12.4	47.7	21	6	AB897225	Abh55958 Human CYP	c 225	12.2	46.9	41	3	AAQ21814	Aaq21814 PCR prime
c 153	12.4	47.7	24	5	AAH55958	Aah55958 Human SCN	c 226	12.2	46.9	42	3	AAK83206	Abk83206 Human cyt
c 154	12.4	47.7	24	6	AB187193	Abi87193 Capture o	c 227	12.2	46.9	42	3	AAK83206	Abk83206 Human cyt
c 155	12.4	47.7	24	6	AB187192	Abi87192 Capture o	c 228	12.2	46.9	43	3	AAT40749	Aat40749 Recombina
c 156	12.4	47.7	24	6	AB187192	Abi87192 Capture o	c 229	12.2	46.9	43	3	AAT40749	Aat40749 Recombina
c 157	12.4	47.7	25	9	ACT42450	Act42450 Human mic	c 230	12.2	46.9	46	4	AAH77976	Aah77976 Oligonuc
c 158	12.4	47.7	25	9	ACT42450	Act42450 Human mic	c 231	12.2	46.9	46	4	AAH77976	Aah77976 Oligonuc
c 159	12.4	47.7	25	9	ACT42450	Act42450 Human mic	c 232	12.2	46.9	48	8	ABZ09274	Abz09274 Human oli
c 160	12.4	47.7	25	9	ACT42450	Act42450 Human mic	c 233	12.2	46.9	48	8	ABZ09274	Abz09274 Human oli
c 161	12.4	47.7	25	9	ACK20277	Ack20277 Human mic	c 234	12.2	46.9	48	8	ABZ09274	Abz09274 Human oli
c 162	12.4	47.7	25	9	ACK20277	Ack20277 Human mic	c 235	12.2	46.9	50	10	ADD31927	Add31927 Human ret
c 163	12.4	47.7	25	9	ACK20277	Ack20277 Human mic	c 236	12.2	46.9	50	10	ADD31911	Add31911 Human ret
c 164	12.4	47.7	25	9	ACK26780	Ack26780 Human mic	c 237	12.2	46.9	50	10	ADD31911	Add31911 Human ret
c 165	12.4	47.7	25	9	ACK26780	Ack26780 Human mic	c 238	12.2	46.9	50	10	ADD31911	Add31911 Human ret
c 166	12.4	47.7	25	9	ACK26780	Ack26780 Human mic	c 239	12.2	46.9	50	10	ADD31911	Add31911 Human ret
c 167	12.4	47.7	25	9	ACK26780	Ack26780 Human mic	c 240	12.2	46.9	50	10	ADD31911	Add31911 Human ret

241	12	46.2	20	12	ADH77273	Adh77273 Human PAZ	C 314	12	46.2	48	10	ADH48220	Adh48220 Primer of
242	12	46.2	21	2	AAQ71151	AAQ71151 Merlin ex	C 315	12	46.2	50	6	ABZ02849	ABZ02849 Human leu
243	12	46.2	21	2	ADRO1317	ADRO1317 Selectabl	C 316	12	46.2	50	6	ABZ05415	ABZ05415 Human leu
244	12	46.2	21	3	AAAL14510	AAAL14510 Primer us	C 317	12	46.2	50	8	ACA15212	ACA15212 Prokaryot
245	12	46.2	21	4	ADL18412	ADL18412 Geneticin	C 318	11.8	45.4	15	12	ADMS3673	ADMS3673 Nucleic a
246	12	46.2	21	4	AAI66711	AAI66711 A. gossyp	C 319	11.8	45.4	17	8	ACD55947	ACD55947 HBV amber
247	12	46.2	21	6	ABK16409	ABK16409 Ashbya go	C 320	11.8	45.4	17	8	ACD54912	ACD54912 HBV DNARY
248	12	46.2	21	9	ACF05776	ACF05776 Geneticin	C 321	11.8	45.4	17	10	ADF62130	ADF62130 Human PCC
249	12	46.2	21	10	ABQ80476	ABQ80476 P. infest	C 322	11.8	45.4	17	12	ADM60370	ADM60370 Hepatitis
250	12	46.2	21	10	ADF75123	ADF75123 PCR prime	C 323	11.8	45.4	17	12	ADM60039	ADM60039 Hepatitis
251	12	46.2	24	6	ABQ06320	ABQ06320 Oligonuc1	C 324	11.8	45.4	18	4	AAAS16132	AAAS16132 Black pan
252	12	46.2	24	6	ABQ06361	ABQ06361 Oligonuc1	C 325	11.8	45.4	18	10	ADB54040	ADB54040 Oligonuc1
253	12	46.2	24	6	ABQ01200	ABQ01200 Oligonuc1	C 326	11.8	45.4	19	4	AAAP29775	AAAP29775 Presenili
254	12	46.2	25	6	ABQ12951	ABQ12951 Oligonuc1	C 327	11.8	45.4	20	3	AAAC82381	AAAC82381 Human amy
255	12	46.2	25	8	ADBO1832	ADBO1832 Human MDZ	C 328	11.8	45.4	20	10	ADG33689	ADG33689 Human PCR
256	12	46.2	25	8	ADBO1837	ADBO1837 Human MDZ	C 329	11.8	45.4	20	12	ADH18431	ADH18431 2'-MOE ga
257	12	46.2	25	8	ADBO1835	ADBO1835 Human MDZ	C 330	11.8	45.4	20	12	ADO32972	ADO32972 Antisense
258	12	46.2	25	8	ADBO1836	ADBO1836 Human MDZ	C 331	11.8	45.4	22	3	AAAS88417	AAAS88417 Sequencin
259	12	46.2	25	8	ADBO1833	ADBO1833 Human MDZ	C 332	11.8	45.4	22	4	AAAS12578	AAAS12578 Primer SR
260	12	46.2	25	8	ADBO1834	ADBO1834 Human MDZ	C 333	11.8	45.4	22	4	AAAS42476	AAAS42476 Schizophr
261	12	46.2	25	9	ACI85237	ACI85237 Human mic	C 334	11.8	45.4	22	4	AAAS43072	AAAS43072 EST AAS26
262	12	46.2	25	9	ACI79051	ACI79051 Human mic	C 335	11.8	45.4	22	5	AAAS23819	AAAS23819 Schizophr
263	12	46.2	25	9	ACI13107	ACI13107 Human mic	C 336	11.8	45.4	22	12	ADO79053	ADO79053 Schizophr
264	12	46.2	25	9	ACK13561	ACK13561 Human mic	C 337	11.8	45.4	22	12	ADO79045	ADO79045 Schizophr
265	12	46.2	25	9	ACK30128	ACK30128 Human mic	C 338	11.8	45.4	23	12	ADK97986	ADK97986 Primer of
266	12	46.2	25	9	ACK30764	ACK30764 Human mic	C 339	11.8	45.4	24	3	AAZ61467	AAZ61467 PCR prime
267	12	46.2	26	12	ADM82860	ADM82860 Human dip	C 340	11.8	45.4	24	6	ABA98776	ABA98776 Neuroplli
268	12	46.2	27	6	ABK15329	ABK15329 PCR prime	C 341	11.8	45.4	24	6	AAAD40792	AAAD40792 Magnaport
269	12	46.2	28	2	AAK78219	AAK78219 Melon MBE	C 342	11.8	45.4	25	2	AAV53692	AAV53692 Nucleotid
270	12	46.2	30	3	AAAG1690	AAAG1690 Saccharom	C 343	11.8	45.4	25	2	AAAS99464	AAAS99464 Complemen
271	12	46.2	30	10	ADC15686	ADC15686 E. intest	C 344	11.8	45.4	25	2	AAI69860	AAI69860 Transcrip
272	12	46.2	30	10	ADO20556	ADO20556 Hansenula	C 345	11.8	45.4	25	9	ACI70511	ACI70511 Human mic
273	12	46.2	30	12	ADN43250	ADN43250 Brassica	C 346	11.8	45.4	25	9	ACI54752	ACI54752 Human mic
274	12	46.2	31	2	AAAX39096	AAAX39096 Human gen	C 347	11.8	45.4	25	9	ACI27369	ACI27369 Human mic
275	12	46.2	32	3	AAAG4038	AAAG4038 Stereoseel	C 348	11.8	45.4	25	9	ACI99063	ACI99063 Human mic
276	12	46.2	33	8	ABZ23954	ABZ23954 A. radiob	C 349	11.8	45.4	25	9	ACK04428	ACK04428 Human mic
277	12	46.2	33	12	ADO24653	ADO24653 Primer pk	C 350	11.8	45.4	25	9	ACK02646	ACK02646 Human mic
278	12	46.2	34	12	ADG31153	ADG31153 PCR prime	C 351	11.8	45.4	25	9	ACI17527	ACI17527 Human mic
279	12	46.2	35	3	AAAT72692	AAAT72692 PCR prime	C 352	11.8	45.4	25	9	ACI70510	ACI70510 Human mic
280	12	46.2	35	8	ACAT5320	ACAT5320 Corynebac	C 353	11.8	45.4	25	9	ACI80465	ACI80465 Human mic
281	12	46.2	36	2	AAAT92325	AAAT92325 MonKey/hu	C 354	11.8	45.4	25	9	ACK26653	ACK26653 Human mic
282	12	46.2	36	2	AAAT62897	AAAT62897 Human or	C 355	11.8	45.4	25	9	ACI07850	ACI07850 Human mic
283	12	46.2	36	2	AAAT95150	AAAT95150 Human/mon	C 356	11.8	45.4	25	9	ACI61953	ACI61953 Human mic
284	12	46.2	36	2	AAV05678	AAV05678 Human/mon	C 357	11.8	45.4	25	9	ACI67194	ACI67194 Human mic
285	12	46.2	36	2	AAV23788	AAV23788 Primer fo	C 358	11.8	45.4	25	9	ACI62614	ACI62614 Human mic
286	12	46.2	36	2	AAV31410	AAV31410 Human or	C 359	11.8	45.4	25	9	ACI22409	ACI22409 Human mic
287	12	46.2	36	8	ABX76665	ABX76665 Immunoglo	C 360	11.8	45.4	25	9	ACI76474	ACI76474 Human mic
288	12	46.2	36	10	ADE31620	ADE31620 Immunoglo	C 361	11.8	45.4	25	9	ACI54753	ACI54753 Human mic
289	12	46.2	38	2	AAQ74239	AAQ74239 Plasmid v	C 362	11.8	45.4	27	4	AAAF84932	AAAF84932 PCR prime
290	12	46.2	38	2	AAAT01161	AAAT01161 Kanamycin	C 363	11.8	45.4	27	6	AAAF38888	AAAF38888 Alfalfa n
291	12	46.2	38	2	AAAT15482	AAAT15482 5' primer	C 364	11.8	45.4	28	2	AAAX90648	AAAX90648 Primer De
292	12	46.2	38	2	AAAT40765	AAAT40765 Primer to	C 365	11.8	45.4	28	6	AAAL40714	AAAL40714 Rat VEGF
293	12	46.2	38	2	AAAT29803	AAAT29803 Primer #1	C 366	11.8	45.4	29	8	AAAD72336	AAAD72336 RACE PCR
294	12	46.2	38	2	AAAT85547	AAAT85547 V1R vecto	C 367	11.8	45.4	29	2	AAV07678	AAV07678 Mycobacte
295	12	46.2	38	2	AAV21774	AAV21774 V1R vacci	C 368	11.8	45.4	30	2	ABL58865	ABL58865 Helicobac
296	12	46.2	38	2	AAV58410	AAV58410 Primer fo	C 369	11.8	45.4	30	6	AAAX62542	AAAX62542 Granule b
297	12	46.2	38	2	AAV31783	AAV31783 Nucleotid	C 370	11.8	45.4	31	2	AAAX62542	AAAX62542 Granule b
298	12	46.2	38	3	AAZ46125	AAZ46125 PCR prime	C 371	11.8	45.4	31	6	ABLA11550	ABLA11550 Plasmid p
299	12	46.2	38	4	ADAO9619	ADAO9619 Vaccine v	C 372	11.8	45.4	31	6	AAAT72463	AAAT72463 Soybean i
300	12	46.2	38	4	ADAO9433	ADAO9433 Vector v1	C 373	11.8	45.4	32	8	AAAD51365	AAAD51365 Soybean i
301	12	46.2	38	12	ADO58168	ADO58168 Human inf	C 374	11.8	45.4	32	10	ADC85151	ADC85151 Ion trans
302	12	46.2	39	9	AAAL55522	AAAL55522 LINE retr	C 375	11.8	45.4	33	4	AAAI68366	AAAI68366 Human imm
303	12	46.2	41	4	AAAF81873	AAAF81873 HBV gene	C 376	11.8	45.4	33	4	AAAH91257	AAAH91257 Human inf
304	12	46.2	41	6	ABZ46317	ABZ46317 Human ald	C 377	11.8	45.4	33	12	ADM93361	ADM93361 Chimeric
305	12	46.2	41	6	ABZ48829	ABZ48829 Human ald	C 378	11.8	45.4	34	2	AAV62792	AAV62792 PCR prime
306	12	46.2	41	12	ADP07504	ADP07504 PCR prime	C 379	11.8	45.4	34	2	AAV81643	AAV81643 Oligonuc1
307	12	46.2	42	6	ABT12767	ABT12767 Thermomyc	C 380	11.8	45.4	35	2	AAAT44106	AAAT44106 Human G-P
308	12	46.2	42	6	ABT12768	ABT12768 Thermomyc	C 381	11.8	45.4	36	2	AAQ06085	AAQ06085 Junction
309	12	46.2	43	2	AAAT39128	AAAT39128 Reporter	C 382	11.8	45.4				
310	12	46.2	43	2	AAAT97605	AAAT97605 Shigella	C 383	11.8	45.4				
311	12	46.2	46	6	ABK10302	ABK10302 Directed	C 384	11.8	45.4				
312	12	46.2	48	6	AAAS20445	AAAS20445 Prion pro	C 385	11.8	45.4				
313	12	46.2	48	6	AAAS20440	AAAS20440 Prion pro	C 386	11.8	45.4				

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C 387	11.8	45.4	36	2	AAT36574	Thermococ
C 388	11.8	45.4	36	2	AAT11699	H. influe
C 389	11.8	45.4	36	6	ABL88047	Aquifex a
C 390	11.8	45.4	36	6	AA141434	DNA regio
C 391	11.8	45.4	37	3	AA96063	Oligonucl
C 392	11.8	45.4	37	3	AA96063	Oligonucl
C 393	11.8	45.4	37	4	AD13055	Human ubi
C 394	11.8	45.4	37	12	ADJ46078	Primer fo
C 395	11.8	45.4	38	2	AAT14566	Recombina
C 396	11.8	45.4	38	2	AAV62791	PCR prime
C 397	11.8	45.4	39	4	AAV81642	Oligonucl
C 398	11.8	45.4	39	10	ADC38577	Transloca
C 399	11.8	45.4	40	2	AAT70771	Stenotic
C 400	11.8	45.4	40	2	AAH08534	Oligonucl
C 401	11.8	45.4	40	4	AAH22855	Nucleotid
C 402	11.8	45.4	40	6	ABL88042	Aquifex a
C 403	11.8	45.4	40	6	ABz44032	Human NDU
C 404	11.8	45.4	40	6	ABz44976	Human NDU
C 405	11.8	45.4	40	6	ABT12137	E coli ex
C 406	11.8	45.4	40	9	ACD32837	Synthetic
C 407	11.8	45.4	41	6	ABz50210	Human NDU
C 408	11.8	45.4	41	6	ABz44198	Human ATP
C 409	11.8	45.4	41	6	ABz44750	Human ATP
C 410	11.8	45.4	41	6	ABz47247	Human ATP
C 411	11.8	45.4	41	8	ACC00163	Probe #1
C 412	11.8	45.4	42	3	AAA26033	Oestrogen
C 413	11.8	45.4	42	6	ABK91231	A. thalia
C 414	11.8	45.4	42	9	ADA66107	DNAP-rela
C 415	11.8	45.4	44	2	AAT03290	Primer fo
C 416	11.8	45.4	44	2	AAT86013	PCR prime
C 417	11.8	45.4	45	3	AAT86664	VEGF nucl
C 418	11.8	45.4	45	6	ABL41143	RNase-T1
C 419	11.8	45.4	47	3	AAZ66705	Nucleotid
C 420	11.8	45.4	47	3	AAZ66705	Human map
C 421	11.8	45.4	47	4	AAH88615	Human map
C 422	11.8	45.4	48	4	AAH88615	CNS disor
C 423	11.8	45.4	48	4	AAH88615	Human VEG
C 424	11.8	45.4	48	4	AAH88615	Human VEG
C 425	11.8	45.4	48	6	AAH88615	Human VEG
C 426	11.8	45.4	48	6	AAH88615	Human VEG
C 427	11.8	45.4	48	6	AAH88615	Human VEG
C 428	11.8	45.4	48	6	AAH88615	Human VEG
C 429	11.8	45.4	48	6	AAH88615	Human VEG
C 430	11.8	45.4	48	6	AAH88615	Human VEG
C 431	11.8	45.4	48	6	AAH88615	Human VEG
C 432	11.8	45.4	48	6	AAH88615	Human VEG
C 433	11.8	45.4	48	6	AAH88615	Human VEG
C 434	11.8	45.4	48	6	AAH88615	Human VEG
C 435	11.8	45.4	48	6	AAH88615	Human VEG
C 436	11.8	45.4	48	6	AAH88615	Human VEG
C 437	11.8	45.4	48	6	AAH88615	Human VEG
C 438	11.8	45.4	48	6	AAH88615	Human VEG
C 439	11.8	45.4	48	6	AAH88615	Human VEG
C 440	11.8	45.4	48	6	AAH88615	Human VEG
C 441	11.8	45.4	48	10	ADC72955	HEX-label
C 442	11.8	45.4	49	2	AAQ93271	Family 1A
C 443	11.8	45.4	49	4	AAQ93271	Family 1A
C 444	11.8	45.4	49	4	AAQ93271	Family 1A
C 445	11.8	45.4	49	4	AAQ93271	Family 1A
C 446	11.8	45.4	49	4	AAQ93271	Family 1A
C 447	11.8	45.4	49	4	AAQ93271	Family 1A
C 448	11.8	45.4	49	4	AAQ93271	Family 1A
C 449	11.8	45.4	49	4	AAQ93271	Family 1A
C 450	11.8	45.4	49	4	AAQ93271	Family 1A
C 451	11.8	45.4	49	4	AAQ93271	Family 1A
C 452	11.8	45.4	49	4	AAQ93271	Family 1A
C 453	11.8	45.4	49	4	AAQ93271	Family 1A
C 454	11.8	45.4	49	4	AAQ93271	Family 1A
C 455	11.8	45.4	49	4	AAQ93271	Family 1A
C 456	11.8	45.4	49	4	AAQ93271	Family 1A
C 457	11.8	45.4	49	4	AAQ93271	Family 1A
C 458	11.8	45.4	49	4	AAQ93271	Family 1A
C 459	11.8	45.4	49	4	AAQ93271	Family 1A

533	11.6	44.6	35	3	AAX290495	Aax290495 Sequence	c 606	11.4	43.8	25	9	ACI98089	AcI98089 Human mic
534	11.6	44.6	35	8	ABX15633	Abx15633 Tnos PCR	c 607	11.4	43.8	25	9	ACI49917	AcI49917 Human mic
535	11.6	44.6	36	6	ABX70346	Abx70346 Novel Hel	c 608	11.4	43.8	25	9	ACI30979	AcI30979 Human mic
536	11.6	44.6	37	3	AAV66669	Aav66669 Human Fas	609	11.4	43.8	25	9	ACI72528	AcI72528 Human mic
537	11.6	44.6	37	3	AAV78368	Aav78368 Fas anti-g	610	11.4	43.8	25	9	ACI52935	AcI52935 Human mic
538	11.6	44.6	37	6	ABK59397	Abk59397 Human CLC	c 611	11.4	43.8	25	9	ACK28857	AcK28857 Human mic
539	11.6	44.6	37	6	ACN19291	Acn19291 WNV Zinzv	c 612	11.4	43.8	25	9	ACK07439	AcK07439 Human mic
540	11.6	44.6	37	6	ACN19753	Acn19753 WNV Zinzv	613	11.4	43.8	25	9	ACI39623	AcI39623 Human mic
541	11.6	44.6	37	6	ACN19000	Acn19000 WNV Zinzv	c 614	11.4	43.8	25	9	ACI98088	AcI98088 Human mic
542	11.6	44.6	37	6	ACN19455	Acn19455 WNV Zinzv	615	11.4	43.8	25	9	ACI49161	AcI49161 Human mic
543	11.6	44.6	37	6	ACN19555	Acn19555 WNV Zinzv	c 616	11.4	43.8	25	9	ACI85897	AcI85897 Human mic
544	11.6	44.6	37	6	ACN31203	Acn31203 WNV minus	c 617	11.4	43.8	25	9	ACI35967	AcI35967 Human mic
545	11.6	44.6	37	8	ACA08036	AcA08036 Necrosis	c 618	11.4	43.8	25	9	ACI97203	AcI97203 Human mic
546	11.6	44.6	39	2	AAV30724	Aav30724 Telomeras	619	11.4	43.8	25	9	ACI86858	AcI86858 Human mic
547	11.6	44.6	39	2	AAV30728	Aav30728 Telomeras	c 620	11.4	43.8	25	9	ACK19084	AcK19084 Human mic
548	11.6	44.6	39	2	AAV30722	Aav30722 Telomeras	621	11.4	43.8	25	9	ACK31020	AcK31020 Human mic
549	11.6	44.6	39	2	AAV30726	Aav30726 Telomeras	c 622	11.4	43.8	25	9	ACI12246	AcI12246 Human mic
550	11.6	44.6	39	6	ABS61143	AbS61143 Human pol	c 623	11.4	43.8	25	9	ACI93626	AcI93626 Human mic
551	11.6	44.6	39	6	ABS61155	AbS61155 Human pol	c 624	11.4	43.8	25	9	ACK13413	AcK13413 Human mic
552	11.6	44.6	39	10	ADG78919	Adg78919 Schizophr	625	11.4	43.8	25	9	ACI50282	AcI50282 Human mic
553	11.6	44.6	39	12	ADI82353	Adi82353 Amorphe-4	c 626	11.4	43.8	25	9	ACI50666	AcI50666 Human mic
554	11.6	44.6	40	4	ACA91706	AcA91706 Mouse fat	c 627	11.4	43.8	25	9	ACK26538	AcK26538 Human mic
555	11.6	44.6	41	2	AAX89736	Aax89736 CLQ502 SY	c 628	11.4	43.8	25	9	ACI27383	AcI27383 Human mic
556	11.6	44.6	41	6	ABA99841	AbA99841 Human TGF	c 629	11.4	43.8	25	9	ACI66176	AcI66176 Human mic
557	11.6	44.6	42	3	AAX47004	Aax47004 Primer TA	c 630	11.4	43.8	25	9	ACI26227	AcI26227 Human mic
558	11.6	44.6	43	12	ADP97045	Adp97045 C. albica	c 631	11.4	43.8	25	9	ACI90735	AcI90735 Human mic
559	11.6	44.6	44	2	AAT01107	Aat01107 V1J-SIV M	632	11.4	43.8	25	9	ACK23318	AcK23318 Human mic
560	11.6	44.6	44	2	AAQ85223	Aaq85223 Ureaplas	c 633	11.4	43.8	25	9	ACI77433	AcI77433 Human mic
561	11.6	44.6	44	2	AAQ85171	Aaq85171 Ureaplas	c 634	11.4	43.8	25	9	ACI10182	AcI10182 Human mic
562	11.6	44.6	44	2	AAQ85225	Aaq85225 Ureaplas	c 635	11.4	43.8	25	9	ACI38924	AcI38924 Human mic
563	11.6	44.6	44	2	AAQ85224	Aaq85224 Ureaplas	636	11.4	43.8	25	9	ACK15053	AcK15053 Human mic
564	11.6	44.6	46	2	AAQ69267	Aaq69267 Human ara	637	11.4	43.8	25	9	ACH63928	AcH63928 DNA targe
565	11.6	44.6	46	2	AAT63729	Aat63729 Human ara	c 638	11.4	43.8	25	9	ACC84715	AcC84715 Interleuk
566	11.6	44.6	46	2	AAT79510	Aat79510 Primer St	639	11.4	43.8	25	12	ADP15866	Adp15866 Renal cel
567	11.6	44.6	46	2	AAX17017	Aax17017 Test sequ	c 640	11.4	43.8	25	12	ADP15284	Adp15284 Renal cel
568	11.6	44.6	46	6	ABK82508	AbK82508 DNA bindi	c 641	11.4	43.8	26	5	AAF17327	Aaf17327 Informati
569	11.6	44.6	46	10	ADL07701	Adl07701 Group II	c 642	11.4	43.8	26	5	AAH68490	AaH68490 C glutami
570	11.6	44.6	46	10	ADL07699	Adl07699 Group II	643	11.4	43.8	26	6	ABK99870	AbK99870 Babesia c
571	11.6	44.6	46	12	ADE80047	Ade80047 Duplex ol	c 644	11.4	43.8	27	2	AAV94096	Aav94096 Human II-
572	11.6	44.6	47	3	AAX67096	Aax67096 Human map	645	11.4	43.8	27	3	AAV58532	Aav58532 Human PRO
573	11.6	44.6	47	12	ADG83281	Adg83281 Primer sp	646	11.4	43.8	28	2	AAV81576	Aav81576 Oligonucle
574	11.6	44.6	50	2	AAX88053	Aax88053 Ku protei	647	11.4	43.8	28	2	AAV81575	Aav81575 Oligonucle
575	11.6	44.6	50	4	ABZ130002	Abz130002 Human SNP	c 648	11.4	43.8	28	3	AAZ88942	AaZ88942 Human sol
576	11.6	44.6	50	6	ABZ17038	Abz17038 Arabidops	c 649	11.4	43.8	28	3	AAF86148	AaF86148 RACE prim
577	11.6	44.6	50	6	ABZ06478	Abz06478 Human leu	c 650	11.4	43.8	28	4	AAH47085	AaH47085 ROH from
578	11.6	44.6	50	6	ABZ064931	Abz064931 Human leu	c 651	11.4	43.8	29	4	AAH47085	AaH47085 ROH from
579	11.6	44.6	50	6	ABZ07204	Abz07204 Human leu	c 652	11.4	43.8	29	4	AAH47085	AaH47085 ROH from
580	11.6	44.6	50	6	ABZ06541	Abz06541 Human leu	653	11.4	43.8	30	3	AAH47085	AaH47085 ROH from
581	11.6	44.6	50	6	ABZ06868	Abz06868 Human leu	c 654	11.4	43.8	30	4	AAH47085	AaH47085 ROH from
582	11.6	44.6	50	12	ADQ94817	Adq94817 Generic b	c 655	11.4	43.8	30	4	AAH47085	AaH47085 ROH from
583	11.6	44.6	50	12	ADQ94816	Adq94816 Generic b	656	11.4	43.8	30	5	AAH47085	AaH47085 ROH from
584	11.6	44.6	50	17	ADF62125	Adf62125 Human PCC	c 657	11.4	43.8	30	6	ABX69882	AbX69882 Novel Hel
585	11.4	43.8	18	4	AAF26868	Aaf26868 SR alpha	c 658	11.4	43.8	30	6	ABK43299	AbK43299 Human KHN
586	11.4	43.8	20	2	AAX94016	Aax94016 PCR prime	659	11.4	43.8	30	6	ABK53800	AbK53800 DMS:accep
587	11.4	43.8	20	4	AAF26867	Aaf26867 SR alpha	c 660	11.4	43.8	31	2	AAQ99845	AaQ99845 Haematopo
588	11.4	43.8	20	8	ABX94761	Abx94761 Human gam	661	11.4	43.8	31	2	AAQ26721	AaQ26721 PCR prime
589	11.4	43.8	20	10	ADC26014	Adc26014 Sense PCR	c 662	11.4	43.8	31	3	AAZ37461	AaZ37461 PCR prime
590	11.4	43.8	20	12	ADJ32597	Adj32597 Ovine GDF	c 663	11.4	43.8	31	3	AAZ13344	AaZ13344 PCR prime
591	11.4	43.8	21	2	AAQ11247	Aaq11247 env/U3 pr	c 664	11.4	43.8	31	4	AAH47085	AaH47085 ROH from
592	11.4	43.8	21	3	AAQ60710	Aaq60710 Rice cyto	c 665	11.4	43.8	31	4	AAH47085	AaH47085 ROH from
593	11.4	43.8	21	3	ADE80904	AdE80904 Streptoco	c 666	11.4	43.8	31	6	AAH47085	AaH47085 ROH from
594	11.4	43.8	21	10	ADD31208	AdD31208 RT-PCR pr	c 667	11.4	43.8	31	6	AAH47085	AaH47085 ROH from
595	11.4	43.8	21	10	ACF79836	AcF79836 siRNA to	c 668	11.4	43.8	31	8	ABX16162	AbX16162 Human hae
596	11.4	43.8	23	2	AAT01519	Aat01519 Human her	669	11.4	43.8	32	2	AAT75945	Aat75945 DEN-2 clo
597	11.4	43.8	23	2	AAV17059	Aav17059 Wound ind	c 670	11.4	43.8	32	2	AAT75945	Aat75945 DEN-2 clo
598	11.4	43.8	23	2	AAV12236	Aav12236 Varicella	c 671	11.4	43.8	32	6	ABSS2870	AbSS2870 Plasmid P
599	11.4	43.8	23	2	AAX91454	Aax91454 T. gondii	672	11.4	43.8	32	12	ADI38951	AdI38951 Glucose-6
600	11.4	43.8	23	2	AAX58942	Aax58942 Tomato TI	c 673	11.4	43.8	33	2	AAQ29504	AaQ29504 neoT3-567
601	11.4	43.8	23	4	AAS42777	Aas42777 T. gondii	674	11.4	43.8	33	2	AAQ46748	AaQ46748 HIV captu
602	11.4	43.8	23	6	ABA93038	AbA93038 Gancorma	675	11.4	43.8	33	2	AAQ89524	AaQ89524 Human imm
603	11.4	43.8	23	10	ADG17384	Adg17384 T. gondii	c 676	11.4	43.8	33	2	AAT63540	Aat63540 Killer to
604	11.4	43.8	25	3	ACI95953	AcI95953 HLA HLA-B	c 677	11.4	43.8	33	2	AAT63542	Aat63542 Atterf3 PC
605	11.4	43.8	25	9	ACI60782	AcI60782 Human mic	678	11.4	43.8	33	6	ABA04379	AbA04379 Atterf3 PC

679	11.4	43.8	34	6	ABL88053	AbL88053 Thymotog	C 752	11.2	43.1	20	10	AA155537	Aa155537 qSH-1 gen
680	11.4	43.8	34	6	AA521189	AA521189 Transmiss	C 753	11.2	43.1	20	12	ADH18782	Adh18782 Human apo
681	11.4	43.8	34	12	ADH10208	Adh10208 npt gene	754	11.2	43.1	20	12	ADH18461	Adh18461 2'-MOS ga
C 682	11.4	43.8	35	2	AT86112	Aat86112 Human sol	755	11.2	43.1	20	12	ADO33002	Ado33002 Antisense
C 683	11.4	43.8	35	2	AT89119	Aat89119 Synthetic	C 756	11.2	43.1	20	12	ADO33323	Ado33323 Human apo
C 684	11.4	43.8	35	2	AA199119	Aa199119 PCR prime	C 757	11.2	43.1	20	12	ADO33323	Ado33323 Human apo
C 685	11.4	43.8	35	2	AA199119	Aa199119 PCR prime	C 757	11.2	43.1	20	12	ADO33323	Ado33323 Human apo
C 686	11.4	43.8	35	2	AA199119	Aa199119 PCR prime	C 758	11.2	43.1	21	3	AA14887	Aa14887 PCR prime
C 687	11.4	43.8	35	6	AA199119	Aa199119 PCR prime	C 759	11.2	43.1	21	6	AA14887	Aa14887 PCR prime
C 688	11.4	43.8	35	6	AA199119	Aa199119 PCR prime	C 760	11.2	43.1	21	8	AA15895	Aa15895 Forward P
C 689	11.4	43.8	36	12	ADL65354	AdL65354 Comamonas	761	11.2	43.1	22	10	ACC59547	Acc59547 Chlamydia
C 690	11.4	43.8	36	12	ADL65354	AdL65354 Comamonas	762	11.2	43.1	22	12	ADN97998	Adn97998 Human pho
C 691	11.4	43.8	37	2	AA175490	Aa175490 Primer E	C 763	11.2	43.1	23	12	ADO10863	Ado10863 Single mu
C 692	11.4	43.8	37	2	AA175490	Aa175490 Primer E	C 764	11.2	43.1	24	8	ABQ03283	Abq03283 Oligonucle
C 693	11.4	43.8	38	4	AAH96464	AaH96464 Human Chk	765	11.2	43.1	24	6	ABQ03283	Abq03283 Oligonucle
C 694	11.4	43.8	38	12	ADO36264	Ado36264 Intracell	766	11.2	43.1	24	10	AA155537	Aa155537 qSH-1 gen
C 695	11.4	43.8	39	2	AA155537	Aa155537 qSH-1 gen	767	11.2	43.1	24	12	ADK48909	Adk48909 Chase AC
C 696	11.4	43.8	40	2	AA155537	Aa155537 qSH-1 gen	768	11.2	43.1	24	12	ADK48909	Adk48909 Chase AC
C 697	11.4	43.8	40	2	AA155537	Aa155537 qSH-1 gen	769	11.2	43.1	25	2	AAQ67981	Aaq67981 Sequence
C 698	11.4	43.8	40	12	ADK98514	AdK98514 Animal fe	770	11.2	43.1	25	2	AAQ67981	Aaq67981 Sequence
C 699	11.4	43.8	40	12	ADK98514	AdK98514 Animal fe	771	11.2	43.1	25	2	AAQ67981	Aaq67981 Sequence
C 700	11.4	43.8	41	6	AB248053	Ab248053 Human ATP	C 772	11.2	43.1	25	6	AB230156	Ab230156 Candida a
C 701	11.4	43.8	41	6	AB248053	Ab248053 Human ATP	C 773	11.2	43.1	25	6	AB230156	Ab230156 Candida a
C 702	11.4	43.8	41	6	AB248053	Ab248053 Human ATP	C 774	11.2	43.1	25	6	AB230156	Ab230156 Candida a
C 703	11.4	43.8	42	11	ADU95848	AdU95848 Rotavirus	775	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 704	11.4	43.8	42	11	ADU95848	AdU95848 Rotavirus	776	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 705	11.4	43.8	42	11	ADU95848	AdU95848 Rotavirus	777	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 706	11.4	43.8	43	2	AAV12249	AaV12249 Varicella	778	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 707	11.4	43.8	44	6	AAV12249	AaV12249 Varicella	C 779	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 708	11.4	43.8	44	6	AAV12249	AaV12249 Varicella	C 780	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 709	11.4	43.8	45	12	ADH73687	Adh73687 Novel rec	781	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 710	11.4	43.8	45	12	ADH73687	Adh73687 Novel rec	C 782	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 711	11.4	43.8	45	12	ADH73687	Adh73687 Novel rec	C 783	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 712	11.4	43.8	46	10	ACA92292	AcA92292 PCR prime	784	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 713	11.4	43.8	46	12	ADN43281	Adn43281 Nucleotid	C 785	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 714	11.4	43.8	47	3	AAZ66809	Aaz66809 Human map	786	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 715	11.4	43.8	47	3	AAZ66809	Aaz66809 Human map	787	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 716	11.4	43.8	47	4	AAZ66809	Aaz66809 Human map	788	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 717	11.4	43.8	47	5	AAZ66809	Aaz66809 Human map	C 789	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 718	11.4	43.8	49	2	AAZ66809	Aaz66809 Human map	790	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 719	11.4	43.8	49	3	AAZ66809	Aaz66809 Human map	C 791	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 720	11.4	43.8	50	3	AAZ66809	Aaz66809 Human map	792	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 721	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 793	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 722	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	794	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 723	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 795	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 724	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	796	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 725	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 797	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 726	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 798	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 727	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 799	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 728	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	800	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 729	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 801	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 730	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	802	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 731	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 803	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 732	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	804	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 733	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 805	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 734	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 806	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 735	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 807	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 736	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 808	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 737	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 809	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 738	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 810	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 739	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	811	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 740	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	812	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 741	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 813	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 742	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	814	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 743	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 815	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 744	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 816	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 745	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 817	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 746	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 818	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 747	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 819	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 748	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 820	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 749	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	C 821	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 750	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	822	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 751	11.4	43.8	50	6	AAZ66809	Aaz66809 Human map	823	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
							824	11.2	43.1	25	9	ACK16719	Ack16719 Human mic

825	11.2	43.1	28	2	AAT97359	Construct	Aat97359	Construct	c 898	11.2	43.1	38	2	AAT48478	Class B T
826	11.2	43.1	28	2	AAT220499	PCR prime	Aax20499	PCR prime	c 899	11.2	43.1	38	2	AAV60086	Class D t
827	11.2	43.1	28	2	AAV68127	Oligonucle	Aav68127	Oligonucle	c 900	11.2	43.1	38	2	AAV60087	Class E t
828	11.2	43.1	28	2	AAV99477	PCR prime	Aav99477	PCR prime	c 901	11.2	43.1	38	2	AAZ06714	Primer fo
829	11.2	43.1	28	2	AAT220489	PCR prime	Aaz20489	PCR prime	c 902	11.2	43.1	38	2	AAZ57632	Mutagenic
830	11.2	43.1	28	3	AAT255040	Neisseria	Aaz55040	Neisseria	c 903	11.2	43.1	38	2	AAZ60053	Class E t
831	11.2	43.1	28	3	AAK63096	Antisense	Aak63096	Antisense	c 904	11.2	43.1	38	2	AAK60052	Class D t
832	11.2	43.1	28	3	ABK49268	CDK4 gene	Abk49268	CDK4 gene	c 905	11.2	43.1	38	2	AAK15361	Mutagenic
833	11.2	43.1	28	3	AAK58636	Nucleotid	Aak58636	Nucleotid	c 906	11.2	43.1	38	3	AAZ56134	Class E t
834	11.2	43.1	28	5	AAAF67615	Oligonucle	Aaf67615	Oligonucle	c 907	11.2	43.1	38	3	AAZ56133	Class D t
835	11.2	43.1	28	5	AAAF67621	Fragment	Aaf67621	Fragment	c 908	11.2	43.1	38	3	AAZ292035	PCR prime
836	11.2	43.1	28	5	AAAF67622	Fragment	Aaf67622	Fragment	c 909	11.2	43.1	38	3	AAZ58633	Nucleotid
837	11.2	43.1	28	5	AAAS44081	Neisseria	Aas44081	Neisseria	c 910	11.2	43.1	38	3	AAAS58635	Nucleotid
838	11.2	43.1	28	6	AAAS17782	Human igG	Aas17782	Human igG	c 911	11.2	43.1	38	4	AAAC61973	Nucleotid
839	11.2	43.1	28	6	AAQ78248	Primer us	Aaq78248	Primer us	c 912	11.2	43.1	38	4	AAAC61974	Nucleotid
840	11.2	43.1	28	6	ABK67061	Human gen	Abk67061	Human gen	c 913	11.2	43.1	38	4	AAH47639	Nucleotid
841	11.2	43.1	28	6	ABK64363	Retrovira	Abk64363	Retrovira	c 914	11.2	43.1	38	4	AAH47638	Nucleotid
842	11.2	43.1	28	8	ABX10455	Human non	Abx10455	Human non	c 915	11.2	43.1	38	5	AAH25579	Nucleotid
843	11.2	43.1	28	10	ABBS57859	Rat G-pro	Abbs57859	Rat G-pro	c 916	11.2	43.1	38	5	AAH25580	Nucleotid
844	11.2	43.1	28	12	ADBE84735	Lymphocyt	Ade84735	Lymphocyt	c 917	11.2	43.1	38	6	ABK98650	Transposo
845	11.2	43.1	28	12	ADO24644	Primer 13	Ado24644	Primer 13	c 918	11.2	43.1	38	8	ACA94741	Class D t
846	11.2	43.1	29	2	AAV81779	Human ALK	Aav81779	Human ALK	c 919	11.2	43.1	38	8	ACA94742	Class E t
847	11.2	43.1	29	2	AAX200019	Anti sens	Aax200019	Anti sens	c 920	11.2	43.1	38	8	ABX16494	Tet opera
848	11.2	43.1	29	2	AAX88115	Antifreez	Aax88115	Antifreez	c 921	11.2	43.1	38	8	ABX16495	Tet opera
849	11.2	43.1	29	2	AAX76793	PCR prime	Aax76793	PCR prime	c 922	11.2	43.1	38	8	ABX04774	Thymidine
850	11.2	43.1	29	8	ACC80932	Primer #2	Acc80932	Primer #2	c 923	11.2	43.1	38	9	ACD13901	Tetracycl
851	11.2	43.1	30	4	AAF58777	Oligonuc	Aaf58777	Oligonuc	c 924	11.2	43.1	38	9	ACC84798	Nucleotid
852	11.2	43.1	30	6	ABS59788	Streptoco	Ab59788	Streptoco	c 925	11.2	43.1	38	10	ADBS23398	Tet opera
853	11.2	43.1	31	2	AAX62409	Granule b	Aax62409	Granule b	c 926	11.2	43.1	38	10	ADBS23397	Tet opera
854	11.2	43.1	31	3	AAAS4005	PCR prime	Aas4005	PCR prime	c 927	11.2	43.1	38	10	ADFS38943	Transposo
855	11.2	43.1	31	3	AAAF60717	Oligonuc	Aaf60717	Oligonuc	c 928	11.2	43.1	40	2	AAT69405	Plasmid p
856	11.2	43.1	31	3	AAAF3690	Primer is	Aaf3690	Primer is	c 929	11.2	43.1	40	2	AAT69405	Plasmid p
857	11.2	43.1	31	4	AAF58793	Avian E c	Aaf58793	Avian E c	c 930	11.2	43.1	40	2	AAAX36168	Probe use
858	11.2	43.1	31	6	ADH76359	E. coli i	Adh76359	E. coli i	c 931	11.2	43.1	40	2	AAAX88877	Circular
859	11.2	43.1	32	12	ADJ92431	Human cys	Adj92431	Human cys	c 932	11.2	43.1	40	2	AAAX88828	Circular
860	11.2	43.1	32	2	AAT10320	PCR prime	Aat10320	PCR prime	c 933	11.2	43.1	40	3	AAAS8639	Nucleotid
861	11.2	43.1	32	3	AAAS8637	Nucleotid	Aas8637	Nucleotid	c 934	11.2	43.1	40	6	ABA98152	Oligonuc
862	11.2	43.1	32	8	ACA61036	Cytochrom	Aca61036	Cytochrom	c 935	11.2	43.1	40	6	ABA98103	Synthetic
863	11.2	43.1	32	9	ADA67749	K. pneumo	Ada67749	K. pneumo	c 936	11.2	43.1	40	6	ABL99281	Oligonuc
864	11.2	43.1	33	6	ABK50695	PCR prime	Abk50695	PCR prime	c 937	11.2	43.1	40	8	ABT17495	Selection
865	11.2	43.1	33	8	AAAL52142	Fungus-or	Aal52142	Fungus-or	c 938	11.2	43.1	41	3	AAAF71003	Molecular
866	11.2	43.1	33	9	ACC84745	E. coli p	Acc84745	E. coli p	c 939	11.2	43.1	41	3	AAAF71007	Molecular
867	11.2	43.1	34	2	AAX08626	Primer us	Aax08626	Primer us	c 940	11.2	43.1	41	6	ABZ43442	Human NQO
868	11.2	43.1	34	2	AAX08618	Primer us	Aax08618	Primer us	c 941	11.2	43.1	41	6	ABZ43442	Human NQO
869	11.2	43.1	34	2	AAX08622	Primer us	Aax08622	Primer us	c 942	11.2	43.1	41	8	ACC00164	Probe #2
870	11.2	43.1	34	2	AAAX01640	Triabody	Aax01640	Triabody	c 943	11.2	43.1	41	10	ADD053343	DNA methy
871	11.2	43.1	34	2	AAAX01634	Anti-B7.1	Aax01634	Anti-B7.1	c 944	11.2	43.1	42	3	AAZ64546	Hairpin r
872	11.2	43.1	34	3	AAAS6734	Beta-lact	Aas6734	Beta-lact	c 945	11.2	43.1	42	3	AAZ64546	Hairpin r
873	11.2	43.1	34	11	ADQ96818	Novel zin	Adq96818	Novel zin	c 946	11.2	43.1	42	3	AAA26006	Oestrogen
874	11.2	43.1	34	12	ADI28634	Mycoplasma	Adi28634	Mycoplasma	c 947	11.2	43.1	42	3	AAA88303	High mobi
875	11.2	43.1	34	12	ADI28635	Mycoplasma	Adi28635	Mycoplasma	c 948	11.2	43.1	42	8	ADA47348	Mutagenic
876	11.2	43.1	35	2	AAT94502	PCR prime	Aat94502	PCR prime	c 949	11.2	43.1	42	10	ABS56914	Rat high
877	11.2	43.1	35	10	ADC36233	Weed cont	Adc36233	Weed cont	c 950	11.2	43.1	42	12	ADP88463	Antibody
878	11.2	43.1	35	12	ADH10520	S. enteri	Adh10520	S. enteri	c 951	11.2	43.1	42	12	ADQ90881	Rat high
879	11.2	43.1	36	3	AAAS8638	Nucleotid	Aas8638	Nucleotid	c 952	11.2	43.1	43	2	AAQ23173	HPV probe
880	11.2	43.1	36	3	AAAS8630	Nucleotid	Aas8630	Nucleotid	c 953	11.2	43.1	43	2	AAQ23173	HPV probe
881	11.2	43.1	36	3	AAAS8630	Nucleotid	Aas8630	Nucleotid	c 954	11.2	43.1	43	2	AAV10879	Human pap
882	11.2	43.1	36	3	AAAS8641	Nucleotid	Aas8641	Nucleotid	c 955	11.2	43.1	43	6	ABZ27894	Human MLH
883	11.2	43.1	36	3	AAAS8632	Nucleotid	Aas8632	Nucleotid	c 956	11.2	43.1	43	6	ABZ27894	Candida e
884	11.2	43.1	36	3	AAAS8642	Nucleotid	Aas8642	Nucleotid	c 957	11.2	43.1	43	12	ADP97154	C. albica
885	11.2	43.1	36	3	AAAS8631	Nucleotid	Aas8631	Nucleotid	c 958	11.2	43.1	44	3	AAAS8640	Nucleotid
886	11.2	43.1	36	6	AD45167	Flea chit	Ad45167	Flea chit	c 959	11.2	43.1	44	10	ACC59552	Chlamydia
887	11.2	43.1	36	10	AD41754	Bacillus	Ad41754	Bacillus	c 960	11.2	43.1	45	2	AAZ33934	Human PRO
888	11.2	43.1	36	12	ADL15684	Murine im	Adl15684	Murine im	c 961	11.2	43.1	45	3	AACT8631	Human PRO
889	11.2	43.1	37	4	AAQ90262	Primer #1	Aaq90262	Primer #1	c 962	11.2	43.1	45	6	AAAL47218	Single-st
890	11.2	43.1	37	6	ACN19955	WNV Zinz	Acn19955	WNV Zinz	c 963	11.2	43.1	45	6	AAAL47219	Single-st
891	11.2	43.1	37	10	ADC98725	PCR prime	Adc98725	PCR prime	c 964	11.2	43.1	45	8	ACA63502	Novel hum
892	11.2	43.1	37	10	ADK71442	Drug-tole	Adk71442	Drug-tole	c 965	11.2	43.1	45	8	ACA71666	Human PRO
893	11.2	43.1	38	2	AAQ90044	B. anyloli	Aaq90044	B. anyloli	c 966	11.2	43.1	45	8	ACA92306	Human PRO
894	11.2	43.1	38	2	AAT11363	Class D t	Aat11363	Class D t	c 967	11.2	43.1	45	8	ACA66047	Human sec
895	11.2	43.1	38	2	AAT11364	Class E t	Aat11364	Class E t	c 968	11.2	43.1	45	9	ADA24589	Secreted
896	11.2	43.1	38	2	AAT45714	Class D T	Aat45714	Class D T	c 969	11.2	43.1	45	9	ACD29648	Novel hum
897	11.2	43.1	38	2	AAT45715	Class E T	Aat45715	Class E T	c 970	11.2	43.1	45	9	ADAL2250	Human sec

[illegible]XX
DE
HCV DNA amplifying PCR primer, ST280pc.

Amplification of a target nucleic acid region using control sequences.
Example 2; Fig 3; 29pp; English.

XX The invention relates to a method for amplification of a target nucleic
 CC acid region. The method is useful for amplification of a nucleic acid
 CC molecule using control nucleic acid sequences. The control nucleic acid
 CC sequences are at least in part parallel-complementary to the sequence of
 CC the target nucleic acid. The present sequence is HCV DNA amplifying PCR
 CC primer. Note: This sequence is stated to be same as that shown as SEQ ID
 CC NO:8 in sequence listing. However this sequence has additional A at its
 CC 3' end. (Updated on 07-AUG-2003 to correct OS field.)
 XX

XX SQ Sequence 27 BP; 5 A; 8 C; 5 G; 9 T; 0 U; 0 Other;
 Query Match 100.0%; Score 26; DB 6; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 1 CGTCTTTCGCAGATCGGTACCTCAAT 26
 |||||
 DB 1 CGTCTTTCGCAGATCGGTACCTCAAT 26
 |||||

RESULT 3
 AC153779/c
 ID AC153779 standard; DNA; 25 BP.
 XX
 AC AC153779;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 53770.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 FN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 53770; 9pp; English.
 XX

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX

XX SQ Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 65.4%; Score 17; DB 9; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX

QY 2 GTCCTTTCGCAGATCGGTACCTCAAT 26
 |||||
 DB 25 GTACTTCGCGATAGGTACCTCTAT 1
 |||||

RESULT 4
 ACH57122/c
 ID ACH57122 standard; DNA; 25 BP.
 XX
 AC ACH57122;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #6258 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;
 KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 FN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 XX
 PI Mittmann M;
 XX
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analysing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 6258; 9pp; English.
 XX

XX The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, Northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in

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CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
CC
SQ Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 59.2%; Score 15.4; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 GCTTTTCGAGATCGGTACCTCAAT 26
Db 25 GTACTTCGCGAAGGTACCTCTAT 1
RESULT 6
ACH57668/c
ID ACH57668 standard; DNA; 25 BP.
XX
AC ACH57668;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #6804 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
XX US2003082596-A1.
XX
XX 01-MAY-2003.
XX
XX 08-AUG-2002; 2002US-00215112.
XX
XX 08-AUG-2001; 2001US-0311040P.
XX
XX (MITT/) MITTMANN M.
XX
XX Mittmann M;
XX
XX WPI; 2003-576608/54.
XX
XX New probe array useful e.g. for monitoring gene expression levels, for
XX analyzing genetic variations, or for hybridizing tag-labeled compounds,
XX comprises multiple nucleic acid probes.
XX
XX Claim 1; SEQ ID NO 6804; 9pp; English.
XX
XX The present invention relates to nucleic acid sequences that are
XX complementary to particular genes, and can be used as probes for a
XX variety of analyses such as gene expression analysis. Each probe
XX comprises 9 or more consecutive nucleotides from at least one of 14936
XX nucleotide sequences defined in the patent, or their perfect sense match,
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.
XX The probes may be used in an array comprising at least 10 distinct
XX nucleic acid probes. The array is useful in monitoring gene expression
XX levels by hybridisation to a DNA library, in analysing genetic
XX variations, and in hybridising tag-labelled compounds. The probes are
XX useful for identifying family members of a gene. The probes are also
XX useful in situ hybridisations, in screening cDNA or genomic libraries
XX (or derived subclones) for additional clones containing segments of DNA
XX that have been previously isolated and sequenced, in Southern, northern,
XX or dot-blot hybridisation of genomic DNA to identify or detect the
XX sequence of any gene or detect specific mutations in any gene, and in
XX mapping the 5' termini of mRNA molecules by primer extensions. The
XX nucleic acid sequences of the invention are also useful as PCR primers.

CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH5260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/psipdsIDEntry.html
CC
SQ Sequence 25 BP; 5 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 61.5%; Score 16; DB 9; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 GCTTTTCGAGATCGGTACCTCAA 25
Db 24 GTCATTTCGAGACCGGTACCTCGA 1
RESULT 5
ACI53778/c
ID ACI53778 standard; DNA; 25 BP.
XX
AC ACI53778;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 53769.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 53769; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones

CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
 XX
 XX Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 58.5%; Score 15.2; DB 9; Length 25;
 Best Local Similarity 85.0%; Pred. No. 1.1e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACTCTCAAT 26
 ||||| ||||| ||||| |||||
 Db 21 TCACAGACAGGTACTCTCAAT 2

RESULT 7
 ACH57794/c
 ID ACH57794 standard; DNA; 25 BP.
 XX
 AC ACH57794;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #6930 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;
 KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 XX
 PI Mittmann M;
 XX
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analysing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.

Claim 1; SEQ ID NO 6930; 9pp; English.
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' termini of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.

CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
 XX
 XX Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 58.5%; Score 15.2; DB 9; Length 25;
 Best Local Similarity 85.0%; Pred. No. 1.1e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACTCTCAAT 26
 ||||| ||||| ||||| |||||
 Db 21 TCACAGACAGGTACTCTCAAT 2

RESULT 8
 ACH54380/c
 ID ACH54380 standard; DNA; 25 BP.
 XX
 AC ACH54380;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #3516 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;
 KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 XX
 PI Mittmann M;
 XX
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analysing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.

Claim 1; SEQ ID NO 3516; 9pp; English.
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' termini of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.

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can be amplified in the same reaction by targeting multiple sequences with (EP). Simultaneous amplification and detection is facilitated using detection probes associated with a substrate. Multiplex detection can be facilitated by an array of detection probes with different detection probes at different locations of a substrate. The present sequence is a primer used in the TEX method to detect/amplify HCV (Hepatitis C virus) target sequences.

Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 57.7%; Score 15; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 CGCTCTTCGAGATC 15
DB 4 CGCTCTTCGAGATC 18

RESULT 10
AC127637/c
ID AC127637 standard; DNA; 25 BP.
XX AC
AC AC127637;
XX DT
DT 13-OCT-2003 (first entry)
XX DE
DE Human microarray DNA oligonucleotide SEQ ID NO 27628.
XX KW
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW
KW genetic variation; biallelic marker; polymorphism; human;
XX KW
KW cross-species comparison.
XX OS
OS Homo sapiens.
XX PN
PN US2003104410-A1.
XX PD
PD 05-JUN-2003.
XX PF
PF 15-MAR-2002; 2002US-00098263.
XX PR
PR 16-MAR-2001; 2001US-0276759P.
XX PA
PA (AFY-) APFYMATRIX INC.
XX PI
PI Mittmann MP;
XX DR
DR WPI; 2003-567953/53.
XX PT
PT New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
XX PT
PT
XX PS
PS Claim 1; SEQ ID NO 27628; 9pp; English.
XX SS
SS The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones

The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH50865-ACH5260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipdbEntry.html

Sequence 25 BP; 6 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 58.5%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3;

QY 7 TCGCAGATCGGTACTCAAT 26
DB 22 TCACAGACAGGTACTCAAT 3

RESULT 9
ADP87820
ID ADP87820 standard; DNA; 18 BP.
XX AC
AC ADP87820;
XX DT
DT 09-SEP-2004 (first entry)
XX DE
DE Primer for TEX detection of Hepatitis C virus T1.
XX KW
KW TEX; thermodynamic equilibrium extension of primers; HCV; ss; primer.
XX OS
OS Hepatitis C virus.
XX PN
PN US2004115643-A1.
XX PD
PD 17-JUN-2004.
XX PF
PF 12-DEC-2002; 2002US-00318416.
XX PR
PR 12-DEC-2002; 2002US-00318416.
XX PA
PA (LIZA/) LIZARDI P M.
XX PA
PA (GRIB/) GRIBANOV O G.
XX PI
PI Lizardi PM, Gribanov OG;
XX DR
DR WPI; 2004-468050/44.
XX SS
SS Amplifying nucleic acid for detecting nucleic acid, by extension of one or more primers using target templates having replication terminating feature, dissociation of primer from templates to produce multiple extended primers.
XX PT
PT
XX PS
PS Disclosure; Fig 8; 75pp; English.
XX SS
SS The invention relates to amplifying (M1) a nucleic acid, involving contacting one or more extension primers (EP) and target templates and incubating under conditions to promote interaction of (EP) and templates, extension of (EP) using the interacting (TT), and dissociation of the extended (EP) from (TT), to produce multiple extended (EP) from at least one (TT), where each (TT) comprise a replication terminating feature. In (M1), (EP) and target templates are incubated under isothermal conditions or single set of conditions. The target templates are nucleic acid sequences of interest. Each of (EP) comprises or consists of a target complement portion, preferably nucleotides, where the nucleotides consist of the target complement portion. Each (EP) further comprises non-target complement portion. The method is known as TEX (thermodynamic equilibrium extension of primers). The method is useful for amplifying nucleic acid and for detecting nucleic acid sequences which involves performing (M1), and detecting one or more of the extended (EP). In (M1), only those sequences targeted by (EP) are amplified, thus allowing specific sequences to be targeted for amplification. Flexibility in the location of replication terminating feature allows flexibility in targeting sequences. If a targeted sequence is not present, the sequence will not be amplified. Multiple sequences

CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 56.2%; Score 14.6; DB 9; Length 25;
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCCTTCGAGATCGGTACTC 23
 ||||| ||||| ||||| |||||
 Db 23 TCCTTCGGGGATCGGTACCAC 3

RESULT 11

AAT31022/c

ID AAT31022 standard; DNA; 41 BP.

XX AAT31022;

AC AAT31022;

DT 26-SEP-1996 (first entry)

XX Human endothelin-1 gene promoter PCR primer F.

DE Gene therapy; hypoxia related enhancer element; HREE; ischaemia;

XX reperfusion; promoter; endothelin-1; endothelium; PCR; primer;

KW polymerase chain reaction; ss.

KW Synthetic.

XX WO9620276-A1.

XX 04-JUL-1996.

XX 13-NOV-1995; 95WO-IB000996.

XX 23-DEC-1994; 94US-00365486.

XX (STRI) SRI INT.

XX Webster KA, Bishopric NH, Murphy B, Laderoute KR, Green CJ;

XX WPI; 1996-321849/32.

XX Chimeric gene contg. therapeutic gene linked to HREE - partic. for

PT expressing SOD etc. in hypoxic tissue to reduce tissue injury caused by

PT ischaemia or reperfusion.

XX Example 1; Page 46; 118pp; English.

XX A DNA fragment (AAT31013) contg. 700 bp of the human endothelin (ET-1)

CC gene promoter was created by PCR using HeLa genomic DNA as template. ET-1

CC specific primers were based on the ET-1 gene promoter sequence. The

CC forward primer (AAT31022) contained PstI and KpnI sites, and the reverse

CC primer (AAT31023) contained HindIII and XbaI sites. The PCR product was

CC cloned into pGL2BV. The promoter can be used to target hypoxia-regulated

CC genes specifically to cells of the vascular endothelium, since it

CC contains elements conferring tissue specificity as well as hypoxia

CC response enhancer elements able to up-regulate transcription of a

CC (therapeutic) gene under hypoxic conditions

XX Sequence 41 BP; 12 A; 8 C; 12 G; 9 T; 0 U; 0 Other;

XX Query Match 56.2%; Score 14.6; DB 2; Length 41;

XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;

XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTCCTTCGAGATCGGTACTC 22

||||| ||||| ||||| |||||

Db 30 GTCCTTCCTTCGGTACTC 10

RESULT 12

ABS97227

XX ABS97227 standard; DNA; 21 BP.

AC ABS97227;

XX ABS97227;

XX 23-DEC-2002 (first entry)

XX Human CYP4502E1 promoter polymorphism #13.

XX Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;

KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; ELAP;

KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;

KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;

KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

KW multidrug resistance associated protein 3; cancer; prostate;

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KW altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; pulmonary; immunological; SNF;

KW single nucleotide polymorphism.

XX Homo sapiens.

OS WO200257410-A2.

XX 25-JUL-2002.

XX 28-NOV-2001; 2001WO-US044838.

XX 28-NOV-2000; 2000US-00724389.

XX (DNAS-) DNA SCI LAB INC.

XX Guida M, Hall J;

XX WPI; 2002-698522/75.

XX Isolated nucleic acid molecules having polymorphisms in known human genes

XX e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers

XX for locating, identifying and characterizing the genes responsible for

XX disorder-related traits.

XX Example 3; Page 104; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid

XX molecule comprising at least one base variation from that of a known

XX human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),

XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),

XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator

XX (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding

XX inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating

XX protein (fLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl

XX transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl

XX sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4

XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

XX transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1

XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3

XX (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic

XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.

XX The polymorphisms in the human genes cited in the invention are useful as

XX genetic linkage markers for locating and characterising the genes that

XX are responsible for specific traits within the genome and eventually

XX identifying the genes responsible for a variety of disorder-related

CC The present primer was used in the preparation of a Thermococcus
 CC peptonophilus derived thermostable DNA polymerase cDNA. The enzyme can be
 CC used for nucleic acid sequence amplification, e.g. PCR
 XX
 SQ Sequence 23 BP; 4 A; 7 C; 3 G; 5 T; 0 U; 4 Other;
 Query Match 55.4%; Score 14.4; DB 2; Length 23;
 Best Local Similarity 71.4%; Pred. No. 2.8e+03;
 Matches 15; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 4 CTTTCGACATCGGTACTCTCA 24
 DB 2 CTTTCGACATCGGTACTCTCA 22
 RESULT 14
 ACI61181
 ID ACI61181 standard; DNA; 25 BP.
 XX ACI61181;
 XX ACI61181;
 DT 13-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 61172.
 DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX Homo sapiens.
 OS US2003104410-A1.
 PN 05-JUN-2003.
 PD 15-MAR-2002; 2002US-00098263.
 XX 16-MAR-2001; 2001US-0276759P.
 PR (AFFY-) AFFYMETRIX INC.
 PA Mittmann MP;
 PI WPI; 2003-567953/53.
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 XX Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS Claim 1; SEQ ID NO 61172; 9pp; English.
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence of mRNA molecules by
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly

CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC ARNT, BPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDRI and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDRI and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered serine
 CC immunological or haematological function, in ILK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 55.4%; Score 14.4; DB 6; Length 21;
 Best Local Similarity 93.8%; Pred. No. 2.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 GCAGATCGGTACTCTCA 24
 DB 6 GCAGATCGGTACTCTCA 21
 RESULT 13
 AAT88375
 ID AAT88375 standard; DNA; 23 BP.
 XX AAT88375;
 AC AAT88375;
 DT 28-JAN-1998 (first entry)
 XX Primer for T. peptonophilus thermostable DNA polymerase cDNA.
 DE Thermostable; DNA polymerase; nucleic acid sequence amplification;
 KW primer; PCR; ss.
 KW Synthetic.
 OS Thermococcus peptonophilus.
 XX Key Location/Qualifiers
 FH modified_base 3 /*tag= a
 FT /*mod_base= i
 FT modified_base 9 /*tag= b
 FT /*mod_base= i
 FT modified_base 15 /*tag= c
 FT /*mod_base= i
 XX JF09252776-A.
 PN 30-SEP-1997.
 PD 19-MAR-1996; 96JP-00063112.
 XX 19-MAR-1996; 96JP-00063112.
 PR (TOYM) TOYBO KK.
 PA WPI; 1997-530149/49.
 DR Thermococcus peptonophilus thermostable DNA polymerase - useful for
 PT nucleic acid sequence amplification, e.g. polymerase chain reaction.
 XX Example 1; Page 24; 27pp; Japanese.
 PS
 XX


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CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match      55.4%; Score 14.4; DB 9; Length 25;
  Best Local Similarity 93.8%; Pred. No. 2.9e+03;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TCAGATCGGTACCT 22
Db 1 TCAGATCGGTACCT 16

RESULT 15
ACH57248/c
ID ACH57248 standard; DNA; 25 BP.
XX
AC ACH57248;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #6384 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
FN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mittmann M;
XX
WPI; 2003-576608/54.

New probe array useful e.g. for monitoring gene expression levels, for
analyzing genetic variations, or for hybridizing tag-labeled compounds,
comprises multiple nucleic acid probes.

Claim 1; SEQ ID NO 6384; 9pp; English.

The present invention relates to nucleic acid sequences that are
complementary to particular genes, and can be used as probes for a
variety of analyses such as gene expression analysis. Each probe
comprises 9 or more consecutive nucleotides from at least one of 14936
nucleotide sequences defined in the patent, or their perfect sense match,
sense mismatch, antisense match or antisense mismatch oligonucleotides.
The probes may be used in an array comprising at least 10 distinct
nucleic acid probes. The array is useful in monitoring gene expression
levels by hybridisation to a DNA library, in analysing genetic
variations, and in hybridising tag-labelled compounds. The probes are
useful for identifying family members of a gene. The probes are also
useful in situ hybridisations, in screening cDNA or genomic libraries
(or derived subclones) for additional clones containing segments of DNA
that have been previously isolated and sequenced, in Southern, northern,
or dot-blot hybridisation of genomic DNA to identify or detect the
sequence of any gene or detect specific mutations in any gene, and in
mapping the 5' termini of mRNA molecules by primer extensions. The
nucleic acid sequences of the invention are also useful as PCR primers.
The invention provides a large collection of nucleic acid sequences
complementary to particular genes with a wide range of analytical uses.
ACH50855-ACH5260 represent the target sequences of the invention. Note:
The sequence data for this patent was obtained in electronic format
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CC directly from the USPTO web site at seqdata.uspto.gov/psipidsEntry.html
XX
SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match      55.4%; Score 14.4; DB 9; Length 25;
  Best Local Similarity 75.0%; Pred. No. 2.9e+03;
  Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACAGTCGGTACCTCA 25
Db 24 GTCATTCGAGTCGGTACCTCGA 1

RESULT 16
AAA65754/c
ID AAA65754 standard; DNA; 40 BP.
XX
AC AAA65754;
XX
DT 21-NOV-2000 (first entry)
XX
DE Streptococcus pneumoniae BVH-3 PCR primer SEQ ID NO:29.
XX
KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal; PCR primer; ss.
XX
OS Streptococcus pneumoniae.
XX
FN WO2000039299-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-CA001218.
XX
PR 23-DEC-1998; 98US-0113800P.
XX
PA (BIOC-) BIOCHEM PHARMA INC.
XX
PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX
WPI; 2000-452397/39.

Streptococcal antigens useful for vaccinating against e.g. meningitis,
otitis media, bacteraemia and/or pneumonia.

Example 8; Page 49; 106pp; English.

The present invention describes nucleic acids (I) encoding protein
antigens (II) from Streptococcus pneumoniae. The protein antigens have
bactericidal activity. The nucleic acids, encoding the protein antigens,
may be used for the recombinant production of the proteins they encode.
The protein antigens may then be used as vaccines for the prevention and
treatment of Streptococcal infections in mammals (especially humans)
which result in, e.g. meningitis, otitis media, bacteraemia and/or
pneumonia. The present sequence represents a PCR primer for a S.
pneumoniae GAS BVH-71 protein antigen, which is used in an example from
the present invention

XX
SQ Sequence 40 BP; 14 A; 6 C; 6 G; 14 T; 0 U; 0 Other;

  Query Match      55.4%; Score 14.4; DB 3; Length 40;
  Best Local Similarity 75.0%; Pred. No. 3e+03;
  Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCCTTTCGACAGTCGGTACCTCAAT 26
Db 37 TTTTTCACAGATAGGTACTTCCAT 14

RESULT 17
ABK33676/c
ID ABK33676 standard; DNA; 40 BP.
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us-10-087-631b-8.max.rng

XX AC ABK33676;
XX DT 08-MAY-2002 (first entry)
XX DE S. pneumoniae BVH-3 gene, PCR primer HAM7 281.
XX KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia;
XX KW streptococcal bacterial infection; PCR; primer; ss.
XX OS Streptococcus pneumoniae.
XX PN W0200198334-A2.
XX PD 27-DEC-2001.
XX PF 19-JUN-2001; 2001WO-CA000908.
XX PR 20-JUN-2000; 2000US-0212683P.
XX PA (SHIR-) SHIRE BIOCHEM INC.
XX PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX DR WPI; 2002-122272/16.
XX KW New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing
XX PT polypeptides, useful as vaccine components for treating or preventing
XX PT streptococcal infections such as otitis media, meningitis, and
XX PT bacteremia.
XX PS Example 1; Page 30; 113pp; English.
XX CC The invention describes an isolated polypeptide (I) with 70-90% identity
XX CC to Streptococcus pneumoniae protein BVH-3, BVH-11, variants of BVH-3 or
XX CC BVH-11, or chimeric sequences derived from them. A vaccine (II)
XX CC comprising (I) is useful for therapeutic or prophylactic treatment of
XX CC meningitis, otitis media, bacteraemia or pneumonia infection in an
XX CC individual susceptible to these disorders. (II) is also useful for
XX CC therapeutic or prophylactic treatment of any streptococcal bacterial
XX CC infection (e.g., caused by Streptococcus pneumoniae, group A
XX CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
XX CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nodocardia or
XX CC Streptococcus aureus) in an individual susceptible to the infection. A
XX CC polynucleotide (III) encoding (I) is useful in DNA immunisation
XX CC techniques. The Streptococcus polypeptides are useful in a diagnostic
XX CC test for S. pneumoniae infection. (III) is useful for designing DNA
XX CC probes for use in detecting the presence of Streptococcus in a biological
XX CC sample suspected of containing the bacteria. The DNA probes may also be
XX CC used for detecting circulating S. pneumoniae nucleic acid in a sample for
XX CC diagnosing streptococcal infections. This sequence represents a primer
XX CC used for the isolation of S. pneumoniae genes from which the antigenic
XX CC peptides of the invention are derived
XX SQ Sequence 40 BP; 14 A; 6 C; 6 G; 14 T; 0 U; 0 Other;
Query Match 55.4%; Score 14.4; DB 6; Length 40;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 TCTTTCGACGATCGGTACTCAAT 26
Db 37 TTTTTCACAGTAGGTACTTCCAT 14
RESULT 18
ACK29528/c
ID ACK29528 standard; DNA; 25 BP.
XX AC ACK29528;
XX DT 14-OCT-2003 (first entry)
XX

DE Human microarray DNA oligonucleotide SEQ ID NO 129509.
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX OS Homo sapiens.
XX US2003104410-A1.
PN 05-JUN-2003.
PD 15-MAR-2002; 2002US-00098263.
PF 16-MAR-2001; 2001US-0276759P.
PR (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
XX WPI; 2003-567953/53.
DR New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX Claim 1; SEQ ID NO 129509; 9pp; English.
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX SQ Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 54.6%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 TCGCAGATCGGTACTCA 25
Db 19 TCACAGACAGGTACTCA 1
RESULT 19
ACH56079/c
ID ACH56079 standard; DNA; 25 BP.
XX AC ACH56079;
XX DT 16-OCT-2003 (first entry)
XX DE DNA target sequence #5215 useful in array for genetic analyses.
XX

Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.

Unidentified.

US2003082596-A1.

01-MAY-2003.

08-AUG-2002; 2002US-00215112.

08-AUG-2001; 2001US-0311040P.

(MITT) MITTMANN M.

Mittmann M;

WPI; 2003-576608/54.

New probe array useful e.g. for monitoring gene expression levels, for analysing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.

Claim 1; SEQ ID NO 5215; 9pp; English.

The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also useful in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH50865-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsIDEntry.html

Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 54.6%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCA 25

Db 19 TCACAGACAGGTACCTCAA 1

RESULT 20

AAI72282/c

ID AAI72282 standard; DNA; 30 BP.

XX

AC AAI72282;

XX

DT 15-APR-2002 (first entry)

XX

DE 7013 marker primer P10.

XX

KW Lung; cancer; metastasis; solid tumour; blood; bone marrow; syndecan 1;
KW collagen 1 alpha 2; 7013; 7018; amplification; mammal; human; dog; cat;
KW bile duct; colon; breast; uterus; oesophagus; larynx; liver; brain; PCR;
KW remission; relapse; polymerase chain reaction; primer; amplify; ss.
XX
OS Synthetic.

XX WO200198539-A2.

XX 27-DEC-2001.

XX 21-JUN-2001; 2001WO-US019980.

XX 21-JUN-2000; 2000US-0215727P.

XX 27-OCT-2000; 2000US-0243976P.

XX (HITB) HITACHI CHEM CO LTD.

XX (HITB) HITACHI CHEM RES CENT INC.

XX (HITA) HITACHI LTD.

XX Mitsuhashi M, Kambara H, Matsunaga H, Kawamura M;

XX WPI; 2002-098233/13.

XX Identifying lung cancer/metastasis of solid tumor in patient by isolating blood or non-lung tissue, or bone marrow from patient and identifying presence of marker e.g. syndecan 1, collagen 1 alpha 2, 7013, or 7018.

XX Example 3; Page 9; 29pp; English.

XX The sequences given AAI72277-86 are primers which were used to identify markers in normal lung cells and lung cell lines. The primers amplify sequences which were identified using the method of the invention for identifying lung cancer or metastasis of a solid tumour. The method comprises isolating blood (or non-lung tissue in the case of identifying lung cancer, or bone marrow in case of identifying metastasis) from a patient, and identifying the presence of at least one marker (M) such as syndecan 1, collagen 1 alpha 2, 7013, or 7018. The method of the invention is useful for identifying lung cancer in a mammal e.g., human, dog or cat, and identifying metastasis of solid tumour in a patient, where the solid tumour is of bile duct, colon, breast, uterus, oesophagus or larynx. The method is useful for identifying presence of lung cancer cells in the blood or bone marrow, and also for identifying metastasis and thus for identifying lung cancer cells in an organ such as liver or brain. The method is useful to identify the presence of lung cancer cells at a very early stage in the disease, or after remission or to identify a relapse

XX SQ Sequence 30 BP; 12 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 54.6%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CGCAGATCGGTACCTCAAT 26

Db 30 CGCAGATCGGAACCTTAAT 12

RESULT 21

ACI42451/c

ID ACI42451 standard; DNA; 25 BP.

XX

AC ACI42451;

XX

DT 13-OCT-2003 (first entry)

XX

DE Human microarray DNA oligonucleotide SEQ ID NO 42442.

XX

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;

XX genetic variation; biallelic marker; polymorphism; human;

XX cross-species comparison.

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us-10-087-631b-8.max.rng

OS Homo sapiens.
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PP 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 42442; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 6 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 53.8%; Score 14; DB 9; Length 25;
 Best Local Similarity 77.3%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 GTCTTTTCGACAGTCGGTACCTC 23
 Db 22 GTCTTTTCGACAGTCGGTACCTC 1
 XX
 RESULT 22
 ACK26781/c
 ID ACK26781 standard; DNA; 25 BP.
 XX
 AC ACK26781;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 126762.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX

PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PP 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 126762; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 11 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 53.8%; Score 14; DB 9; Length 25;
 Best Local Similarity 77.3%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CGTCTTTTCGACAGTCGGTACCT 22
 Db 23 CGTCTTTTCGACAGTCGGTACCT 2
 XX
 RESULT 23
 ABQ07185/c
 ID ABQ07185 standard; DNA; 24 BP.
 XX
 AC ABQ07185;
 XX
 DT 11-JUN-2002 (first entry)
 XX
 DE Oligonucleotide adapter/capture probe 7176.
 XX
 KW Oligonucleotide array; adapter sequence; probe; ss.
 XX
 OS Synthetic.
 XX
 PN WO200216649-A2.
 XX
 PD 28-FEB-2002.
 XX

PF 27-AUG-2001; 2001WO-US026519.
 XX 25-AUG-2000; 2000US-0227948P.
 PR 29-AUG-2000; 2000US-0228854P.
 XX (ILLU-) ILLUMINA INC.
 PA Gunderson K;
 PI WPI; 2002-292068/33.
 DR Array comprising adapter sequences useful for immobilizing or detecting a
 PT target nucleic acid sequence, has different addresses comprising
 PT different specific capture probes.
 XX Claim 1; Page 178; 261pp; English.
 XX The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
 CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
 CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
 CC and contacting the modified target nucleic acid with (I). The steps of
 CC above method is useful for detecting a target nucleic acid, which further
 CC comprises detecting the presence of the modified target nucleic acid
 XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 U; 0 Other;
 SQ Query Match 53.1%; Score 13.8; DB 6; Length 24;
 Best Local Similarity 88.2%; Pred. No. 5.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 10 CAGATCGGTACCTCAAT 26
 DB ||||| ||||| |||||
 22 CAGATCGGTACCCCAAT 6
 RESULT 24
 ABQ07226
 ID ABQ07226 standard; DNA; 24 BP.
 AC ABQ07226;
 XX 11-JUN-2002 (first entry)
 DT Oligonucleotide adapter/capture probe 7217.
 DE Oligonucleotide array; adapter sequence; probe; ss.
 KW Synthetic.
 OS WO200216649-A2.
 XX 28-FEB-2002.
 PD 27-AUG-2001; 2001WO-US026519.
 XX 25-AUG-2000; 2000US-0227948P.
 PR 29-AUG-2000; 2000US-0228854P.
 XX (ILLU-) ILLUMINA INC.
 PA Gunderson K;
 PI WPI; 2002-292068/33.
 DR Array comprising adapter sequences useful for immobilizing or detecting a
 PT target nucleic acid sequence, has different addresses comprising
 PT different specific capture probes.
 XX Claim 1; Page 178; 261pp; English.

CC The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
 CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
 CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
 CC and contacting the modified target nucleic acid with (I). The steps of
 CC above method is useful for detecting a target nucleic acid, which further
 CC comprises detecting the presence of the modified target nucleic acid
 XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 U; 0 Other;
 SQ Query Match 53.1%; Score 13.8; DB 6; Length 24;
 Best Local Similarity 88.2%; Pred. No. 5.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 10 CAGATCGGTACCTCAAT 26
 DB ||||| ||||| |||||
 3 CAGATCGGTACCCCAAT 19
 RESULT 25
 ABQ01619/c
 ID ABQ01619 standard; DNA; 24 BP.
 XX AC ABQ01619;
 XX 11-JUN-2002 (first entry)
 DT Oligonucleotide adapter/capture probe 1610.
 DE Oligonucleotide array; adapter sequence; probe; ss.
 KW Synthetic.
 OS WO200216649-A2.
 XX 28-FEB-2002.
 PD 27-AUG-2001; 2001WO-US026519.
 XX 25-AUG-2000; 2000US-0227948P.
 PR 29-AUG-2000; 2000US-0228854P.
 XX (ILLU-) ILLUMINA INC.
 PA Gunderson K;
 PI WPI; 2002-292068/33.
 DR Array comprising adapter sequences useful for immobilizing or detecting a
 PT target nucleic acid sequence, has different addresses comprising
 PT different specific capture probes.
 XX Claim 1; Page 82; 261pp; English.
 XX The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
 CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
 CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
 CC and contacting the modified target nucleic acid with (I). The steps of
 CC above method is useful for detecting a target nucleic acid, which further
 CC comprises detecting the presence of the modified target nucleic acid
 XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 U; 0 Other;
 SQ Query Match 53.1%; Score 13.8; DB 6; Length 24;
 Best Local Similarity 88.2%; Pred. No. 5.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 10 CAGATCGGTACCTCAAT 26

Db	22	CAGATCCGTAACCCCAAT	6
RESULT 26			
ADF42309/c			
ID	ADF42309	standard; DNA; 32 BP.	
XX			
AC	ADF42309;		
XX			
DT	12-FEB-2004	(first entry)	
XX			
DE	Arabidopsis GUS PCR primer SEQ ID NO:67.		
XX			
KW	site-specific recombination; transgenic plant cell; integrase;		
KW	int recognition site; crop improvement; herbicide tolerance;		
KW	pathogen resistance; stress tolerance; enhanced nutritional quality;		
KW	yield stability; PCR primer; ss.		
XX			
OS	Synthetic.		
OS	Arabidopsis thaliana.		
XX			
PN	WO2003083045-A2.		
XX			
PD	09-OCT-2003.		
XX			
PF	28-MAR-2003; 2003WO-US010124.		
XX			
PR	29-MAR-2002; 2002US-0369041P.		
PR	12-NOV-2002; 2002US-0425512P.		
XX			
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.		
XX			
PI	Suttie JL, Chilton M, Que Q, Deframond A;		
XX			
DR	WPI; 2003-876984/81.		
XX			
PT	Performing site-specific recombination of DNA within a plant cell, useful		
PT	for crop improvement, comprises introducing into a plant cell a target		
PT	sequence, a donor sequence, and an integrase or an integrase complex.		
XX			
PS	Example 20; SEQ ID NO 67; 214pp; English.		
XX			
CC	The present invention describes a method for performing site-specific		
CC	recombination of DNA within a plant cell by introducing into a plant cell		
CC	a target sequence comprising a first integrase (int) recognition site, a		
CC	donor sequence comprising a second integrase complex, and introducing		
CC	into the plant cell an integrase or integrase complex. Also described:		
CC	(1) manipulating a target sequence within a plant cell, comprising: (a)		
CC	introducing into a plant cell a target sequence comprising a first int		
CC	recognition site and a second int recognition site that are capable of		
CC	recombining with each other, and a first nucleotide sequence that is		
CC	situated between the first and second int recognition sites; (b)		
CC	introducing into the plant cell an integrase or integrase complex; and		
CC	(c) identifying a recombination product comprising an altered target		
CC	sequence; (2) a transgenic plant cell obtained by the method of (1)		
CC	comprising at least one int recognition site; and (3) a transgenic plant		
CC	cell comprising the transgenic plant cell described above. The method is		
CC	useful in integrating foreign DNA at a pre-selected site in the genome of		
CC	a plant or in effecting site-specific recombination of DNA within a plant		
CC	cell. The method may be used in the field of crop improvement, for		
CC	example to confer herbicide tolerance, resistance to pathogens, stress		
CC	tolerance, enhanced nutritional quality, yield stability or enhancement,		
CC	or improved performance in an industrial process. The present sequence is		
CC	used in the exemplification of the present invention.		
XX			
SQ	Sequence 32 BP; 7 A; 8 C; 9 G; 8 T; 0 U; 0 Other;		
	Query Match	53.1%;	Score 13.8; DB 10; Length 32;
	Best Local Similarity	88.2%;	Pred. No. 5.9e+03;
	Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	6	TTCCGAGATCGGTACTT	22

Db	26	TTCCGAGCTTGTTACTT	10
RESULT 27			
ADF42313/c			
ID	ADF42313	standard; DNA; 32 BP.	
XX			
AC	ADF42313;		
XX			
DT	12-FEB-2004	(first entry)	
XX			
DE	Arabidopsis GUS PCR primer SEQ ID NO:71.		
XX			
KW	site-specific recombination; transgenic plant cell; integrase;		
KW	int recognition site; crop improvement; herbicide tolerance;		
KW	pathogen resistance; stress tolerance; enhanced nutritional quality;		
KW	yield stability; PCR primer; ss.		
XX			
OS	Synthetic.		
OS	Arabidopsis thaliana.		
XX			
PN	WO2003083045-A2.		
XX			
PD	09-OCT-2003.		
XX			
PF	28-MAR-2003; 2003WO-US010124.		
XX			
PR	29-MAR-2002; 2002US-0369041P.		
PR	12-NOV-2002; 2002US-0425512P.		
XX			
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.		
XX			
PI	Suttie JL, Chilton M, Que Q, Deframond A;		
XX			
DR	WPI; 2003-876984/81.		
XX			
PT	Performing site-specific recombination of DNA within a plant cell, useful		
PT	for crop improvement, comprises introducing into a plant cell a target		
PT	sequence, a donor sequence, and an integrase or an integrase complex.		
XX			
PS	Example 20; SEQ ID NO 71; 214pp; English.		
XX			
CC	The present invention describes a method for performing site-specific		
CC	recombination of DNA within a plant cell by introducing into a plant cell		
CC	a target sequence comprising a first integrase (int) recognition site, a		
CC	donor sequence comprising a second integrase complex, and introducing		
CC	into the plant cell an integrase or integrase complex. Also described:		
CC	(1) manipulating a target sequence within a plant cell, comprising: (a)		
CC	introducing into a plant cell a target sequence comprising a first int		
CC	recognition site and a second int recognition site that are capable of		
CC	recombining with each other, and a first nucleotide sequence that is		
CC	situated between the first and second int recognition sites; (b)		
CC	introducing into the plant cell an integrase or integrase complex; and		
CC	(c) identifying a recombination product comprising an altered target		
CC	sequence; (2) a transgenic plant cell obtained by the method of (1)		
CC	comprising at least one int recognition site; and (3) a transgenic plant		
CC	cell comprising the transgenic plant cell described above. The method is		
CC	useful in integrating foreign DNA at a pre-selected site in the genome of		
CC	a plant or in effecting site-specific recombination of DNA within a plant		
CC	cell. The method may be used in the field of crop improvement, for		
CC	example to confer herbicide tolerance, resistance to pathogens, stress		
CC	tolerance, enhanced nutritional quality, yield stability or enhancement,		
CC	or improved performance in an industrial process. The present sequence is		
CC	used in the exemplification of the present invention.		
XX			
SQ	Sequence 32 BP; 7 A; 8 C; 9 G; 8 T; 0 U; 0 Other;		
	Query Match	53.1%;	Score 13.8; DB 10; Length 32;
	Best Local Similarity	88.2%;	Pred. No. 5.9e+03;
	Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	6	TTCCGAGATCGGTACTT	22

Db 26 TTCGACGCTCGTACCT 10

RESULT 28

ABZ01654
ID ABZ01654 standard; DNA; 50 BP.

XX AC
XX ABZ01654;

DT 09-JAN-2003 (first entry)

DE Human leukocyte gene expression profiling probe SEQ ID NO 1645.

XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.

XX Homo sapiens.

OS WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.
XX 20-OCT-2000; 2000US-0241994P.
XX 08-JUN-2001; 2001US-0296764P.

XX (BIOC-) BIOTEC INC.

XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 378; Opp; English.

XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 15 A; 12 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 53.1%; Score 13.8; DB 6; Length 50;

Best Local Similarity 72.0%; Pred. No. 6.3e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GTCTTTTCGACGATCGGTACCTCAAT 26

Db 4 GTCTCAGGGTATCGGTACCTCAAT 28

RESULT 29

ACH54506/c
ID ACH54506 standard; DNA; 25 BP.

XX AC
XX ACH54506;

DT 16-OCT-2003 (first entry)

XX DNA target sequence #3642 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.

XX Unidentified.

XX US2003082596-A1.

XX 01-MAY-2003.

XX 08-AUG-2002; 2002US-00215112.

XX 08-AUG-2001; 2001US-0311040P.

XX (MITT/) MITTMANN M.

XX Mittmann M;

XX WPI; 2003-576608/54.

XX New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX Claim 1; SEQ ID NO 3642; 9pp; English.

XX The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH5260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/peipsIDentry.html

XX Sequence 25 BP; 6 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 52.3%; Score 13.6; DB 9; Length 25;

Best Local Similarity 80.0%; Pred. No. 7.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26

Db 22 TCACAGACGCTACCTCAAT 3

RESULT 30

AAV74227
ID AAV74227 standard; DNA; 34 BP.

XX AC
XX AAV74227;

Wed Nov 24 08:46:10 2004

20-MAR-2003 (revised)
 15-MAR-1999 (first entry)
 CpG-N motif PCR primer Mu- (4+5)R.
 CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;
 viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
 toxins; tumour suppressor; cytokine; apoptotic protein; interferon;
 hormone; clotting factor; ligand; receptor; PCR primer; ss.
 Synthetic.
 WO9852581-A1.
 26-NOV-1998.
 20-MAY-1998; 98WO-US010408.
 20-MAY-1997; 97US-0047209P.
 20-MAY-1997; 97US-0047233P.
 (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
 (IOWA) UNIV IOWA RES FOUND.
 (QIAG-) QIAGEN GMBH.
 Davis HL, Krieg AM, Schorr J, Wu T;
 WPI; 1999-059712/05.
 Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
 enhancing the immunostimulatory effect of an antigen or enhancing the
 expression of a therapeutic polypeptide.
 Example 1; Page 58; 109pp; English.
 AAU74209-V74236 are PCR primers used to describe a method for enhancing
 the immunostimulatory effect of an antigen encoded by nucleic acid
 contained in a nucleic acid construct. The method involves determining
 the CpG-N and CpG-S motifs present in the construct, removing
 neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG
 (CpG-S) motifs in the construct, thereby producing a nucleic acid
 construct having enhanced immunostimulatory efficacy. The method can be
 used for immunisation against viral antigens, e.g. from hepatitis B virus
 (HBV), bacterial antigens or an antigen derived from a parasite. They can
 also be used for expression of a therapeutic polypeptide, e.g. growth
 factors, toxins, tumour suppressors, cytokines, apoptotic proteins,
 interferons, hormones, clotting factors, ligands and receptors. (Updated
 on 20-MAR-2003 to correct PA field.)
 Sequence 34 BP; 9 A; 7 C; 10 G; 8 T; 0 U; 0 Other;
 Query Match 52.3%; Score 13.6; DB 2; Length 34;
 Best Local Similarity 80.0%; Pred. No. 7.5e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7 TCGCAGATCGGTACCTCAAT 26
 Db 10 TCGCAGATCGGTACCTCAAT 29
 RESULT 31
 AAC66050
 ID AAC66050 standard; DNA; 40 BP.
 XX AC
 AAC66050;
 22-FEB-2001 (first entry)
 DE E.coli ygbp primer YGBP2A.
 XX YJEE; KDTB; YQGF; YGGF; YHBC; YGCB; YGBB; YCHB; antibacterial; treatment;
 infection; primer; ss.
 XX

Escherichia coli.
 DE19916176-A1.
 12-OCT-2000.
 10-APR-1999; 99DE-01016176.
 10-APR-1999; 99DE-01016176.
 (FARB) BAYER AG.
 Broetz H, Ehler K, Freiberg C, Spaltmann F, Wieland B;
 Labischinski H;
 WPI; 2000-639611/62.
 Essential genes from bacteria, useful in screening for antimicrobial
 agents, and related proteins, transformants and antisense sequences.
 Example 2; Page 26; 28pp; German.
 This invention describes novel Escherichia coli genes (I) encoding
 proteins (II) designated YQGF, YHBC, YGGJ, YGGB, YCHB, YJEE and
 KDTB, and genes (Ia) that encode orthologous gene products (IIa) in other
 microorganisms and which have antibacterial activity. Recombinant
 microorganisms in which expression of (I) or (Ia) can be regulated are
 used to identify compounds that bind to the gene products, particularly
 in affinity selection assays. (II) and (IIa) are used to identify, or
 prepare, antibodies and other proteins that bind to the gene products.
 Substances that bind to (II) or (IIa) are potentially useful as
 antibacterials for treating a wide range of infections in humans and
 animals. Sequences antisense to (I) and (Ia) can also be used as
 antibacterials. The specified genes are widely distributed in bacteria
 but have no close homologs in eukaryotic cells
 Sequence 40 BP; 9 A; 12 C; 10 G; 9 T; 0 U; 0 Other;
 Query Match 52.3%; Score 13.6; DB 3; Length 40;
 Best Local Similarity 80.0%; Pred. No. 7.7e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 TTTCGACATCGGTACCTCA 24
 Db 9 TTTCGACATCGGTACCTCA 28
 RESULT 32
 ADG69940/c
 ID ADG69940 standard; DNA; 24 BP.
 XX AC
 ADG69940;
 11-MAR-2004 (first entry)
 DT Mouse interleukin-6, IL-6, RT-PCR primer #1.
 DE Mouse; interleukin; IL-6; RT-PCR; primer; PCR; reverse transcriptase PCR;
 cytotkine; wild yam; polysaccharide extract; indigestion; anorexia;
 diarrhoea; diabetes; vaccine; infection; ss.
 XX OS
 Mus sp.
 XX US2003224066-A1.
 PN 04-DEC-2003.
 XX 30-MAY-2002; 2002US-00160670.
 XX 30-MAY-2002; 2002US-00160670.
 (WURR/) WU R.
 XX

PI Wu R;
 XX WPI; 2004-051892/05.
 XX
 XX
 PT Oral composition for enhancing immunological effects of oral vaccine
 PT comprising microbial antigen and inducing cytokine gene expression in
 PT lamina propria, has polysaccharide extract of Dioscorea species.
 XX
 XX Example 2; SEQ ID NO 5; 21pp; English.
 XX
 XX The invention relates to an oral composition comprising a polysaccharide
 CC extract of Dioscorea sp (wild yam) prepared by a process which involves
 CC extracting tuber of yam using alcohol-based solvent in the presence of
 CC acid to obtain insoluble solid portion which is subjected to aqueous
 CC solvent in presence of starch hydrolysing enzyme to obtain aqueous
 CC solution and subjecting the aqueous solution to the solvent so that a
 CC polysaccharide extract of yam is precipitated and collected from aqueous
 CC solution. The polysaccharide extract is an enhancer of immunological
 CC activity by inducing cytokine gene expression in the small intestine.
 CC Mice were fed the extract and then the lamina propria cells from the
 CC Peyer's patch were isolated. RT (reverse transcriptase) PCR was performed
 CC using primer for certain cytokines. The results showed that the gene
 CC expression of interferon-alpha (IFN-alpha), interleukin-4 (IL-4) and IL-6
 CC in Peyer's patch were increased, especially IL-4 and in lamina propria,
 CC the gene expression of IFN-alpha, IL-4, IL-6 and transforming growth
 CC factor-beta (TGF-beta) were increased, especially IL-6. The extract is
 CC thus useful for eliciting the induction of cytokine (interleukin-2 (IL-
 CC 2), interferon-alpha, IL-4, IL-5, IL-6, IL-10 or transforming growth
 CC factor-beta) gene expression in intestinal epithelium lymphocytes, lamina
 CC propria, and Peyer's patch of the subject. The extract is also useful for
 CC enhancing the immunological effects of an oral vaccine to a subject, by
 CC enhancing the systemic Igg and mucosal Iga antibody responses of subject
 CC upon vaccination with an oral vaccine that comprises a microbial antigen.
 CC Preferably, the oral vaccine is Pneumovax 23. The extract also inhibits
 CC the oral tolerance induced by orally administered protein antigen. The
 CC extract is useful for enhancing immunity and for enhancing the systemic
 CC and mucosal immune responses of a subject upon vaccination with oral
 CC vaccine. The extract also offers a more efficacious vaccination for the
 CC elderly or patients with immunodeficiencies and is safer than the
 CC currently used cholera toxin. The polysaccharides are orally active in
 CC immunomodulating effect, enhancement of mucosal and systemic immunities
 CC and elimination of oral tolerance. Yam extract have been used in Chinese
 CC medicine for treatment of indigestion, anorexia, diarrhoea and diabetes.
 CC The present sequence is an RT-PCR primer for a cytokine (or control) used
 CC in the above experiment.
 XX
 XX SQ Sequence 24 BP; 7 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 51.5%; Score 13.4; DB 12; Length 24;
 Best Local Similarity 73.9%; Pred. No. 9.1e+03;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 2 GTCTTTTCGACGATCGGTACTCTCA 24
 ||||| ||||| ||||| |||||
 Db 24 GTCTTTTCGACGAGGAAGTCTCA 2
 RESULT 33
 AD071456/c
 ID AD071456 standard; DNA; 24 BP.
 XX
 XX AC AD071456;
 XX
 XX DT 26-AUG-2004 (first entry)
 XX
 XX DE IL-6 sense primer.
 XX
 XX KW Gastrointestinal; Antiinflammatory;
 XX KW Corticotropin-releasing hormone receptor 1;
 XX KW Corticotropin-releasing hormone receptor 2; CRH-R1; CRH-R2;
 XX KW inflammatory disease; primer; ss; IL-6.
 XX
 XX OS Synthetic.

XX WO2004047866-A2.
 XX
 XX PD 10-JUN-2004.
 XX
 XX PF 26-NOV-2003; 2003WO-IB005429.
 XX
 XX PR 26-NOV-2002; 2002GR-00100513.
 XX
 XX PA (BION-) BIONATURE EA LTD.
 XX
 XX PI Margioris AN, Gravanis A;
 XX WPI; 2004-441105/41.
 XX
 XX PT Use of synthetic corticotropin releasing hormone receptor antagonists
 PT and/or agonists in the treatment of inflammatory diseases e.g. chronic
 PT inflammatory bowel disease and idiopathic inflammatory disease.
 XX
 XX PS Disclosure; Page 15; 44pp; English.
 XX
 XX CC The present invention relates to a method for treating inflammatory
 CC disease using a corticotropin-releasing hormone-receptor 1 (CRH-R1)
 CC antagonist and/or CRH-R2 agonist. Antalarmin is specifically claimed as
 CC the synthetic CRH-R1 antagonist. The CRH-R1 antagonist and/or CRH-R2
 CC agonist modifies the response of monocyte/macrophage cell activation,
 CC proliferation, differentiation, apoptosis or cytokine production, thereby
 CC subsequently controls the magnitude of the inflammatory response. The
 CC invention is useful in the manufacture of pharmaceutical composition for
 CC the treatment of inflammatory diseases or condition e.g. chronic
 CC inflammatory bowel disease, idiopathic inflammatory disease, inflammatory
 CC disorders of connective tissue, inflammatory demyelinating
 CC polyneuropathies, inflammatory myopathies, inflammatory diseases of
 CC joints including bursitis, fibromyalgia syndrome and inflammatory disease
 CC of upper gastrointestinal tract. The present sequence is a primer used to
 CC illustrate the invention.
 XX
 XX SQ Sequence 24 BP; 6 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 51.5%; Score 13.4; DB 12; Length 24;
 Best Local Similarity 73.9%; Pred. No. 9.1e+03;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 2 GTCTTTTCGACGATCGGTACTCTCA 24
 ||||| ||||| ||||| |||||
 Db 23 GTCTTTTCGACGAGGAAGTCTCA 1
 RESULT 34
 AAV54074/c
 ID AAV54074 standard; DNA; 25 BP.
 XX
 XX AC AAV54074;
 XX
 XX DT 02-DEC-1998 (first entry)
 XX
 XX DE Nucleotide sequence of (interleukin-6) IL-6 PCR primer 1.
 XX KW PCR; primer; amplification; microglia; carrier; brain; cerebral disease;
 XX KW interleukin-6; IL-6; ss.
 XX
 XX OS Synthetic.
 XX
 XX FN WO9839415-A1.
 XX
 XX PD 11-SEP-1998.
 XX
 XX PF 05-MAR-1998; 98WO-JP000949.
 XX
 XX PR 05-MAR-1997; 97JP-00050448.
 XX
 XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX

PI Sawada M;
XX WPI; 1998-495834/42.
XX
XX Microglia with brain affinity - formulable as drug compositions, useful
PT as carrier for introduction of gene or drugs for treatment of cerebral
PT diseases.
XX
XX Example 1; Page 11; 36pp; Japanese.
XX
XX This is the nucleotide sequence of a PCR primer used for amplification in
CC the method of the invention. The process involves the use of established
CC microglia as carriers for introducing gene, drugs as well as other
CC chemical substances e.g. in drug compositions especially to the brain,
CC particularly useful in the treatment of cerebral diseases. The microglia
CC can be stably expressed in a vector and have specific affinity to the
CC brain
XX
XX Sequence 25 BP; 7 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 51.5%; Score 13.4; DB 2; Length 25;
Best Local Similarity 73.9%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 GTCTTTCGACGATCGGTACTCA 24
Db 24 GTCTTTCGACGAGGAACTTCA 2
RESULT 35
AAD24887/c
ID AAD24887 standard; DNA; 25 BP.
XX
XX AAD24887;
XX
XX 12-MAR-2002 (first entry)
XX
XX Interleukin-6 (IL-6) cDNA amplifying sense RT-PCR primer.
XX
XX Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;
XX immune response; apoptosis; Alzheimer's disease; Parkinson's disease;
KW rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;
KW liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;
KW amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;
KW head injury damage; aplastic anaemia; tumour; organ transplantation;
KW cerebral infarction; follicular lymphomas; systemic lupus erythematosus;
KW viral infection; glomerulonephritis; apoptosis; autoimmune disorder;
KW sepsis; RT-PCR primer; ss.
XX
XX Unidentified.
XX
XX WO200185910-A2.
XX
XX 15-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US014508.
XX
XX 05-MAY-2000; 2000US-0202274P.
PR 17-JAN-2001; 2001US-0262321P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Raz E, Lois AP, Takabayashi K;
XX
XX WPI; 2002-062244/08.
XX
XX Modulating cell death or reducing DNA damage in eukaryotic cells, useful
PT for reducing cell death in individual or organ, comprises contacting cell
PT with agent modulating biological activity of DNA-dependent protein
PT kinase.
XX
XX Example 1; Page 30; 57pp; English.
XX

CC The invention relates to a method for modulating cell death or reducing
CC DNA damage in an eukaryotic cell by contacting the cell with an agent
CC that modulates the biological activity of DNA-dependent protein kinase
CC (DNA-PK). The invention also relates nucleic acids which modulate the
CC immune response binding to Ku antigen, resulting in activation of DNA-PK.
CC The method is useful for modulating cell death or reducing DNA damage in
CC an eukaryotic cell, for treating any disorder resulting from a genotoxic
CC insert to a cell e.g., necrosis, apoptosis. The method is also useful for
CC treating cell death-related indications such as Alzheimer's disease,
CC Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
CC central nervous system inflammation, osteoporosis, degenerative liver
CC disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,
CC amyotrophic lateral sclerosis, myocardial infarction, head injury damage,
CC acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral
CC infarction, bypass heart surgery, organ transplantation. The method is
CC also useful for treating follicular lymphomas, carcinomas, autoimmune
CC disorders (systemic lupus erythematosus), hormone dependent tumours,
CC immune mediated glomerulonephritis; apoptosis and viral infections. The
CC present sequence is a reverse transcription (RT) PCR primer used for
CC amplifying interleukin-6 (IL-6) cDNA used in the exemplification of the
CC invention
XX
XX Sequence 25 BP; 7 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 51.5%; Score 13.4; DB 6; Length 25;
Best Local Similarity 73.9%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 GTCTTTCGACGATCGGTACTCA 24
Db 24 GTCTTTCGACGAGGAACTTCA 2
RESULT 36
ACI80464/c
ID ACI80464 standard; DNA; 25 BP.
XX
XX ACI80464;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 80455.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 80455; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used

CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 9; Length 25;
 Best Local Similarity 73.9%; Pred. No. 9.1e+03;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGTCTTTGCGAGATCGGTACCTC 23
 ||||| || ||||| |||||
 Db 23 CGTCTCCAGATCGGTCTC 1

RESULT 37
 AAX24768
 ID AAX24768 standard; DNA; 30 BP.
 XX
 AC AAX24768;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Human glandular kallikrein hKLK2 gene PCR primer 51.70.2.
 XX
 KW Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;
 KW therapy; PCR; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO9906576-A1.
 XX
 PD 11-FEB-1999.
 XX
 PF 04-AUG-1998; 98WO-US016312.
 XX
 PR 04-AUG-1997; 97US-0054523P.
 PR 02-MAR-1998; 98US-0076545P.
 PR 03-AUG-1998; 98US-00127834.
 XX
 PA (CALY-) CALYDON INC.
 XX
 PI Yu D, Herdenson DR, Schuur ER;
 XX
 DR WPI; 1999-153804/13.
 XX
 PT New nucleic acid containing the human glandular kallikrein enhancer -
 PT providing increased expression of heterologous sequences in prostatic
 PT cells, and related adenoviral vectors for treating prostatic cancer.
 XX
 PS Example 2; Page 77; 179pp; English.
 XX

CC Primer 51.70.2 was used with primer 51.70.1 (see AAX24767) to amplify a
 CC fragment of the 5' flanking region of the hKLK2 gene. A series of
 CC constructs was generated by inserting hKLK2 5' flanking regions upstream
 CC of a luciferase reporter gene, and the activity of these fragments was

CC compared with that of CN299, a plasmid with the full hKLK2 promoter (-607
 CC to +33) driving expression of luciferase. hKLK2 gene enhancers were
 CC identified (see AAX24755) that increase the transcription of cis-linked
 CC coding sequences in prostate cells. Methods of using DNA constructs
 CC comprising the enhancers to control transcription of heterologous
 CC polynucleotides are provided. Adenoviral vectors in which one or more
 CC genes are under transcriptional control of a hKLK2 transcription
 CC regulatory element are claimed, and can be used to confer selective
 CC cytotoxicity in mammalian cells for use e.g. in the treatment of prostate
 CC cancer
 XX

SQ Sequence 30 BP; 9 A; 8 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 2; Length 30;
 Best Local Similarity 93.3%; Pred. No. 9.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAAT 26
 ||||| ||||| |||||
 Db 1 GATCGGTACCTCACT 15

RESULT 38
 AAT73409
 ID AAT73409 standard; DNA; 31 BP.
 XX
 AC AAT73409;
 XX
 DT 14-JAN-1998 (first entry)
 XX
 DE S182 gene mutation detection intron 2/exon 3 boundary.
 XX
 KW S182 gene; Alzheimer's disease; polymorphism; mismatch; mutation;
 KW intronic sequence; polymerase chain reaction; primer; ss.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT intron 1..21
 FT /*tag= a
 FT /number= 2
 FT /note= "End of intron 2"
 FT exon 22..31
 FT /*tag= b
 FT /number= 3
 FT /note= "Start of exon 3"

WO9715689-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017132.
 XX
 PR 25-OCT-1995; 95US-0007048P.
 XX
 PA (UNIW) UNIV WASHINGTON SCHOOL MED.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Hardy JA, Goate AM;
 XX
 DR WPI; 1997-259039/23.
 XX

PT Diagnosing Alzheimer's disease by detecting polymorphism in the S182 gene
 PT - using mismatch polymerase chain reaction primers derived from intronic
 PT sequences.
 XX

PS Example 2; Fig 1; 30pp; English.

CC A method has been developed for the detection of polymorphism (mutations)
 CC in the S182 gene. The mutations are detected using selected mismatch
 CC polymerase chain reaction (PCR) primers derived from intronic sequences
 CC of the gene. The present sequence represents the intron 2/ exon 3
 CC boundary. Mutations in the S182 gene indicate that a subject is

CC susceptible to late onset Alzheimer's disease. The method allows rapid
CC analysis of many samples by PCR, restriction enzyme digestion and gel
CC electrophoresis. Use of intronic sequences allows mutations to be
CC detected in splice donor and acceptor sites (this would be almost
CC impossible without intronic primers)

XX Sequence 31 BP; 6 A; 8 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 2; Length 31;

Best Local Similarity 73.9%; Pred. No. 9.4e+03; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 6;

QY 3 TCTTTCCGACATCGGTACTCAA 25

Db 7 TCTTTCCCTTTTCAGACCTCAA 29

RESULT 39

ADB23049

ID ADB23049 standard; DNA; 31 BP.

XX AC ADB23049;

XX DT 20-NOV-2003 (first entry)

XX DE Tobacco methionine synthase oligonucleotide #4.

XX KW ss; plant; methionine synthase; methionine; seed; transformed plant;
XX KW transgenic; tobacco.

XX OS Nicotiana tabacum.

XX PN US2003088886-A1.

XX PD 08-MAY-2003.

XX PF 28-JAN-2002; 2002US-00989339.

XX PR 30-AUG-1995; 95US-0002973P.

XX PR 27-AUG-1996; 96US-00703829.

XX PR 19-AUG-1999; 99US-00377431.

XX PA (FALC/) FALCO S C.

XX PA (FAMO/) FAMODU O O.

XX PA (RAPA/) RAFALSKI J A.

XX PA (RAMA/) RAMAKER M L.

XX PA (TARC/) TARCZYNSKI M C.

XX PA (THOR/) THORPE C.

XX PI Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC;

XX PT Thorpe C;

XX WI WI; 2003-657990/62.

XX PT New nucleic acid fragments encoding a plant 5-methyltetra-
XX PT hydroxyethylglutamate-homocysteine methyl transferase or methionine
XX PT synthase, useful for producing increased levels of methionine in the
XX PT seeds of transformed plants.

XX PS Example 2; Page 42; 69pp; English.

XX CC The invention relates to an isolated nucleic acid fragment encoding a
XX CC plant methionine synthase. The nucleic acid fragments and chimeric genes
XX CC are useful for producing increased levels of methionine in the seeds of
XX CC transformed plants. The present sequence represents the amino acid
XX CC sequence of a plant methionine synthase associated oligonucleotide.

XX SQ Sequence 31 BP; 6 A; 7 C; 10 G; 8 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 9; Length 31;

Best Local Similarity 93.3%; Pred. No. 9.4e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1;

QY 12 GATCGGTACTCAAT 26

Db 1 GATCGGTACTCACT 15

RESULT 40

AAI64730/c

ID AAI64730 standard; DNA; 32 BP.

XX AC AAI64730;

XX DT 07-DEC-2001 (first entry)

XX DE Human line 1-12 PCR primer 4.

XX KW Human, line 1-12; cytostatic; virucidal; immunomodulatory;
XX KW antiinflammatory; haemostatic; malignant tumour; HIV; infection;
XX KW human immunodeficiency virus; immunological disease; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200173068-A1.

XX PD 04-OCT-2001.

XX PF 26-MAR-2001; 2001WO-CN000495.

XX PR 27-MAR-2000; 2000CN-00115143.

XX PA (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.

XX PI Mao Y, Xie Y;

XX WI WI; 2001-597126/67.

XX PT Line 1-12 and encoded polynucleotide, used in diagnosis and treatment of
XX PT malignant tumors, hemopathy, human immunodeficiency virus infection,
XX PT immunological diseases and inflammation.

XX PS Example 5; Page 17; 33pp; Chinese.

XX CC The invention relates to human line 1-12 with cytostatic, virucidal,
XX CC immunomodulatory, antiinflammatory and haemostatic activity. The protein
XX CC and encoding polynucleotide are used in diagnosis and treatment of
XX CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)
XX CC infection, immunological diseases and various inflammations. The present
XX CC sequence is that of a human line 1-12 PCR primer, useful to the invention

XX SQ Sequence 32 BP; 8 A; 7 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 5; Length 32;

Best Local Similarity 73.9%; Pred. No. 9.4e+03; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 6;

QY 1 CGTCTTTTCGACATCGGTACTC 23

Db 26 CTTCTTTTCGCAACCGGGAATTC 4

Search completed: November 23, 2004, 17:29:51
Job time : 160.543 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 30.0899 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631B-8

Perfect score: 26

Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.2	58.5	44	1	US-08-344-695-5
C 2	14.6	56.2	41	2	US-08-365-486A-4
C 3	14.6	56.2	41	3	US-08-880-342-4
C 4	14	53.8	47	4	US-09-641-638-998
C 5	14	53.8	47	4	US-10-170-097-998
C 6	13.6	52.3	34	3	US-09-082-649B-41
C 7	13.4	51.5	25	4	US-09-180-394-3
C 8	13.4	51.5	31	3	US-08-738-381-24
C 9	13.4	51.5	39	3	US-08-845-546-22
C 10	13.2	50.8	32	4	US-09-714-550-6
C 11	13	50.0	30	4	US-09-553-867A-31
C 12	13	50.0	50	1	US-08-171-389-583
C 13	13	50.0	50	1	US-08-123-916-583
C 14	13	50.0	50	2	US-08-475-228A-583
C 15	13	50.0	50	3	US-08-482-080A-583
C 16	13	50.0	50	3	US-09-354-947-583
C 17	13	50.0	50	5	PCT-US93-12388-583
C 18	12.8	49.2	38	1	US-08-485-971-12
C 19	12.8	49.2	38	1	US-08-275-876-12
C 20	12.8	49.2	38	1	US-08-383-754-12
C 21	12.8	49.2	38	1	US-08-485-978-12
C 22	12.8	49.2	38	2	US-08-486-814-12
C 23	12.8	49.2	38	2	US-08-487-472-12
C 24	12.8	49.2	38	3	US-08-485-740-12
C 25	12.8	49.2	38	3	US-09-162-184-12
C 26	12.8	49.2	38	3	US-09-161-902-12
C 27	12.8	49.2	38	3	US-09-489-777A-12

C 28	12.8	49.2	38	5	PCT-US95-08179-12	Sequence 12, Appl
C 29	12.6	48.5	26	4	US-09-976-667-15	Sequence 15, Appl
C 30	12.6	48.5	26	6	RE34606-8	Patent No. RE34,60
C 31	12.4	47.7	28	4	US-09-672-810-15	Sequence 15, Appl
C 32	12.4	47.7	35	3	US-09-455-960-28	Sequence 28, Appl
C 33	12.4	47.7	35	4	US-10-051-325-28	Sequence 28, Appl
C 34	12.4	47.7	37	4	US-08-641-294-4	Sequence 4, Appl
C 35	12.4	47.7	40	6	5256558-14	Patent No. 5256558
C 36	12.4	47.7	42	3	US-08-879-565-6	Sequence 6, Appl
C 37	12.4	47.7	45	3	US-09-217-228-4	Sequence 4, Appl
C 38	12.2	46.9	18	1	US-08-363-240A-1102	Sequence 1102, Ap
C 39	12.2	46.9	24	3	US-03-165-934-2	Sequence 2, Appli
C 40	12.2	46.9	24	4	US-03-343-494-5	Sequence 5, Appli
C 41	12.2	46.9	31	4	US-09-831-842-59	Sequence 69, Appl
C 42	12.2	46.9	33	4	US-09-828-310-23	Sequence 23, Appl
C 43	12.2	46.9	33	4	US-09-828-310-37	Sequence 37, Appl
C 44	12.2	46.9	33	4	US-09-828-310-44	Sequence 44, Appl
C 45	12.2	46.9	36	4	US-09-173-053-15	Sequence 15, Appl
C 46	12.2	46.9	36	4	US-09-331-793-15	Sequence 15, Appl
C 47	12.2	46.9	38	6	RE34606-9	Patent No. RE34,60
C 48	12.2	46.9	43	3	US-09-351-814-18	Sequence 18, Appl
C 49	12.2	46.9	48	2	US-08-924-695A-27	Sequence 27, Appl
C 50	12	46.2	20	4	US-09-198-452A-4650	Sequence 4650, Ap
C 51	12	46.2	21	1	US-08-171-718-92	Sequence 92, Appl
C 52	12	46.2	21	3	US-08-478-087-92	Sequence 92, Appl
C 53	12	46.2	21	3	US-08-998-416-9	Sequence 9, Appl
C 54	12	46.2	21	3	US-09-415-522-16	Sequence 16, Appl
C 55	12	46.2	21	3	US-09-588-256-14	Sequence 14, Appl
C 56	12	46.2	21	3	US-09-625-188-24	Sequence 24, Appl
C 57	12	46.2	32	4	US-09-527-522-11	Sequence 11, Appl
C 58	12	46.2	32	4	US-10-067-291-11	Sequence 11, Appl
C 59	12	46.2	36	1	US-08-478-039-46	Sequence 46, Appl
C 60	12	46.2	36	1	US-08-476-349A-46	Sequence 46, Appl
C 61	12	46.2	36	3	US-08-523-894-39	Sequence 39, Appl
C 62	12	46.2	38	1	US-08-338-992B-12	Sequence 12, Appl
C 63	12	46.2	38	3	US-09-010-733-12	Sequence 12, Appl
C 64	12	46.2	38	4	US-09-340-798A-46	Sequence 46, Appl
C 65	12	46.2	38	5	PCT-US95-09057-12	Sequence 12, Appl
C 66	12	46.2	43	1	US-08-629-600-18	Sequence 18, Appl
C 67	12	46.2	43	3	US-08-973-131-28	Sequence 28, Appl
C 68	12	46.2	43	3	US-08-863-859-19	Sequence 19, Appl
C 69	11.8	45.4	24	4	US-09-336-946B-67	Sequence 67, Appl
C 70	11.8	45.4	24	4	US-09-362-842-30	Sequence 30, Appl
C 71	11.8	45.4	24	4	US-09-993-170-27	Sequence 27, Appl
C 72	11.8	45.4	25	1	US-07-936-163-22	Sequence 22, Appl
C 73	11.8	45.4	25	3	US-08-729-601A-62	Sequence 62, Appl
C 74	11.8	45.4	25	3	US-09-097-319A-42	Sequence 42, Appl
C 75	11.8	45.4	25	4	US-09-643-971-42	Sequence 42, Appl
C 76	11.8	45.4	27	4	US-09-678-300-28	Sequence 28, Appl
C 77	11.8	45.4	30	4	US-08-693-234-3	Sequence 3, Appli
C 78	11.8	45.4	30	4	US-08-693-234-4	Sequence 4, Appli
C 79	11.8	45.4	31	3	US-08-679-645-417	Sequence 417, App
C 80	11.8	45.4	32	1	US-07-936-163-26	Sequence 26, Appl
C 81	11.8	45.4	32	3	US-08-729-601A-65	Sequence 65, Appl
C 82	11.8	45.4	32	3	US-09-355-434-16	Sequence 16, Appl
C 83	11.8	45.4	32	3	US-09-097-319A-45	Sequence 45, Appl
C 84	11.8	45.4	32	4	US-09-371-772B-14224	Sequence 14224, A
C 85	11.8	45.4	32	4	US-09-643-971-45	Sequence 45, Appl
C 86	11.8	45.4	34	1	US-08-181-271A-58	Sequence 58, Appl
C 87	11.8	45.4	34	1	US-08-449-315-58	Sequence 58, Appl
C 88	11.8	45.4	34	1	US-08-444-803-58	Sequence 58, Appl
C 89	11.8	45.4	34	1	US-08-449-063A-58	Sequence 58, Appl
C 90	11.8	45.4	34	1	US-08-456-265A-58	Sequence 58, Appl
C 91	11.8	45.4	34	1	US-08-455-416-58	Sequence 58, Appl
C 92	11.8	45.4	34	1	US-08-455-244-58	Sequence 58, Appl
C 93	11.8	45.4	34	1	US-08-454-876-58	Sequence 58, Appl
C 94	11.8	45.4	34	2	US-08-457-364-58	Sequence 58, Appl
C 95	11.8	45.4	34	2	US-08-456-262-58	Sequence 58, Appl
C 96	11.8	45.4	34	2	US-08-456-240-58	Sequence 58, Appl
C 97	11.8	45.4	34	2	US-08-455-736-58	Sequence 58, Appl
C 98	11.8	45.4	34	2	US-08-971-217-58	Sequence 58, Appl
C 99	11.8	45.4	34	3	US-09-350-600-58	Sequence 58, Appl
C 100	11.8	45.4	34	4	US-09-906-234-58	Sequence 58, Appl

us-10-087-631b-8.max.rn1

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c 101	11.8	45.4	36	1	US-08-066-961-38	Sequence 38, Appl	c 174	11.6	44.6	36	3	US-09-129-740-4	Sequence 4, Appl
c 102	11.8	45.4	36	1	US-08-375-134-4	Sequence 4, Appl	c 175	11.6	44.6	36	3	US-09-568-527-4	Sequence 4, Appl
c 103	11.8	45.4	36	5	PCT-US95-15263-4	Sequence 4, Appl	176	11.6	44.6	39	3	US-08-974-549A-498	Sequence 498, Appl
c 104	11.8	45.4	37	3	US-09-424-120-1	Sequence 1, Appl	177	11.6	44.6	39	3	US-08-974-549A-500	Sequence 500, Appl
c 105	11.8	45.4	37	3	US-09-424-120-3	Sequence 3, Appl	178	11.6	44.6	39	3	US-08-974-549A-502	Sequence 502, Appl
c 106	11.8	45.4	38	1	US-08-181-271A-57	Sequence 57, Appl	179	11.6	44.6	39	3	US-08-974-549A-504	Sequence 504, Appl
c 107	11.8	45.4	38	1	US-08-449-315-57	Sequence 57, Appl	180	11.6	44.6	39	4	US-08-912-951-265	Sequence 265, Appl
c 108	11.8	45.4	38	1	US-08-449-043-57	Sequence 57, Appl	181	11.6	44.6	39	4	US-08-912-951-267	Sequence 267, Appl
c 109	11.8	45.4	38	1	US-08-449-043-57	Sequence 57, Appl	182	11.6	44.6	39	4	US-08-912-951-269	Sequence 269, Appl
c 110	11.8	45.4	38	1	US-08-456-265A-57	Sequence 57, Appl	183	11.6	44.6	39	4	US-08-912-951-271	Sequence 271, Appl
c 111	11.8	45.4	38	1	US-08-455-416-57	Sequence 57, Appl	184	11.6	44.6	39	4	US-09-402-181B-498	Sequence 498, Appl
c 112	11.8	45.4	38	1	US-08-455-244-57	Sequence 57, Appl	185	11.6	44.6	39	4	US-09-402-181B-500	Sequence 500, Appl
c 113	11.8	45.4	38	1	US-08-454-876-57	Sequence 57, Appl	186	11.6	44.6	39	4	US-09-402-181B-502	Sequence 502, Appl
c 114	11.8	45.4	38	2	US-08-457-364-57	Sequence 57, Appl	187	11.6	44.6	39	4	US-09-402-181B-504	Sequence 504, Appl
c 115	11.8	45.4	38	2	US-08-456-262-57	Sequence 57, Appl	188	11.6	44.6	39	4	US-09-721-456-498	Sequence 498, Appl
c 116	11.8	45.4	38	2	US-08-456-262-57	Sequence 57, Appl	189	11.6	44.6	39	4	US-09-721-456-500	Sequence 500, Appl
c 117	11.8	45.4	38	2	US-08-455-735-57	Sequence 57, Appl	190	11.6	44.6	39	4	US-09-721-456-502	Sequence 502, Appl
c 118	11.8	45.4	38	2	US-08-971-217-57	Sequence 57, Appl	191	11.6	44.6	39	4	US-09-721-456-504	Sequence 504, Appl
c 119	11.8	45.4	38	2	US-09-350-600-57	Sequence 57, Appl	192	11.6	44.6	41	1	US-08-664-449-26	Sequence 26, Appl
c 120	11.8	45.4	38	4	US-09-906-234-57	Sequence 57, Appl	193	11.6	44.6	41	1	US-08-664-449-27	Sequence 27, Appl
c 121	11.8	45.4	40	3	US-09-485-737B-6	Sequence 6, Appl	194	11.6	44.6	42	4	US-09-622-951-6	Sequence 6, Appl
c 122	11.8	45.4	44	4	US-08-823-823-31	Sequence 31, Appl	195	11.6	44.6	44	4	US-08-109-037-30	Sequence 30, Appl
c 123	11.8	45.4	45	1	US-08-447-169A-229	Sequence 229, Appl	196	11.6	44.6	44	4	US-08-109-037-118	Sequence 118, Appl
c 124	11.8	45.4	45	1	US-09-860-474-229	Sequence 229, Appl	197	11.6	44.6	44	4	US-08-109-037-119	Sequence 119, Appl
c 125	11.8	45.4	47	4	US-09-422-978-162	Sequence 162, Appl	198	11.6	44.6	44	4	US-08-109-037-120	Sequence 120, Appl
c 126	11.8	45.4	49	1	US-08-384-708A-114	Sequence 114, Appl	199	11.6	44.6	46	1	US-08-171-389-17	Sequence 17, Appl
c 127	11.8	45.4	49	3	US-08-687-421-114	Sequence 114, Appl	200	11.6	44.6	46	2	US-08-123-936-17	Sequence 17, Appl
c 128	11.8	45.4	49	3	US-08-442-423-114	Sequence 114, Appl	201	11.6	44.6	46	2	US-08-475-228A-17	Sequence 17, Appl
c 129	11.8	45.4	50	1	US-08-701-26	Sequence 112, Appl	202	11.6	44.6	46	3	US-08-482-080A-17	Sequence 17, Appl
c 130	11.8	45.4	50	3	US-08-687-421-112	Sequence 112, Appl	203	11.6	44.6	46	3	US-09-354-947-17	Sequence 17, Appl
c 131	11.8	45.4	50	3	US-08-563-524A-13	Sequence 13, Appl	204	11.6	44.6	46	4	PCT-US93-12388-17	Sequence 17, Appl
c 132	11.8	45.4	50	3	US-08-563-524A-14	Sequence 14, Appl	205	11.6	44.6	47	4	US-09-422-978-2653	Sequence 2653, Appl
c 133	11.8	45.4	50	3	US-08-563-524A-15	Sequence 15, Appl	206	11.6	44.6	48	1	US-08-664-449-32	Sequence 32, Appl
c 134	11.8	45.4	50	3	US-08-563-524A-16	Sequence 16, Appl	207	11.6	44.6	48	1	US-09-198-452A-3342	Sequence 3342, Appl
c 135	11.8	45.4	50	3	US-08-563-524A-17	Sequence 17, Appl	208	11.4	43.8	21	1	US-07-908-679-1	Sequence 1, Appl
c 136	11.8	45.4	50	3	US-08-563-524A-18	Sequence 18, Appl	209	11.4	43.8	21	4	US-09-393-858-26	Sequence 26, Appl
c 137	11.8	45.4	50	3	US-08-563-524A-19	Sequence 19, Appl	210	11.4	43.8	21	5	US-10-190-279-26	Sequence 1, Appl
c 138	11.8	45.4	50	3	US-08-563-524A-20	Sequence 20, Appl	211	11.4	43.8	21	5	PCT-US92-09475-1	Sequence 1, Appl
c 139	11.8	45.4	50	3	US-08-563-524A-21	Sequence 21, Appl	212	11.4	43.8	23	4	US-09-216-393B-334	Sequence 334, Appl
c 140	11.8	45.4	50	3	US-08-563-524A-22	Sequence 22, Appl	213	11.4	43.8	27	1	US-09-216-393B-334	Sequence 334, Appl
c 141	11.6	44.6	20	4	US-09-198-452A-2900	Sequence 2900, Appl	214	11.4	43.8	28	2	US-08-758-306-422	Sequence 9, Appl
c 142	11.6	44.6	20	4	US-09-112-580-104	Sequence 104, Appl	215	11.4	43.8	28	2	US-09-075-395-9	Sequence 10, Appl
c 143	11.6	44.6	24	4	US-09-522-433B-2	Sequence 2, Appl	216	11.4	43.8	28	2	US-09-075-395-10	Sequence 24, Appl
c 144	11.6	44.6	29	3	US-09-485-737B-82	Sequence 82, Appl	217	11.4	43.8	29	4	US-09-645-593-24	Sequence 24, Appl
c 145	11.6	44.6	30	2	US-08-421-155-7	Sequence 7, Appl	218	11.4	43.8	30	3	US-09-540-014-22	Sequence 22, Appl
c 146	11.6	44.6	31	3	US-08-294-386C-12	Sequence 12, Appl	219	11.4	43.8	30	3	US-09-540-014-22	Sequence 4, Appl
c 147	11.6	44.6	31	3	US-08-679-645-496	Sequence 496, Appl	220	11.4	43.8	31	2	US-08-187-186A-4	Sequence 4, Appl
c 148	11.6	44.6	31	4	US-09-302-357-8	Sequence 8, Appl	221	11.4	43.8	31	2	US-08-442-497C-4	Sequence 4, Appl
c 149	11.6	44.6	31	4	PCT-US95-10224-12	Sequence 12, Appl	222	11.4	43.8	32	4	US-09-333-033-4	Sequence 4, Appl
c 150	11.6	44.6	31	5	US-08-181-271A-60	Sequence 60, Appl	223	11.4	43.8	32	4	US-10-004-832-4	Sequence 2, Appl
c 151	11.6	44.6	32	1	US-08-449-315-60	Sequence 60, Appl	224	11.4	43.8	32	4	US-08-744-685-2	Sequence 2, Appl
c 152	11.6	44.6	32	1	US-08-449-315-60	Sequence 60, Appl	225	11.4	43.8	33	3	US-09-029-267-33	Sequence 33, Appl
c 153	11.6	44.6	32	1	US-08-449-315-60	Sequence 60, Appl	226	11.4	43.8	33	3	US-09-029-267-35	Sequence 35, Appl
c 154	11.6	44.6	32	1	US-08-449-315-60	Sequence 60, Appl	227	11.4	43.8	33	3	US-08-169-715-50	Sequence 50, Appl
c 155	11.6	44.6	32	1	US-08-449-315-60	Sequence 60, Appl	228	11.4	43.8	33	5	PCT-US92-01358-3	Sequence 3, Appl
c 156	11.6	44.6	32	1	US-08-456-265A-60	Sequence 60, Appl	229	11.4	43.8	34	4	US-09-862-847-4	Sequence 4, Appl
c 157	11.6	44.6	32	1	US-08-455-416-60	Sequence 60, Appl	230	11.4	43.8	35	3	US-09-178-089-10	Sequence 10, Appl
c 158	11.6	44.6	32	1	US-08-455-416-60	Sequence 60, Appl	231	11.4	43.8	35	3	US-09-194-613-7	Sequence 7, Appl
c 159	11.6	44.6	32	1	US-08-454-876-60	Sequence 60, Appl	232	11.4	43.8	35	3	US-09-253-586-11	Sequence 11, Appl
c 160	11.6	44.6	32	2	US-08-456-262-60	Sequence 60, Appl	233	11.4	43.8	35	4	US-09-142-027A-1	Sequence 1, Appl
c 161	11.6	44.6	32	2	US-08-456-262-60	Sequence 60, Appl	234	11.4	43.8	37	4	US-09-463-402-4	Sequence 4, Appl
c 162	11.6	44.6	32	2	US-08-455-736-60	Sequence 60, Appl	235	11.4	43.8	37	4	US-09-117-447-4	Sequence 4, Appl
c 163	11.6	44.6	32	2	US-08-455-736-60	Sequence 60, Appl	236	11.4	43.8	38	4	US-09-529-239D-41	Sequence 28, Appl
c 164	11.6	44.6	32	2	US-08-971-217-60	Sequence 60, Appl	237	11.4	43.8	38	5	PCT-US96-03916-28	Sequence 14, Appl
c 165	11.6	44.6	32	4	US-09-350-600-60	Sequence 60, Appl	238	11.4	43.8	39	4	US-08-318-794-14	Sequence 14, Appl
c 166	11.6	44.6	33	3	US-09-906-234-60	Sequence 1, Appl	239	11.4	43.8	44	3	US-08-470-106-14	Sequence 1086, Appl
c 167	11.6	44.6	33	3	US-09-129-740-1	Sequence 1, Appl	240	11.4	43.8	47	4	US-09-641-638-1086	Sequence 1086, Appl
c 168	11.6	44.6	33	3	US-09-568-527-1	Sequence 1, Appl	241	11.4	43.8	47	4	US-09-422-978-1052	Sequence 1052, Appl
c 169	11.6	44.6	35	1	US-08-294-386C-13	Sequence 13, Appl	242	11.4	43.8	47	4	US-10-170-097-1086	Sequence 25, Appl
c 170	11.6	44.6	35	2	US-07-814-220-37	Sequence 37, Appl	243	11.4	43.8	49	3	US-09-244-794A-25	Sequence 25, Appl
c 171	11.6	44.6	35	2	US-07-812-421-37	Sequence 37, Appl	244	11.4	43.8	49	3	US-09-007-005-25	Sequence 25, Appl
c 172	11.6	44.6	35	2	US-09-353-242A-13	Sequence 13, Appl	245	11.4	43.8	49	3	US-09-244-796-25	Sequence 25, Appl
c 173	11.6	44.6	35	5	PCT-US95-10224-13	Sequence 13, Appl	246	11.4	43.8	49	4	US-09-238-710-25	Sequence 25, Appl

c 247	11.4	43.8	50	3	US-09-315-886C-14	Sequence 14, Appl	c 320	11.2	43.1	40	2	US-08-425-684-6	Sequence 6, Appl
c 248	11.2	43.1	18	3	US-09-071-433-32	Sequence 32, Appl	321	11.2	43.1	40	2	US-08-425-684-55	Sequence 55, Appl
c 249	11.2	43.1	19	4	US-09-696-791-238	Sequence 238, Appl	c 322	11.2	43.1	40	2	US-08-675-502-6	Sequence 6, Appl
250	11.2	43.1	20	1	US-08-146-422-10	Sequence 10, Appl	323	11.2	43.1	40	2	US-08-675-502-55	Sequence 55, Appl
251	11.2	43.1	20	1	US-08-146-424-10	Sequence 10, Appl	c 324	11.2	43.1	40	4	US-09-245-802-6	Sequence 6, Appl
252	11.2	43.1	20	1	US-08-626-554-26	Sequence 26, Appl	c 325	11.2	43.1	40	4	US-09-245-802-55	Sequence 55, Appl
253	11.2	43.1	20	1	US-08-693-709-24	Sequence 24, Appl	c 326	11.2	43.1	42	3	US-09-248-574A-2	Sequence 2, Appl
c 254	11.2	43.1	20	3	US-09-359-757-33	Sequence 33, Appl	c 327	11.2	43.1	42	4	US-09-929-962-2	Sequence 2, Appl
255	11.2	43.1	20	4	US-09-198-452A-2584	Sequence 2584, Ap	c 328	11.2	43.1	42	4	US-09-503-632-2	Sequence 2, Appl
c 256	11.2	43.1	20	4	US-09-198-452A-6523	Sequence 6523, Ap	c 329	11.2	43.1	42	4	US-08-316-293-43	Sequence 43, Appl
257	11.2	43.1	24	2	US-08-948-717A-2	Sequence 2, Appl	c 330	11.2	43.1	47	2	US-08-422-333-5	Sequence 5, Appl
c 258	11.2	43.1	26	3	US-09-202-712-26	Sequence 26, Appl	c 331	11.2	43.1	47	2	US-08-422-333-6	Sequence 6, Appl
259	11.2	43.1	28	1	US-07-988-194A-17	Sequence 17, Appl	c 332	11.2	43.1	47	4	US-09-478-189-179	Sequence 179, App
260	11.2	43.1	28	1	US-08-258-152-19	Sequence 19, Appl	c 333	11.2	43.1	47	4	US-09-422-978-65	Sequence 65, Appl
261	11.2	43.1	28	2	US-08-076-299A-19	Sequence 19, Appl	c 334	11.2	43.1	47	4	US-09-422-978-1443	Sequence 1443, Ap
262	11.2	43.1	28	2	US-08-438-582-19	Sequence 19, Appl	c 335	11.2	43.1	49	2	US-08-392-771-3	Sequence 3, Appl
263	11.2	43.1	28	2	US-09-035-593-8	Sequence 8, Appl	c 336	11.2	43.1	50	2	US-08-583-276-3	Sequence 3, Appl
c 264	11.2	43.1	28	2	US-08-859-998-1149	Sequence 1149, Ap	c 337	11.2	43.1	50	3	US-08-985-162-1696	Sequence 1696, Ap
265	11.2	43.1	28	3	US-08-266-596-19	Sequence 19, Appl	c 338	11.2	43.1	50	4	US-08-956-1718-2020	Sequence 2020, Ap
c 266	11.2	43.1	28	3	US-08-479-737-17	Sequence 17, Appl	c 339	11.2	43.1	50	4	US-09-401-063-1696	Sequence 1696, Ap
c 267	11.2	43.1	28	3	US-09-225-928-1149	Sequence 1149, Ap	c 340	11.2	43.1	50	4	US-08-781-986A-2020	Sequence 2020, Ap
268	11.2	43.1	28	4	US-08-475-442A-17	Sequence 17, Appl	c 341	11.2	42.3	20	4	US-09-331-359-6	Sequence 6, Appl
c 269	11.2	43.1	28	4	US-09-225-201B-1149	Sequence 1149, Ap	c 342	11.2	42.3	20	4	US-09-198-452A-4777	Sequence 4777, Ap
270	11.2	43.1	28	4	US-09-944-411-19	Sequence 19, Appl	c 343	11.2	42.3	21	1	US-07-747-785-2	Sequence 2, Appl
c 271	11.2	43.1	28	4	US-08-608-958-26	Sequence 26, Appl	c 344	11.2	42.3	21	3	US-09-195-817-3	Sequence 3, Appl
c 272	11.2	43.1	28	4	US-09-608-958-32	Sequence 32, Appl	c 345	11.2	42.3	21	4	US-09-379-615-3	Sequence 3, Appl
c 273	11.2	43.1	28	4	US-09-608-958-33	Sequence 33, Appl	c 346	11.2	42.3	24	1	US-08-361-920-80	Sequence 80, Appl
274	11.2	43.1	29	2	US-07-814-220-38	Sequence 38, Appl	c 347	11.2	42.3	24	1	US-08-479-939-80	Sequence 80, Appl
275	11.2	43.1	29	2	US-07-812-421-38	Sequence 38, Appl	c 348	11.2	42.3	24	1	US-08-483-432-80	Sequence 80, Appl
276	11.2	43.1	29	3	US-09-189-462-43	Sequence 43, Appl	c 349	11.2	42.3	24	4	US-09-687-538B-17	Sequence 17, Appl
277	11.2	43.1	29	4	US-08-863-040-43	Sequence 43, Appl	c 350	11.2	42.3	24	4	US-10-309-437-17	Sequence 17, Appl
278	11.2	43.1	31	3	US-09-023-221A-13	Sequence 13, Appl	c 351	11.2	42.3	25	3	US-08-544-381B-99	Sequence 99, Appl
279	11.2	43.1	31	3	US-09-282-352A-13	Sequence 13, Appl	c 352	11.2	42.3	25	3	US-09-014-065-11	Sequence 11, Appl
c 280	11.2	43.1	31	3	US-08-679-645-284	Sequence 284, App	c 353	11.2	42.3	25	4	US-09-495-406-27	Sequence 27, Appl
281	11.2	43.1	32	3	US-08-931-952-7	Sequence 7, Appl	c 354	11.2	42.3	25	4	US-09-816-028A-41	Sequence 41, Appl
282	11.2	43.1	32	3	US-08-272-247-7	Sequence 7, Appl	c 355	11.2	42.3	25	4	US-10-303-162-41	Sequence 41, Appl
c 283	11.2	43.1	32	5	PCT-US95-08560-7	Sequence 7, Appl	c 356	11.2	42.3	26	3	US-09-005-298-40	Sequence 40, Appl
c 284	11.2	43.1	34	3	US-08-711-218-10	Sequence 10, Appl	c 357	11.2	42.3	26	4	US-08-768-619-40	Sequence 40, Appl
c 285	11.2	43.1	34	3	US-09-485-737B-95	Sequence 95, Appl	c 358	11.2	42.3	27	2	US-08-892-880-8	Sequence 8, Appl
286	11.2	43.1	34	4	US-09-479-479-18	Sequence 18, Appl	c 359	11.2	42.3	27	3	US-09-314-847A-13	Sequence 13, Appl
287	11.2	43.1	34	4	US-09-297-851-18	Sequence 18, Appl	c 360	11.2	42.3	27	4	US-10-037-677A-15	Sequence 15, Appl
c 288	11.2	43.1	35	3	US-09-133-321-12	Sequence 12, Appl	c 361	11.2	42.3	28	1	US-08-601-435-5	Sequence 5, Appl
289	11.2	43.1	36	4	US-09-545-814-38	Sequence 38, Appl	c 362	11.2	42.3	28	2	US-08-930-274-13	Sequence 13, Appl
c 290	11.2	43.1	37	3	US-09-035-665-1	Sequence 1, Appl	c 363	11.2	42.3	28	2	US-08-930-274-14	Sequence 14, Appl
291	11.2	43.1	38	1	US-08-485-971-15	Sequence 15, Appl	c 364	11.2	42.3	28	2	US-08-931-047-5	Sequence 5, Appl
c 292	11.2	43.1	38	1	US-08-485-971-15	Sequence 15, Appl	c 365	11.2	42.3	28	2	US-08-783-202-5	Sequence 5, Appl
c 293	11.2	43.1	38	1	US-08-275-876-14	Sequence 14, Appl	c 366	11.2	42.3	28	3	US-09-165-827C-4	Sequence 4, Appl
c 294	11.2	43.1	38	1	US-08-275-876-15	Sequence 15, Appl	c 367	11.2	42.3	28	3	US-09-165-827C-8	Sequence 8, Appl
c 295	11.2	43.1	38	1	US-08-383-754-15	Sequence 15, Appl	c 368	11.2	42.3	29	2	US-08-892-880-10	Sequence 10, Appl
c 296	11.2	43.1	38	1	US-08-485-978-14	Sequence 14, Appl	c 369	11.2	42.3	29	4	US-07-971-834-9	Sequence 9, Appl
297	11.2	43.1	38	1	US-08-485-978-14	Sequence 14, Appl	c 370	11.2	42.3	29	5	PCT-US93-05240-1	Sequence 1, Appl
c 298	11.2	43.1	38	1	US-08-485-978-15	Sequence 15, Appl	c 371	11.2	42.3	30	4	US-08-896-537A-10	Sequence 10, Appl
c 299	11.2	43.1	38	2	US-08-486-814-14	Sequence 14, Appl	c 372	11.2	42.3	30	4	US-09-912-935-45	Sequence 45, Appl
c 300	11.2	43.1	38	2	US-08-486-814-15	Sequence 15, Appl	c 373	11.2	42.3	31	1	US-08-466-033-150	Sequence 150, App
c 301	11.2	43.1	38	2	US-08-432-871C-10	Sequence 10, Appl	c 374	11.2	42.3	31	1	US-08-444-733-150	Sequence 150, App
302	11.2	43.1	38	2	US-08-487-472-14	Sequence 14, Appl	c 375	11.2	42.3	31	2	US-08-464-134-150	Sequence 150, App
c 303	11.2	43.1	38	2	US-08-487-472-15	Sequence 15, Appl	c 376	11.2	42.3	31	2	US-08-461-361-150	Sequence 150, App
304	11.2	43.1	38	3	US-08-485-740-14	Sequence 14, Appl	c 377	11.2	42.3	31	2	US-08-485-910-150	Sequence 150, App
c 305	11.2	43.1	38	3	US-08-485-740-15	Sequence 15, Appl	c 378	11.2	42.3	31	2	US-09-018-576-8	Sequence 8, Appl
c 306	11.2	43.1	38	3	US-09-162-184-15	Sequence 15, Appl	c 379	11.2	42.3	31	2	US-09-018-576-9	Sequence 9, Appl
c 307	11.2	43.1	38	3	US-09-162-184-15	Sequence 15, Appl	c 380	11.2	42.3	31	3	US-09-248-137-8	Sequence 8, Appl
c 308	11.2	43.1	38	3	US-09-161-902-14	Sequence 14, Appl	c 381	11.2	42.3	31	3	US-09-248-137-9	Sequence 9, Appl
c 309	11.2	43.1	38	3	US-09-161-902-15	Sequence 15, Appl	c 382	11.2	42.3	33	1	US-08-173-510B-52	Sequence 52, Appl
310	11.2	43.1	38	3	US-09-489-777A-14	Sequence 14, Appl	c 383	11.2	42.3	33	2	US-08-458-218-52	Sequence 52, Appl
c 311	11.2	43.1	38	3	US-09-489-777A-15	Sequence 15, Appl	c 384	11.2	42.3	33	2	US-08-450-497-52	Sequence 52, Appl
c 312	11.2	43.1	38	4	US-09-270-956-10	Sequence 10, Appl	c 385	11.2	42.3	34	1	US-07-931-473B-324	Sequence 324, App
313	11.2	43.1	38	5	PCT-US95-08179-14	Sequence 14, Appl	c 386	11.2	42.3	34	1	US-07-714-131C-324	Sequence 324, App
c 314	11.2	43.1	38	5	PCT-US95-08179-15	Sequence 15, Appl	c 387	11.2	42.3	34	1	US-08-412-110-324	Sequence 324, App
315	11.2	43.1	39	3	US-08-445-463B-84	Sequence 84, Appl	c 388	11.2	42.3	34	1	US-08-409-442A-324	Sequence 324, App
316	11.2	43.1	39	3	US-08-445-464C-84	Sequence 84, Appl	c 389	11.2	42.3	34	2	US-08-469-609A-324	Sequence 324, App
317	11.2	43.1	39	4	US-09-402-631A-31	Sequence 31, Appl	c 390	11.2	42.3	34	2	US-08-821-782-16	Sequence 16, Appl
318	11.2	43.1	39	4	US-08-044-857D-84	Sequence 84, Appl	c 391	11.2	42.3	34	3	US-09-143-190-324	Sequence 324, App
319	11.2	43.1	39	5	PCT-US94-03437-84	Sequence 84, Appl	c 392	11.2	42.3	34	3	US-09-292-435A-16	Sequence 16, Appl

c 393	11	42.3	34	3	US-09-502-344-324	Sequence 324, App	466	10.8	41.5	24	3	US-08-949-155-17	Sequence 17, Appl
394	11	42.3	35	4	US-09-614-034-11	Sequence 11, Appl	467	10.8	41.5	24	3	US-08-949-155-19	Sequence 19, Appl
395	11	42.3	35	4	US-09-614-034-12	Sequence 12, Appl	c 468	10.8	41.5	24	3	US-09-230-804-24	Sequence 24, Appl
396	11	42.3	35	4	US-09-614-034-13	Sequence 13, Appl	c 469	10.8	41.5	24	3	US-08-981-653-4	Sequence 4, Appl
397	11	42.3	35	4	US-09-614-034-17	Sequence 17, Appl	470	10.8	41.5	24	3	US-09-819-964-17	Sequence 17, Appl
398	11	42.3	35	4	US-09-614-034-21	Sequence 21, Appl	471	10.8	41.5	24	3	US-09-819-964-19	Sequence 19, Appl
c 399	11	42.3	36	1	US-08-445-640-33	Sequence 33, Appl	472	10.8	41.5	24	3	US-09-033-556-18	Sequence 18, Appl
c 400	11	42.3	36	2	US-08-438-864-5	Sequence 5, Appl	c 473	10.8	41.5	25	1	US-08-153-746-9	Sequence 9, Appl
c 401	11	42.3	36	2	US-08-478-379C-74	Sequence 74, Appl	c 474	10.8	41.5	25	1	US-08-341-148-11	Sequence 11, Appl
c 402	11	42.3	36	2	US-08-170-558-33	Sequence 33, Appl	c 475	10.8	41.5	25	1	US-08-341-148-21	Sequence 21, Appl
c 403	11	42.3	36	3	US-08-146-249A-74	Sequence 74, Appl	c 476	10.8	41.5	25	4	US-09-648-254-27	Sequence 27, Appl
c 404	11	42.3	36	3	US-08-447-314-33	Sequence 33, Appl	c 477	10.8	41.5	25	5	PCT-US94-00771-9	Sequence 9, Appl
c 405	11	42.3	36	3	US-08-445-461-33	Sequence 33, Appl	c 478	10.8	41.5	25	5	PCT-US94-14096-11	Sequence 11, Appl
c 406	11	42.3	36	3	US-08-206-188B-74	Sequence 74, Appl	c 479	10.8	41.5	25	5	PCT-US94-14096-21	Sequence 21, Appl
c 407	11	42.3	36	3	US-08-628-747-5	Sequence 5, Appl	c 480	10.8	41.5	27	3	US-09-008-165-10	Sequence 10, Appl
c 408	11	42.3	36	3	US-08-402-253-5	Sequence 5, Appl	c 481	10.8	41.5	27	3	US-09-253-396A-42	Sequence 42, Appl
c 409	11	42.3	36	3	US-08-443-868B-5	Sequence 5, Appl	c 482	10.8	41.5	27	4	US-09-303-681-50	Sequence 50, Appl
c 410	11	42.3	36	4	US-09-864-866-39	Sequence 39, Appl	c 483	10.8	41.5	28	4	US-10-080-505-57	Sequence 57, Appl
c 411	11	42.3	36	4	US-09-864-866-39	Sequence 36, Appl	c 484	10.8	41.5	30	1	US-08-411-795B-157	Sequence 157, App
c 412	11	42.3	37	3	US-09-320-878-27	Sequence 27, Appl	c 485	10.8	41.5	30	1	US-08-341-148-22	Sequence 22, Appl
c 413	11	42.3	37	3	US-09-141-908-24	Sequence 24, Appl	c 486	10.8	41.5	30	1	US-08-341-148-23	Sequence 23, Appl
c 414	11	42.3	37	4	US-09-657-440-27	Sequence 27, Appl	c 487	10.8	41.5	30	1	US-08-469-319A-157	Sequence 157, App
c 415	11	42.3	37	6	5198342-8	Patent No. 5198342	c 488	10.8	41.5	30	4	US-08-764-114-157	Sequence 157, App
c 416	11	42.3	38	3	US-09-182-859-28	Sequence 28, Appl	c 489	10.8	41.5	30	4	US-08-469-419-157	Sequence 157, App
c 417	11	42.3	38	4	US-09-537-168-27	Sequence 27, Appl	c 490	10.8	41.5	30	4	US-09-593-359-10	Sequence 10, Appl
c 418	11	42.3	38	4	US-09-672-459-28	Sequence 28, Appl	c 491	10.8	41.5	30	4	US-09-937-832-11	Sequence 11, Appl
c 419	11	42.3	38	4	US-10-186-042-28	Sequence 28, Appl	c 492	10.8	41.5	30	5	PCT-US94-14096-22	Sequence 22, Appl
c 420	11	42.3	41	1	US-07-931-473B-274	Sequence 274, App	c 493	10.8	41.5	32	5	PCT-US94-14096-23	Sequence 23, Appl
c 421	11	42.3	41	1	US-07-714-131C-274	Sequence 274, App	c 494	10.8	41.5	32	2	US-09-022-461-3	Sequence 3, Appl
c 422	11	42.3	41	1	US-08-412-110-274	Sequence 274, App	c 495	10.8	41.5	32	3	US-09-138-024-12	Sequence 12, Appl
c 423	11	42.3	41	1	US-08-409-442A-274	Sequence 274, App	c 496	10.8	41.5	32	3	US-09-404-066-12	Sequence 12, Appl
c 424	11	42.3	41	2	US-08-469-609A-274	Sequence 274, App	c 497	10.8	41.5	32	4	US-09-573-322-12	Sequence 12, Appl
c 425	11	42.3	41	2	US-08-143-190-274	Sequence 274, App	c 498	10.8	41.5	32	4	US-09-151-376-70	Sequence 70, Appl
c 426	11	42.3	41	3	US-09-502-344-274	Sequence 274, App	c 499	10.8	41.5	33	1	US-08-173-510B-52	Sequence 52, Appl
c 427	11	42.3	43	1	US-08-720-899-24	Sequence 24, App	c 500	10.8	41.5	33	1	US-08-458-218-52	Sequence 52, Appl
c 428	11	42.3	43	1	US-08-459-610-24	Sequence 24, App	c 501	10.8	41.5	33	1	US-08-690-102A-21	Sequence 21, Appl
c 429	11	42.3	43	2	US-08-343-804-24	Sequence 24, App	c 502	10.8	41.5	33	1	US-08-463-224-20	Sequence 20, Appl
c 430	11	42.3	43	2	US-09-153-310-23	Sequence 23, App	c 503	10.8	41.5	33	2	US-08-463-377-20	Sequence 20, Appl
c 431	11	42.3	45	4	US-09-636-368-13	Sequence 13, App	c 504	10.8	41.5	33	2	US-08-450-497-52	Sequence 52, Appl
c 432	11	42.3	47	1	US-07-931-473B-307	Sequence 307, App	c 505	10.8	41.5	33	2	US-08-874-678-22	Sequence 22, Appl
c 433	11	42.3	47	1	US-07-714-131C-307	Sequence 307, App	c 506	10.8	41.5	33	3	US-08-643-839-22	Sequence 22, Appl
c 434	11	42.3	47	1	US-08-412-110-307	Sequence 307, App	c 507	10.8	41.5	33	3	US-09-127-902-21	Sequence 21, Appl
c 435	11	42.3	47	1	US-08-409-442A-307	Sequence 307, App	c 508	10.8	41.5	33	3	US-09-227-717-9	Sequence 9, Appl
c 436	11	42.3	47	2	US-08-459-609A-307	Sequence 307, App	c 509	10.8	41.5	33	3	US-09-155-107-33	Sequence 33, Appl
c 437	11	42.3	47	2	US-08-910-632-80	Sequence 80, App	c 510	10.8	41.5	33	3	US-09-348-886-22	Sequence 22, Appl
c 438	11	42.3	47	3	US-09-143-190-307	Sequence 307, App	c 511	10.8	41.5	33	4	US-09-589-287B-40	Sequence 40, Appl
c 439	11	42.3	47	3	US-09-502-344-307	Sequence 307, App	c 512	10.8	41.5	33	4	US-09-588-947A-40	Sequence 40, Appl
c 440	11	42.3	47	4	US-09-422-978-3324	Sequence 3324, App	c 513	10.8	41.5	33	4	US-09-589-286A-40	Sequence 40, Appl
c 441	11	42.3	48	4	US-08-786-531B-10	Sequence 10, App	c 514	10.8	41.5	34	5	PCT-US95-09641-21	Sequence 21, Appl
c 442	11	42.3	48	4	US-09-454-204A-25	Sequence 25, App	c 515	10.8	41.5	34	5	US-08-792-832A-13	Sequence 13, Appl
c 443	11	42.3	49	4	US-09-331-793-56	Sequence 56, App	c 516	10.8	41.5	36	1	US-08-411-796-245	Sequence 245, App
c 444	11	42.3	49	4	US-07-727-814B-6	Sequence 6, App	c 517	10.8	41.5	36	1	US-08-411-796-251	Sequence 251, App
c 445	11	42.3	50	1	US-08-258-614-6	Sequence 6, App	c 518	10.8	41.5	36	2	US-08-921-382-7	Sequence 7, Appl
c 446	11	42.3	50	1	US-08-687-580B-11	Sequence 11, App	c 519	10.8	41.5	36	2	US-08-921-382-11	Sequence 11, Appl
c 447	10.8	41.5	14	3	US-09-608-958-14	Sequence 14, App	c 520	10.8	41.5	36	3	US-08-471-039-245	Sequence 245, App
c 448	10.8	41.5	18	4	US-09-608-958-14	Sequence 14, App	c 521	10.8	41.5	36	3	US-08-471-039-251	Sequence 251, App
c 449	10.8	41.5	18	4	US-09-608-958-14	Sequence 14, App	c 522	10.8	41.5	36	3	US-09-098-628-69	Sequence 69, Appl
c 450	10.8	41.5	20	2	US-08-256-426B-287	Sequence 287, App	c 523	10.8	41.5	36	4	US-08-559-390-245	Sequence 245, App
c 451	10.8	41.5	20	3	US-09-418-641-64	Sequence 64, App	c 524	10.8	41.5	36	4	US-08-559-390-251	Sequence 251, App
c 452	10.8	41.5	20	4	US-09-118-452A-6622	Sequence 6622, App	c 525	10.8	41.5	36	4	US-09-386-380-7	Sequence 7, Appl
c 453	10.8	41.5	20	4	US-09-118-452A-6622	Sequence 99, App	c 526	10.8	41.5	36	4	US-09-386-380-11	Sequence 11, Appl
c 454	10.8	41.5	20	4	US-09-418-980-15	Sequence 15, App	c 527	10.8	41.5	36	5	PCT-US93-11198-245	Sequence 245, App
c 455	10.8	41.5	20	4	US-08-701-582D-22	Sequence 22, App	c 528	10.8	41.5	36	5	PCT-US93-11198-251	Sequence 251, App
c 456	10.8	41.5	21	3	US-08-891-463-18	Sequence 18, App	c 529	10.8	41.5	37	2	US-08-700-670A-31	Sequence 31, Appl
c 457	10.8	41.5	22	1	US-08-696-944-14	Sequence 14, App	c 530	10.8	41.5	37	4	US-09-313-221A-54	Sequence 54, Appl
c 458	10.8	41.5	22	2	US-09-433-579-23	Sequence 23, App	c 531	10.8	41.5	38	5	PCT-US92-01015-23	Sequence 23, Appl
c 459	10.8	41.5	22	4	US-09-574-779B-78	Sequence 78, App	c 532	10.8	41.5	38	5	US-09-402-631A-30	Sequence 30, Appl
c 460	10.8	41.5	22	4	US-09-574-779B-78	Sequence 79, App	c 533	10.8	41.5	39	6	RE34606-26	Patent No. RE34,60
c 461	10.8	41.5	24	1	US-08-657-175-3	Sequence 3, App	c 534	10.8	41.5	40	3	US-09-590-061-16	Sequence 16, Appl
c 462	10.8	41.5	24	1	US-08-589-028-43	Sequence 43, App	c 535	10.8	41.5	40	3	US-09-329-920-9	Sequence 9, Appl
c 463	10.8	41.5	24	3	US-08-784-582-43	Sequence 43, App	c 536	10.8	41.5	40	4	US-09-894-788-16	Sequence 16, Appl
c 464	10.8	41.5	24	3	US-08-785-271-43	Sequence 43, App	c 537	10.8	41.5	40	4	US-09-894-208-16	Sequence 16, Appl
c 465	10.8	41.5	24	3	US-08-943-731-334	Sequence 334, App	c 538	10.8	41.5	42	2	US-08-428-197-50	Sequence 50, Appl

C 539	10.8	41.5	42	3	US-08-879-565-9	Sequence 9, Appli	Sequence 9, Appli	10.6	40.8	30	3	US-08-951-923-28	Sequence 28, Appl
C 540	10.8	41.5	42	4	US-09-138-277C-5	Sequence 50, Appli	Sequence 50, Appli	10.6	40.8	30	3	US-08-848-793-13	Sequence 13, Appl
C 541	10.8	41.5	42	5	PCT-US93-10555-50	Sequence 248, App	Sequence 248, App	10.6	40.8	30	4	US-08-322-678-13	Sequence 13, Appl
C 542	10.8	41.5	44	1	US-07-931-473B-248	Sequence 248, App	Sequence 248, App	10.6	40.8	30	4	US-09-769-863-23	Sequence 23, Appl
C 543	10.8	41.5	44	1	US-07-714-131C-248	Sequence 248, App	Sequence 248, App	10.6	40.8	30	4	US-09-741-744A-100	Sequence 100, App
C 544	10.8	41.5	44	1	US-08-412-110-248	Sequence 248, App	Sequence 248, App	10.6	40.8	31	1	US-08-466-033-113	Sequence 113, App
C 545	10.8	41.5	44	1	US-08-409-442A-248	Sequence 248, App	Sequence 248, App	10.6	40.8	31	1	US-08-444-733-113	Sequence 113, App
C 546	10.8	41.5	44	2	US-08-469-609A-248	Sequence 248, App	Sequence 248, App	10.6	40.8	31	2	US-08-464-134-113	Sequence 113, App
C 547	10.8	41.5	44	3	US-09-143-190-248	Sequence 248, App	Sequence 248, App	10.6	40.8	31	2	US-08-461-361-113	Sequence 113, App
C 548	10.8	41.5	44	3	US-09-502-344-248	Sequence 248, App	Sequence 248, App	10.6	40.8	31	2	US-08-485-910-113	Sequence 113, App
C 549	10.8	41.5	47	4	US-09-641-638-1207	Sequence 1207, Ap	Sequence 1207, Ap	10.6	40.8	31	2	US-08-859-998-182	Sequence 182, App
C 550	10.8	41.5	47	4	US-10-170-097-1207	Sequence 1207, Ap	Sequence 1207, Ap	10.6	40.8	31	2	US-09-225-928-182	Sequence 182, App
C 551	10.8	41.5	48	1	US-08-014-153D-14	Sequence 14, Appli	Sequence 14, Appli	10.6	40.8	31	4	US-09-225-928-182	Sequence 182, App
C 552	10.8	41.5	48	3	US-08-532-657A-46	Sequence 46, Appli	Sequence 46, Appli	10.6	40.8	31	5	PCT-US95-06266-94	Sequence 94, Appl
C 553	10.8	41.5	48	3	US-09-248-998-46	Sequence 46, Appli	Sequence 46, Appli	10.6	40.8	32	1	US-08-222-616-40	Sequence 40, Appl
C 554	10.8	41.5	48	4	US-09-248-998-46	Sequence 46, Appli	Sequence 46, Appli	10.6	40.8	32	1	US-08-442-542-41	Sequence 41, Appl
C 555	10.8	41.5	48	4	US-09-610-651-46	Sequence 29, Appli	Sequence 29, Appli	10.6	40.8	32	3	US-08-765-469-41	Sequence 41, Appl
C 556	10.8	41.5	49	4	US-09-395-937-29	Sequence 168, App	Sequence 168, App	10.6	40.8	32	3	US-09-312-285-9	Sequence 9, Appli
C 557	10.8	41.5	50	4	US-09-907-794A-168	Sequence 168, App	Sequence 168, App	10.6	40.8	32	3	US-09-312-286-9	Sequence 9, Appli
C 558	10.8	41.5	50	4	US-09-905-125A-168	Sequence 168, App	Sequence 168, App	10.6	40.8	32	3	US-09-312-038-9	Sequence 9, Appli
C 559	10.8	41.5	50	4	US-09-902-775A-168	Sequence 168, App	Sequence 168, App	10.6	40.8	32	3	US-08-446-648-40	Sequence 40, Appl
C 560	10.8	41.5	50	4	US-09-906-700-168	Sequence 168, App	Sequence 168, App	10.6	40.8	32	3	US-09-728-764-9	Sequence 9, Appli
C 561	10.8	41.5	50	4	US-09-903-603A-168	Sequence 168, App	Sequence 168, App	10.6	40.8	32	4	US-09-312-304B-7	Sequence 7, Appli
C 562	10.6	40.8	17	1	US-07-717-332D-4	Sequence 4, Appli	Sequence 4, Appli	10.6	40.8	32	4	US-09-728-792-9	Sequence 9, Appli
C 563	10.6	40.8	17	3	US-08-673-645-263	Sequence 263, App	Sequence 263, App	10.6	40.8	32	4	US-09-850-964-9	Sequence 9, Appli
C 564	10.6	40.8	18	1	US-08-390-850-1128	Sequence 1128, Ap	Sequence 1128, Ap	10.6	40.8	32	4	US-09-982-610-40	Sequence 40, Appl
C 565	10.6	40.8	18	1	US-08-435-634-1128	Sequence 1128, Ap	Sequence 1128, Ap	10.6	40.8	32	4	US-09-532-806-10	Sequence 10, Appl
C 566	10.6	40.8	18	4	US-09-696-791-4286	Sequence 4286, Ap	Sequence 4286, Ap	10.6	40.8	32	4	PCT-US95-04228-40	Sequence 40, Appl
C 567	10.6	40.8	20	4	US-09-844-634-49	Sequence 49, Appli	Sequence 49, Appli	10.6	40.8	33	1	US-08-049-473-8	Sequence 8, Appli
C 568	10.6	40.8	20	4	US-09-198-452A-2885	Sequence 2885, Ap	Sequence 2885, Ap	10.6	40.8	33	1	US-08-312-648-8	Sequence 8, Appli
C 569	10.6	40.8	20	4	US-09-198-452A-5430	Sequence 5430, Ap	Sequence 5430, Ap	10.6	40.8	33	1	US-08-793-408-10	Sequence 10, Appl
C 570	10.6	40.8	20	4	US-09-198-452A-5996	Sequence 5996, Ap	Sequence 5996, Ap	10.6	40.8	33	3	US-09-139-762A-10	Sequence 10, Appl
C 571	10.6	40.8	20	4	US-09-112-580-210	Sequence 210, App	Sequence 210, App	10.6	40.8	33	3	US-08-891-516-36	Sequence 36, Appl
C 572	10.6	40.8	20	4	US-08-983-605-235	Sequence 235, App	Sequence 235, App	10.6	40.8	33	3	US-08-837-034-36	Sequence 36, Appl
C 573	10.6	40.8	20	5	PCT-US95-04138-2	Sequence 2, Appli	Sequence 2, Appli	10.6	40.8	33	3	US-09-382-616A-27	Sequence 27, Appl
C 574	10.6	40.8	21	3	US-09-376-781-20	Sequence 20, Appli	Sequence 20, Appli	10.6	40.8	33	3	US-09-382-616A-29	Sequence 29, Appl
C 575	10.6	40.8	21	4	US-09-105-058C-16	Sequence 16, Appli	Sequence 16, Appli	10.6	40.8	33	4	US-09-813-781-41	Sequence 41, Appl
C 576	10.6	40.8	22	4	US-08-983-605-115	Sequence 115, App	Sequence 115, App	10.6	40.8	33	4	US-09-728-466-29	Sequence 29, Appl
C 577	10.6	40.8	23	1	US-07-616-022C-11	Sequence 11, Appl	Sequence 11, Appl	10.6	40.8	33	4	US-09-728-466-29	Sequence 29, Appl
C 578	10.6	40.8	24	1	US-08-399-675-16	Sequence 16, Appli	Sequence 16, Appli	10.6	40.8	33	5	PCT-US94-04190-8	Sequence 8, Appli
C 579	10.6	40.8	24	1	US-08-233-030-18	Sequence 18, Appli	Sequence 18, Appli	10.6	40.8	33	5	5316943-4	Patent No. 5316943
C 580	10.6	40.8	24	2	US-08-809-297-36	Sequence 36, Appli	Sequence 36, Appli	10.6	40.8	34	1	US-08-468-036-42	Sequence 42, Appl
C 581	10.6	40.8	24	3	US-09-345-217-24	Sequence 24, Appli	Sequence 24, Appli	10.6	40.8	34	2	US-08-376-843-42	Sequence 42, Appl
C 582	10.6	40.8	24	4	US-09-845-129-24	Sequence 24, Appli	Sequence 24, Appli	10.6	40.8	34	4	US-09-595-344-16	Sequence 16, Appl
C 583	10.6	40.8	24	4	US-09-632-657-21	Sequence 21, Appli	Sequence 21, Appli	10.6	40.8	34	4	US-09-700-293-6	Sequence 6, Appli
C 584	10.6	40.8	25	4	US-09-538-709-299	Sequence 299, App	Sequence 299, App	10.6	40.8	35	1	US-08-401-908-22	Sequence 22, Appl
C 585	10.6	40.8	25	4	US-10-132-920B-24	Sequence 24, Appli	Sequence 24, Appli	10.6	40.8	35	2	US-08-474-379C-70	Sequence 70, Appl
C 586	10.6	40.8	26	1	US-08-627-845-9	Sequence 9, Appli	Sequence 9, Appli	10.6	40.8	36	3	US-09-146-249A-70	Sequence 70, Appl
C 587	10.6	40.8	26	1	US-08-627-845-9	Sequence 9, Appli	Sequence 9, Appli	10.6	40.8	36	3	US-08-206-188B-70	Sequence 70, Appl
C 588	10.6	40.8	26	4	US-09-050-739-117	Sequence 117, App	Sequence 117, App	10.6	40.8	36	3	US-09-522-666-23	Sequence 23, Appl
C 589	10.6	40.8	27	1	US-08-758-306-92	Sequence 92, Appli	Sequence 92, Appli	10.6	40.8	37	1	US-08-276-852-134	Sequence 134, App
C 590	10.6	40.8	27	3	US-08-584-040-551	Sequence 551, App	Sequence 551, App	10.6	40.8	37	1	US-08-077-252B-8	Sequence 8, Appli
C 591	10.6	40.8	27	3	US-08-584-040-6706	Sequence 6706, Ap	Sequence 6706, Ap	10.6	40.8	37	1	US-08-899-575-134	Sequence 134, App
C 592	10.6	40.8	27	3	US-08-584-040-7136	Sequence 7136, Ap	Sequence 7136, Ap	10.6	40.8	37	1	US-08-899-575-134	Sequence 134, App
C 593	10.6	40.8	27	4	US-09-009-893A-12	Sequence 12, Appli	Sequence 12, Appli	10.6	40.8	37	3	US-09-002-753A-8	Sequence 8, Appli
C 594	10.6	40.8	27	4	US-09-009-893A-18	Sequence 18, Appli	Sequence 18, Appli	10.6	40.8	37	3	US-09-657-274-8	Sequence 8, Appli
C 595	10.6	40.8	27	4	US-09-454-204A-23	Sequence 23, Appli	Sequence 23, Appli	10.6	40.8	37	5	PCT-US94-06687-8	Sequence 8, Appli
C 596	10.6	40.8	27	4	US-09-489-155-12	Sequence 12, Appli	Sequence 12, Appli	10.6	40.8	37	5	PCT-US95-08743-134	Sequence 134, App
C 597	10.6	40.8	27	4	US-09-489-155-18	Sequence 18, Appli	Sequence 18, Appli	10.6	40.8	38	2	US-08-432-871C-10	Sequence 10, Appli
C 598	10.6	40.8	27	4	US-09-642-894A-4	Sequence 4, Appli	Sequence 4, Appli	10.6	40.8	38	2	US-08-570-155-6	Sequence 6, Appli
C 599	10.6	40.8	29	3	US-09-446-504-92	Sequence 92, Appli	Sequence 92, Appli	10.6	40.8	38	4	US-09-270-956-10	Sequence 10, Appl
C 600	10.6	40.8	29	3	US-09-712-266-92	Sequence 92, Appli	Sequence 92, Appli	10.6	40.8	38	5	PCT-US95-02861-6	Sequence 6, Appli
C 601	10.6	40.8	29	4	US-09-786-684-7	Sequence 7, Appli	Sequence 7, Appli	10.6	40.8	40	1	US-08-105-483-66	Sequence 66, Appl
C 602	10.6	40.8	29	4	US-09-078-972A-6	Sequence 6, Appli	Sequence 6, Appli	10.6	40.8	40	1	US-08-117-083-4	Sequence 4, Appli
C 603	10.6	40.8	29	4	US-09-291-289-27	Sequence 27, Appli	Sequence 27, Appli	10.6	40.8	40	1	US-08-709-209-66	Sequence 66, Appl
C 604	10.6	40.8	29	4	US-09-786-684-7	Sequence 7, Appli	Sequence 7, Appli	10.6	40.8	40	1	US-08-458-101-66	Sequence 66, Appl
C 605	10.6	40.8	29	4	US-09-623-551-24	Sequence 24, Appli	Sequence 24, Appli	10.6	40.8	40	3	US-08-961-083-358	Sequence 358, App
C 606	10.6	40.8	29	4	US-09-623-551-25	Sequence 25, Appli	Sequence 25, Appli	10.6	40.8	40	3	US-09-633-566-2	Sequence 2, Appli
C 607	10.6	40.8	30	1	US-08-479-487-17	Sequence 17, Appli	Sequence 17, Appli	10.6	40.8	40	4	US-09-536-784-358	Sequence 358, App
C 608	10.6	40.8	30	1	US-08-322-677A-13	Sequence 13, Appli	Sequence 13, Appli	10.6	40.8	40	4	US-09-628-730-19	Sequence 19, Appl
C 609	10.6	40.8	30	1	US-08-322-676-13	Sequence 13, Appli	Sequence 13, Appli	10.6	40.8	40	4	US-09-628-730-36	Sequence 36, Appl
C 610	10.6	40.8	30	3	US-08-898-218-13	Sequence 13, Appli	Sequence 13, Appli	10.6	40.8	40	4	US-09-863-179-6	Sequence 6, Appli
C 611	10.6	40.8	30	3	US-08-951-923-12	Sequence 12, Appli	Sequence 12, Appli	10.6	40.8	40	6	5198342-9	Patent No. 5198342

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686	10.6	40.8	41	3	US-08-813-507-123	Sequence 123, App	c 759	10.4	40.0	28	3	US-08-474-636-24	Sequence 24, Appl
687	10.6	40.8	41	3	US-09-464-453-1	Sequence 1, Appli	c 760	10.4	40.0	28	4	US-07-971-834-13	Sequence 13, Appl
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689	10.6	40.8	42	4	US-09-997-956-3	Sequence 3, Appli	c 762	10.4	40.0	29	1	US-08-222-177A-460	Sequence 460, App
690	10.6	40.8	44	1	US-08-093-741-58	Sequence 58, Appl	c 763	10.4	40.0	29	3	US-08-492-459-25	Sequence 25, Appl
691	10.6	40.8	44	1	US-08-720-012-58	Sequence 58, Appl	c 764	10.4	40.0	29	3	US-08-716-873-39	Sequence 39, Appl
692	10.6	40.8	45	2	US-08-560-098A-25	Sequence 25, Appl	c 765	10.4	40.0	29	3	US-09-001-472-6	Sequence 6, Appli
693	10.6	40.8	46	2	US-08-790-963-69	Sequence 69, Appl	c 766	10.4	40.0	29	3	US-09-368-431-39	Sequence 39, Appl
694	10.6	40.8	46	3	US-09-371-774-69	Sequence 69, Appl	c 767	10.4	40.0	29	3	US-09-414-006-25	Sequence 25, Appl
695	10.6	40.8	47	2	US-08-996-306-57	Sequence 57, Appl	c 768	10.4	40.0	29	4	US-07-971-834-7	Sequence 7, Appli
696	10.6	40.8	47	2	US-08-996-306-60	Sequence 60, Appl	c 769	10.4	40.0	29	4	US-07-971-834-8	Sequence 8, Appli
697	10.6	40.8	47	3	US-09-338-907-57	Sequence 57, Appl	c 770	10.4	40.0	29	4	US-09-775-827A-6	Sequence 39, Appl
698	10.6	40.8	47	3	US-09-338-907-60	Sequence 60, Appl	c 771	10.4	40.0	29	4	US-09-951-217-39	Sequence 17, Appl
699	10.6	40.8	47	3	US-09-218-207-57	Sequence 57, Appl	c 772	10.4	40.0	30	1	US-08-147-696B-17	Sequence 17, Appl
700	10.6	40.8	47	3	US-09-218-207-60	Sequence 60, Appl	c 773	10.4	40.0	30	1	US-08-147-696B-32	Sequence 32, Appl
701	10.6	40.8	47	4	US-09-641-638-1051	Sequence 1051, Ap	c 774	10.4	40.0	30	1	US-08-147-890-8	Sequence 8, Appli
702	10.6	40.8	47	4	US-09-422-978-2410	Sequence 2410, Ap	c 775	10.4	40.0	30	1	US-08-484-334-17	Sequence 17, Appl
703	10.6	40.8	47	4	US-09-422-978-2626	Sequence 2626, Ap	c 776	10.4	40.0	30	1	US-08-484-334-32	Sequence 32, Appl
704	10.6	40.8	47	4	US-09-422-978-3336	Sequence 3336, Ap	c 777	10.4	40.0	30	3	US-09-013-092-17	Sequence 17, Appl
705	10.6	40.8	47	4	US-09-422-978-3324	Sequence 3324, Ap	c 778	10.4	40.0	30	3	US-09-013-092-32	Sequence 32, Appl
706	10.6	40.8	47	4	US-10-170-097-1051	Sequence 1051, Ap	c 779	10.4	40.0	30	3	US-09-280-999-17	Sequence 17, Appl
707	10.6	40.8	49	2	US-08-414-657D-4	Sequence 4, Appli	c 780	10.4	40.0	30	3	US-09-280-999-32	Sequence 32, Appl
708	10.6	40.8	49	4	US-09-135-080-29	Sequence 29, Appl	c 781	10.4	40.0	30	3	US-09-026-408-8	Sequence 8, Appli
709	10.6	40.8	50	4	US-09-849-069-15	Sequence 15, Appl	c 782	10.4	40.0	30	3	US-09-545-244A-1	Sequence 1, Appli
710	10.4	40.0	13	3	US-09-091-058-16	Sequence 16, Appl	c 783	10.4	40.0	30	4	US-09-402-631A-13	Sequence 13, Appl
711	10.4	40.0	16	3	US-09-187-946-14	Sequence 14, Appl	c 784	10.4	40.0	30	4	US-09-173-053-10	Sequence 10, Appl
712	10.4	40.0	16	4	US-09-523-323-62	Sequence 62, Appl	c 785	10.4	40.0	30	4	US-07-971-834-10	Sequence 22, Appl
713	10.4	40.0	17	3	US-09-091-058-17	Sequence 17, Appl	c 786	10.4	40.0	30	4	US-09-646-028-22	Sequence 22, Appl
714	10.4	40.0	20	2	US-08-778-494B-113	Sequence 113, App	c 787	10.4	40.0	30	4	US-08-896-537A-8	Sequence 8, Appli
715	10.4	40.0	21	1	US-07-602-608-20	Sequence 20, Appl	c 788	10.4	40.0	30	4	US-09-902-684-8	Sequence 8, Appli
716	10.4	40.0	21	1	US-08-261-578-20	Sequence 10, Appl	c 789	10.4	40.0	31	1	US-07-867-106-16	Sequence 16, Appl
717	10.4	40.0	21	1	US-08-440-103-10	Sequence 10, Appl	c 790	10.4	40.0	31	1	US-08-147-696B-18	Sequence 18, Appl
718	10.4	40.0	21	1	US-08-426-792-27	Sequence 27, Appl	c 791	10.4	40.0	31	1	US-08-032-846-12	Sequence 12, Appl
719	10.4	40.0	21	1	US-08-231-368-10	Sequence 10, Appl	c 792	10.4	40.0	31	1	US-08-032-846-12	Sequence 18, Appl
720	10.4	40.0	21	1	US-08-440-210-10	Sequence 10, Appl	c 793	10.4	40.0	31	2	US-08-484-334-18	Sequence 9, Appli
721	10.4	40.0	21	3	US-09-046-604-10	Sequence 15, Appl	c 794	10.4	40.0	31	2	US-08-626-169-9	Sequence 4, Appli
722	10.4	40.0	21	3	US-09-452-638-15	Sequence 5, Appli	c 795	10.4	40.0	31	2	US-08-466-120-4	Sequence 9, Appli
723	10.4	40.0	22	1	US-08-425-315-5	Sequence 17, Appl	c 796	10.4	40.0	31	3	US-08-602-359A-9	Sequence 18, Appl
724	10.4	40.0	22	3	US-08-716-190-17	Sequence 17, Appl	c 797	10.4	40.0	31	3	US-09-013-092-18	Sequence 9, Appli
725	10.4	40.0	22	3	US-09-358-972-1	Sequence 281, App	c 798	10.4	40.0	31	3	US-09-164-907-9	Sequence 9, Appli
726	10.4	40.0	22	3	US-09-358-972-281	Sequence 14, Appl	c 799	10.4	40.0	31	3	US-09-280-999-18	Sequence 18, Appl
727	10.4	40.0	22	3	US-09-406-065-14	Sequence 1, Appli	c 800	10.4	40.0	31	4	US-08-474-636-12	Sequence 12, Appl
728	10.4	40.0	22	4	US-09-790-417-1	Sequence 281, App	c 801	10.4	40.0	31	4	US-08-474-636-12	Sequence 4, Appli
729	10.4	40.0	22	4	US-08-790-417-281	Sequence 112, App	c 802	10.4	40.0	31	4	US-08-845-546-17	Sequence 17, Appl
730	10.4	40.0	23	2	US-08-778-494B-112	Sequence 29, Appl	c 803	10.4	40.0	32	2	US-08-997-803-10	Sequence 10, Appl
731	10.4	40.0	23	2	US-08-173-510B-29	Sequence 6, Appli	c 804	10.4	40.0	32	2	US-08-997-803-10	Sequence 15, Appl
732	10.4	40.0	24	1	US-08-458-218-29	Sequence 4, Appli	c 805	10.4	40.0	32	3	US-08-845-546-17	Sequence 15, Appl
733	10.4	40.0	24	1	US-08-816-605-4	Sequence 29, Appl	c 806	10.4	40.0	32	3	US-08-156-163A-15	Sequence 23, Appl
734	10.4	40.0	24	2	US-08-816-605-6	Sequence 6, Appli	c 807	10.4	40.0	32	3	US-09-982-308B-15	Sequence 23, Appl
735	10.4	40.0	24	2	US-08-450-497-29	Sequence 29, Appl	c 808	10.4	40.0	32	4	US-09-758-282B-23	Sequence 24, Appl
736	10.4	40.0	24	2	US-09-866-028-56	Sequence 56, Appl	c 809	10.4	40.0	32	4	US-09-758-282B-23	Sequence 24, Appl
737	10.4	40.0	24	4	US-09-944-457-56	Sequence 56, Appl	c 810	10.4	40.0	32	4	US-09-577-304A-23	Sequence 24, Appl
738	10.4	40.0	24	4	US-09-944-457-56	Sequence 56, Appl	c 811	10.4	40.0	32	4	US-09-577-304A-23	Sequence 24, Appl
739	10.4	40.0	25	2	US-08-671-975A-14	Sequence 14, Appl	c 812	10.4	40.0	32	4	PCT-US96-00547-37	Sequence 37, Appl
740	10.4	40.0	25	2	US-09-758-282B-34	Sequence 34, Appl	c 813	10.4	40.0	32	5	US-08-557-128-16	Sequence 16, Appl
741	10.4	40.0	25	4	US-09-866-108A-13783	Sequence 13783, A	c 814	10.4	40.0	33	2	US-08-874-102-23	Sequence 23, Appl
742	10.4	40.0	25	4	US-09-866-108A-13784	Sequence 13784, A	c 815	10.4	40.0	33	3	US-08-984-919A-23	Sequence 23, Appl
743	10.4	40.0	25	4	US-09-866-108A-13785	Sequence 13785, A	c 816	10.4	40.0	33	3	US-09-477-392-22	Sequence 22, Appl
744	10.4	40.0	25	4	US-09-866-108A-13786	Sequence 13786, A	c 817	10.4	40.0	33	4	US-08-147-696E-29	Sequence 29, Appl
745	10.4	40.0	25	4	US-09-866-108A-13787	Sequence 13787, A	c 818	10.4	40.0	34	1	US-08-484-334-29	Sequence 29, Appl
746	10.4	40.0	25	4	US-09-866-108A-13788	Sequence 13788, A	c 819	10.4	40.0	34	1	US-08-484-334-29	Sequence 33, Appl
747	10.4	40.0	25	4	US-09-577-304A-34	Sequence 34, Appl	c 820	10.4	40.0	34	2	US-08-888-366-33	Sequence 33, Appl
748	10.4	40.0	25	4	US-10-004-993A-2	Sequence 2, Appli	c 821	10.4	40.0	34	2	US-08-888-366-33	Sequence 29, Appl
749	10.4	40.0	26	1	US-08-120-827-60	Sequence 60, Appl	c 822	10.4	40.0	34	3	US-09-013-092-29	Sequence 42, Appl
750	10.4	40.0	26	1	US-08-478-675-60	Sequence 1347, Ap	c 823	10.4	40.0	34	3	US-08-767-128-42	Sequence 29, Appl
751	10.4	40.0	27	3	US-08-985-162-1347	Sequence 1489, Ap	c 824	10.4	40.0	34	3	US-09-280-999-29	Sequence 29, Appl
752	10.4	40.0	27	3	US-08-985-162-1489	Sequence 6997, Ap	c 825	10.4	40.0	34	4	US-09-371-772B-14223	Sequence 33, Appl
753	10.4	40.0	27	3	US-08-584-040-6997	Sequence 21, Appl	c 826	10.4	40.0	35	1	US-08-110-158-8	Sequence 8, Appli
754	10.4	40.0	27	3	US-09-410-464-21	Sequence 21, Appl	c 827	10.4	40.0	35	2	US-07-829-461A-14	Sequence 14, Appl
755	10.4	40.0	27	4	US-09-311-784A-77	Sequence 77, Appl	c 828	10.4	40.0	35	2	US-08-440-845D-14	Sequence 14, Appl
756	10.4	40.0	27	4	US-09-401-063-1347	Sequence 1347, Ap	c 829	10.4	40.0	35	3	US-08-868-458-14	Sequence 14, Appl
757	10.4	40.0	27	4	US-09-401-063-1489	Sequence 1489, Ap	c 830	10.4	40.0	35	3		

C 831	10.4	40.0	35	3	US-09-197-649-15	Sequence 15, Appl	904	10.4	40.0	39	5	PCT-US92-10983-59	Sequence 59, Appl
832	10.4	40.0	35	4	US-09-894-698-13	Sequence 13, Appl	C 905	10.4	40.0	39	5	PCT-US95-05262-5	Sequence 5, Appl
833	10.4	40.0	36	1	US-07-834-539A-10	Sequence 10, Appl	C 906	10.4	40.0	39	6	5256648-26	Patent No. 5256648
834	10.4	40.0	36	1	US-08-053-131-18	Sequence 18, Appl	C 907	10.4	40.0	40	1	US-08-036-210-40	Sequence 40, Appl
835	10.4	40.0	36	1	US-08-478-019-49	Sequence 49, Appl	C 908	10.4	40.0	40	2	US-08-446-345-22	Sequence 22, Appl
836	10.4	40.0	36	1	US-08-645-641-18	Sequence 18, Appl	C 909	10.4	40.0	40	2	US-08-449-609-40	Sequence 40, Appl
837	10.4	40.0	36	1	US-08-476-349A-49	Sequence 49, Appl	C 910	10.4	40.0	40	3	US-09-162-484-8	Sequence 8, Appl
838	10.4	40.0	36	1	US-08-074-121-11	Sequence 11, Appl	C 911	10.4	40.0	40	3	US-09-361-096A-40	Sequence 40, Appl
839	10.4	40.0	36	1	US-07-853-408B-18	Sequence 18, Appl	C 912	10.4	40.0	40	4	US-09-909-650B-2	Sequence 2, Appl
840	10.4	40.0	36	1	US-08-096-762-18	Sequence 18, Appl	C 913	10.4	40.0	41	1	US-08-375-241-17	Sequence 17, Appl
841	10.4	40.0	36	2	US-08-800-353-10	Sequence 10, Appl	C 914	10.4	40.0	41	1	US-08-375-241-29	Sequence 29, Appl
842	10.4	40.0	36	2	US-08-585-684B-898	Sequence 898, App	C 915	10.4	40.0	41	3	US-08-501-253A-8	Sequence 8, Appl
843	10.4	40.0	36	2	US-08-308-865-18	Sequence 18, Appl	C 916	10.4	40.0	41	3	US-08-501-253A-21	Sequence 21, Appl
844	10.4	40.0	36	2	US-08-717-123-9	Sequence 9, Appl	C 917	10.4	40.0	41	3	US-09-622-540A-18	Sequence 18, Appl
845	10.4	40.0	36	3	US-08-889-841B-50	Sequence 50, Appl	C 918	10.4	40.0	41	4	US-09-622-540A-18	Sequence 18, Appl
846	10.4	40.0	36	3	US-08-523-894-42	Sequence 42, Appl	C 919	10.4	40.0	41	5	PCT-US92-06617A-17	Sequence 17, Appl
847	10.4	40.0	36	3	US-09-035-665-2	Sequence 2, Appl	C 920	10.4	40.0	41	5	PCT-US92-06617A-29	Sequence 29, Appl
848	10.4	40.0	36	3	US-09-038-073-898	Sequence 898, App	C 921	10.4	40.0	42	1	US-08-225-224-18	Sequence 18, Appl
849	10.4	40.0	36	3	US-09-042-353-186	Sequence 186, App	C 922	10.4	40.0	42	3	US-08-722-258-18	Sequence 18, Appl
850	10.4	40.0	36	3	US-08-758-417A-34	Sequence 34, Appl	C 923	10.4	40.0	42	5	PCT-US95-04468-18	Sequence 18, Appl
851	10.4	40.0	36	3	US-09-540-014-30	Sequence 30, Appl	C 924	10.4	40.0	43	2	US-08-472-171-49	Sequence 49, Appl
852	10.4	40.0	36	4	US-09-375-257-9	Sequence 9, Appl	C 925	10.4	40.0	43	2	US-08-894-526-49	Sequence 49, Appl
853	10.4	40.0	36	4	US-09-322-624-8	Sequence 8, Appl	C 926	10.4	40.0	43	2	US-09-013-047-49	Sequence 49, Appl
854	10.4	40.0	36	4	US-09-419-362-50	Sequence 50, Appl	C 927	10.4	40.0	43	3	US-09-374-597-49	Sequence 49, Appl
855	10.4	40.0	36	4	US-09-724-138-36	Sequence 36, Appl	C 928	10.4	40.0	44	3	US-09-411-329C-11	Sequence 11, Appl
856	10.4	40.0	36	4	US-09-538-864-33	Sequence 23, Appl	C 929	10.4	40.0	44	4	US-09-477-135A-143	Sequence 143, App
857	10.4	40.0	36	5	PCT-US92-06185-10	Sequence 10, Appl	C 930	10.4	40.0	44	4	US-09-068-821-11	Sequence 11, Appl
858	10.4	40.0	36	5	PCT-US92-10983-18	Sequence 18, Appl	C 931	10.4	40.0	44	4	US-09-846-729A-11	Sequence 11, Appl
859	10.4	40.0	36	5	PCT-US94-06447-11	Sequence 11, Appl	C 932	10.4	40.0	44	4	US-09-371-307-38	Sequence 38, Appl
860	10.4	40.0	37	1	US-08-353-657-1	Sequence 1, Appl	C 933	10.4	40.0	45	1	US-07-885-689A-12	Sequence 12, Appl
861	10.4	40.0	37	1	US-08-353-657-2	Sequence 2, Appl	C 934	10.4	40.0	45	1	US-08-225-224-19	Sequence 19, Appl
862	10.4	40.0	37	1	US-07-951-715A-62	Sequence 62, Appl	C 935	10.4	40.0	45	1	US-08-722-258-19	Sequence 19, Appl
863	10.4	40.0	37	1	US-08-709-982-1	Sequence 1, Appl	C 936	10.4	40.0	45	3	US-09-411-329C-10	Sequence 10, Appl
864	10.4	40.0	37	1	US-08-709-982-2	Sequence 2, Appl	C 937	10.4	40.0	45	3	US-08-874-102-51	Sequence 51, Appl
865	10.4	40.0	37	2	US-08-459-448A-62	Sequence 62, Appl	C 938	10.4	40.0	45	3	US-08-874-102-53	Sequence 53, Appl
866	10.4	40.0	37	2	US-08-982-866-1	Sequence 1, Appl	C 939	10.4	40.0	45	3	US-08-984-519A-51	Sequence 51, Appl
867	10.4	40.0	37	2	US-08-982-866-2	Sequence 2, Appl	C 940	10.4	40.0	45	3	US-08-984-519A-53	Sequence 53, Appl
868	10.4	40.0	37	3	US-08-459-595A-62	Sequence 62, Appl	C 941	10.4	40.0	45	4	US-09-963-137-45	Sequence 45, Appl
869	10.4	40.0	37	3	US-08-459-504B-62	Sequence 62, Appl	C 942	10.4	40.0	45	4	US-09-846-729A-10	Sequence 10, Appl
870	10.4	40.0	37	3	US-08-459-444-62	Sequence 62, Appl	C 943	10.4	40.0	45	4	US-09-866-028-81	Sequence 81, Appl
871	10.4	40.0	37	3	US-09-547-422-62	Sequence 62, Appl	C 944	10.4	40.0	45	4	US-09-944-457-81	Sequence 81, Appl
872	10.4	40.0	37	4	US-09-155-613A-13	Sequence 13, Appl	C 945	10.4	40.0	45	4	US-09-806-871A-3	Sequence 3, Appl
873	10.4	40.0	37	4	US-09-276-533A-14	Sequence 14, Appl	C 946	10.4	40.0	45	5	PCT-US95-04468-19	Sequence 19, Appl
874	10.4	40.0	37	4	US-09-724-138-19	Sequence 19, Appl	C 947	10.4	40.0	46	1	US-08-127-905-2	Sequence 2, Appl
875	10.4	40.0	37	4	US-09-988-462-62	Sequence 62, Appl	C 948	10.4	40.0	46	1	US-08-396-415-2	Sequence 2, Appl
876	10.4	40.0	37	4	US-10-158-735-14	Sequence 14, Appl	C 949	10.4	40.0	46	1	US-08-171-389-271	Sequence 271, App
877	10.4	40.0	37	5	PCT-US94-14181-1	Sequence 1, Appl	C 950	10.4	40.0	46	1	US-08-123-936-271	Sequence 271, App
878	10.4	40.0	37	5	PCT-US94-14181-2	Sequence 2, Appl	C 951	10.4	40.0	46	2	US-08-475-228A-271	Sequence 271, App
879	10.4	40.0	38	4	US-09-371-772B-7669	Sequence 7669, App	C 952	10.4	40.0	46	3	US-08-482-080A-271	Sequence 271, App
880	10.4	40.0	38	4	US-09-371-772B-10992	Sequence 10992, A	C 953	10.4	40.0	46	3	US-09-354-947-271	Sequence 271, App
881	10.4	40.0	38	4	US-09-371-772B-11721	Sequence 11721, A	C 954	10.4	40.0	46	5	PCT-US93-12388-271	Sequence 271, App
882	10.4	40.0	38	4	US-09-371-772B-13881	Sequence 13881, A	C 955	10.4	40.0	47	2	US-08-659-567-7	Sequence 7, Appl
883	10.4	40.0	38	4	US-09-628-730-10	Sequence 10, Appl	C 956	10.4	40.0	47	4	US-09-671-317-600	Sequence 600, App
884	10.4	40.0	38	4	US-09-332-522E-57	Sequence 57, Appl	C 957	10.4	40.0	47	4	US-09-422-378-591	Sequence 591, App
885	10.4	40.0	39	1	US-08-236-520-5	Sequence 5, Appl	C 958	10.4	40.0	47	4	US-09-422-978-938	Sequence 938, App
886	10.4	40.0	39	1	US-07-834-539A-47	Sequence 47, Appl	C 959	10.4	40.0	47	4	US-09-422-978-938	Sequence 938, App
887	10.4	40.0	39	1	US-08-053-131-59	Sequence 59, Appl	C 960	10.4	40.0	47	4	US-09-422-978-2016	Sequence 2016, App
888	10.4	40.0	39	1	US-08-645-641-59	Sequence 59, Appl	C 961	10.4	40.0	47	4	US-09-422-978-3381	Sequence 3381, App
889	10.4	40.0	39	1	US-07-853-408B-59	Sequence 59, Appl	C 962	10.4	40.0	47	4	US-09-422-978-3761	Sequence 3761, App
890	10.4	40.0	39	1	US-07-977-696C-9	Sequence 9, Appl	C 963	10.4	40.0	48	4	US-09-291-874-10	Sequence 10, Appl
891	10.4	40.0	39	1	US-08-129-930B-9	Sequence 9, Appl	C 964	10.4	40.0	48	4	US-09-344-783C-27	Sequence 27, Appl
892	10.4	40.0	39	1	US-08-096-762-59	Sequence 59, Appl	C 965	10.4	40.0	48	4	US-09-428-082B-1124	Sequence 1124, App
893	10.4	40.0	39	1	US-08-800-353-47	Sequence 47, Appl	C 966	10.4	40.0	49	1	US-08-540-448-9	Sequence 9, Appl
894	10.4	40.0	39	2	US-08-308-865-59	Sequence 59, Appl	C 967	10.4	40.0	49	2	US-08-801-898A-29	Sequence 29, Appl
895	10.4	40.0	39	2	US-08-648-506-2	Sequence 2, Appl	C 968	10.4	40.0	49	3	US-08-929-939-9	Sequence 9, Appl
896	10.4	40.0	39	3	US-08-860-483A-11	Sequence 11, Appl	C 969	10.4	40.0	50	1	US-08-171-389-458	Sequence 458, App
897	10.4	40.0	39	3	US-09-277-355-2	Sequence 2, Appl	C 970	10.4	40.0	50	1	US-08-207-901-35	Sequence 35, Appl
898	10.4	40.0	39	3	US-09-042-353-222	Sequence 222, App	C 971	10.4	40.0	50	1	US-08-123-936-458	Sequence 458, App
899	10.4	40.0	39	3	US-08-758-417A-70	Sequence 70, Appl	C 972	10.4	40.0	50	2	US-08-475-228A-458	Sequence 458, App
900	10.4	40.0	39	3	US-08-976-288A-9	Sequence 9, Appl	C 973	10.4	40.0	50	3	US-08-482-080A-458	Sequence 458, App
901	10.4	40.0	39	4	US-09-474-178-24	Sequence 24, Appl	C 974	10.4	40.0	50	3	US-09-390-867A-43	Sequence 43, Appl
902	10.4	40.0	39	4	US-09-806-871A-6	Sequence 6, Appl	C 975	10.4	40.0	50	3	US-09-548-260-43	Sequence 43, Appl
903	10.4	40.0	39	5	PCT-US92-06185-47	Sequence 47, Appl	C 976	10.4	40.0	50	3	US-09-354-947-458	Sequence 458, App

RESULT 1
 US-08-344-695-5/c
 Sequence 5, Application US/08344695
 Patent No. 5614398
 GENERAL INFORMATION:
 APPLICANT: O'BROCHTA, DAVID
 APPLICANT: WARREN, WILLIAM
 APPLICANT: ATKINSON, PETER
 TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,695
 FILING DATE: 18-NOV-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
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 REGISTRATION NUMBER: 30,073
 REFERENCE/DOCKET NUMBER: 2747-058-27
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 44 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 US-08-344-695-5

APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ET-1 primer F
US-08-880-342-4

Query Match 56.2%; Score 14.6; DB 3; Length 41;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACATCGGTACCT 22
||||| |
Db 30 GTCTTTCCTATCGGTACCT 10

RESULT 4
US-09-641-638-998/c
Sequence 998, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 998
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 10-482-145 : polymorphic base A or G
US-09-641-638-998

Query Match 53.8%; Score 14; DB 4; Length 47;
Best Local Similarity 70.8%; Pred. No. 6.5e+02;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACATCGGTACCTCAA 25
||||| |
Db 43 GTCTTTCACAGATAGGAGGTGAA 20

RESULT 5
US-10-170-097-998/c
Sequence 998, Application US/10170097
Patent No. 6794143
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GEN-T114XC2D1
CURRENT APPLICATION NUMBER: US/10/170,097
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 998
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 10-482-145 : polymorphic base A or G
US-10-170-097-998

Query Match 53.8%; Score 14; DB 4; Length 47;
Best Local Similarity 70.8%; Pred. No. 6.5e+02;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACATCGGTACCTCAA 25
||||| |
Db 43 GTCTTTCACAGATAGGAGGTGAA 20

RESULT 6
US-09-082-649B-41
Sequence 41, Application US/09082649B

Patent No. 6339068
 GENERAL INFORMATION:
 APPLICANT: Davis, Heather L.
 APPLICANT: Krieg, Arthur M.
 APPLICANT: Schorr, Joachim
 APPLICANT: Wu, Tong
 TITLE OF INVENTION: Vectors and Methods for Immunization or Therapeutic Protocols
 FILE REFERENCE: C1039/7009
 CURRENT APPLICATION NUMBER: US/09/082,649B
 CURRENT FILING DATE: 1998-05-20
 PRIOR APPLICATION NUMBER: US 60/047,233
 PRIOR FILING DATE: 1997-05-20
 PRIOR APPLICATION NUMBER: US 60/047,209
 PRIOR FILING DATE: 1997-05-20
 NUMBER OF SEQ ID NOS: 85
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 41
 LENGTH: 34
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic oligonucleotide
 US-09-082-649B-41
 Query Match 52.3%; Score 13.6; DB 3; Length 34;
 Best Local Similarity 80.0%; Pred. No. 9.9e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TCGCAGATCGGTACTCAAT 26
 |||||
 DB 10 TCGCAGATCGATACCAGGAT 29

RESULT 7
 US-09-180-394-3/c
 Sequence 3, Application US/09180394
 Patent No. 6673605
 GENERAL INFORMATION:
 APPLICANT: M. Sawada
 TITLE OF INVENTION: ESTABLISHED CELL LINE OF MICROGLIA
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Peter F. Corless
 STREET: Pike, Bronstein, Roberts & Cushman, LLP 130 Water St.
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-4280
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/180,394
 FILING DATE: 1998-11-05
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP98/00949
 FILING DATE: 1998-03-05
 ATTORNEY/AGENT INFORMATION:
 NAME: Peter F. Corless
 REGISTRATION NUMBER: 33,860
 REFERENCE/DOCKET NUMBER: 1526-48781
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)-523-3400
 TELEFAX: (617)-523-6440
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Synthetic DNA
 US-09-180-394-3
 Query Match 51.5%; Score 13.4; DB 4; Length 25;
 Best Local Similarity 73.9%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCTTTCGACAGTCGGTACTCA 24
 |||||
 DB 24 GTCTTTCGACAGAGAACTTCA 2

RESULT 8
 US-08-738-381-24
 Sequence 24, Application US/08738381
 Patent No. 6083694
 GENERAL INFORMATION:
 APPLICANT: John A. Hardy, Alison M. Goate
 TITLE OF INVENTION: Method for Elucidation and Detection of Polymorphisms, Splice Variants and Proximal Coding Using Intronic Sequences of the Mutations Alzheimer's S182 Gene
 TITLE OF INVENTION: Proximal Coding Using Intronic Sequences of the Mutations Alzheimer's S182 Gene
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road, P.O. Box 1539
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406-0939
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
 MEDIUM TYPE: STORAGE
 COMPUTER: IBM 486
 OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/738,381
 FILING DATE: Herewith
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/007,048
 FILING DATE: October 25, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: William T. Han
 REGISTRATION NUMBER: 34,344
 REFERENCE/DOCKET NUMBER: P50388
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5024
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 ANTI-SENSE: NO
 US-08-738-381-24
 Query Match 51.5%; Score 13.4; DB 3; Length 31;
 Best Local Similarity 73.9%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TCCTTCGACAGTCGGTACTCAA 25
 |||||
 DB 7 TCCTTCCTTCGAGAACTCAA 29

RESULT 9
 US-08-845-546-22/c
 Sequence 22, Application US/08845546

```
; Patent No. 6077949
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald
; APPLICANT: Gupta, Ashwani
; APPLICANT: Vyas, Tejal
; APPLICANT: McCallum, Kirk
; APPLICANT: Fan, Ernei
; TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
; TITLE OF INVENTION: 2 RECEPTORS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,546
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8607-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-845-546-22

Query Match      51.5%; Score 13.4; DB 3; Length 39;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 AGATCGGTACCTCAA 25
        |||||
Db      22 AGATCGGTACCTCGA 8

RESULT 10
US-09-714-550-6
; Sequence 6, Application US/09714550
; Patent No. 6558948
; GENERAL INFORMATION:
; APPLICANT: Kochanek, Stefan
; APPLICANT: Schiedner, Gudrun
; TITLE OF INVENTION: Permanent amniocytic cell line, its
; TITLE OF INVENTION: production and use for the production of gene transfer
; FILE REFERENCE: 50125/007002
; CURRENT APPLICATION NUMBER: US/09/714,550
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/167,439
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: primer
US-09-714-550-6
Query Match      50.8%; Score 13.2; DB 4; Length 32;
Best Local Similarity 69.2%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CGTCTTCGCGAGATCGGTACCTCAAT 26
        |||||
Db      3 CGCAATTCATTTCAGTACTCAAT 28

RESULT 11
US-09-553-867A-31
; Sequence 31, Application US/09553867A
; Patent No. 6476188
; GENERAL INFORMATION:
; APPLICANT: Young, Michael W
; APPLICANT: Kloss, Brian
; APPLICANT: Blau, Justin
; APPLICANT: Price, Jeffrey
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Philip, Lowrey L.
; TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE THEREOF
; FILE REFERENCE: 600-1-22INCP
; CURRENT APPLICATION NUMBER: US/09/553,867A
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/090,068
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 09/335,983
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer.
US-09-553-867A-31

Query Match      50.0%; Score 13; DB 4; Length 30;
Best Local Similarity 76.2%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 GTCTTCGCGAGATCGGTACCT 22
        |||||
Db      9 GTCTTCGCGAGATCTACCT 29

RESULT 12
US-08-171-389-583/c
; Sequence 583, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Fenobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,389
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION NUMBER: US 07/996,783
; APPLICATION DATA:
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 583:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site
; INDIVIDUAL ISOLATE: 25954)
; US-08-171-389-583

Query Match 50.0%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 CTTTCGCAGATCGGTACTCA 24
Db 34 CTTTCGCAATTTGTACTCA 14

RESULT 13
US-08-123-936-583/c
; Sequence 583, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 583:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site
; INDIVIDUAL ISOLATE: 25954)
; US-08-171-389-583
```

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;
; APPLICATION NUMBER: US/08/123,936
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 583:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site
; INDIVIDUAL ISOLATE: 25954)
; US-08-123-936-583

Query Match 50.0%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 CTTTCGCAGATCGGTACTCA 24
Db 34 CTTTCGCAATTTGTACTCA 14

RESULT 14
US-08-475-228A-583/c
; Sequence 583, Application US/08475228A
; Patent No. 5869241
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,228A
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
```


APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 583:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site)
INDIVIDUAL ISOLATE: 25954)
US-08-475-228A-583

Query Match 50.0%; Score 13; DB 2; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTTTCGCAGATCGGTACTCA 24
| | | | | | | | | | | | | | | | | |
Db 34 CTTTCGCAAAATTTGTACTGA 14

RESULT 15
US-08-482-080A-583/c
Sequence 583, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 583:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site)
INDIVIDUAL ISOLATE: 25954)
US-08-482-080A-583

Query Match 50.0%; Score 13; DB 3; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTTTCGCAGATCGGTACTCA 24
| | | | | | | | | | | | | | | | | |
Db 34 CTTTCGCAAAATTTGTACTGA 14

RESULT 16
US-09-354-947-583/c
Sequence 583, Application US/09354947
Patent No. 6384208
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:

Wed Nov 24 08:46:10 2004

;; APPLICATION NUMBER: US 07/723,618
;; FILING DATE: 27-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/081,070
;; FILING DATE: 22-JUN-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brady, John F.
;; REGISTRATION NUMBER: 39,118
;; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 324-0880
;; TELEFAX: (650) 324-0960
;; INFORMATION FOR SEQ ID NO: 583:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 50 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site
;; INDIVIDUAL ISOLATE: 25954)
;; US-09-354-947-583

Query Match 50.0%; Score 13; DB 3; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

Qy 4 CTTTCGAGATCGGTACCTCA 24
Db 34 CTTTCGAAATTTGTACCTGA 14

RESULT 17
PCT-US93-12388-583/c
; Sequence 583, Application PC/TUS9312388
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12388
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 583:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 50 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site
;; INDIVIDUAL ISOLATE: 25954)
;; PCT-US93-12388-583

Query Match 50.0%; Score 13; DB 5; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTTTCGAGATCGGTACCTCA 24
Db 34 CTTTCGAAATTTGTACCTGA 14

RESULT 18
US-08-485-971-12/c
; Sequence 12, Application US/08485971
; Patent No. 5589362
; GENERAL INFORMATION:
; APPLICANT: Bujard, Hermann
; APPLICANT: Gossen, Manfred
; APPLICANT: Hillen, Wolfgang
; APPLICANT: Helbl, Vera
; APPLICANT: Schnappinger, Dirk
; TITLE OF INVENTION: Tetracycline-Regulated Transcriptional
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,971
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/383,754
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/270,637
; FILING DATE: 01-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,452
; FILING DATE: 14-JUNE-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,327
; FILING DATE: 14-JUNE-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,726
; FILING DATE: 14-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-009CP7
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-485-971-12

Query Match 49.2%; Score 12.8; DB 1; Length 38;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 3 TCTTTCCGAGATCGGTACTCTCAAT 26
Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 19

US-08-275-876-12/c
Sequence 12, Application US/08275876
Patent No. 5654168

GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
APPLICANT: Gossen, Manfred
TITLE OF INVENTION: Tetracycline-Inducible Transcriptional
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,876

FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 01-JULY-94
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009CP

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-275-876-12

Query Match 49.2%; Score 12.8; DB 1; Length 38;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 3 TCTTTCCGAGATCGGTACTCTCAAT 26
Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 20

US-08-383-754-12/c
Sequence 12, Application US/08383754
Patent No. 5789156

GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
APPLICANT: Gossen, Manfred
TITLE OF INVENTION: Tetracycline-Regulated Transcriptional
TITLE OF INVENTION: Inhibitors
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,754

FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-94
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-94
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,452

FILING DATE: 14-JUNE-94
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726

FILING DATE: 14-JUNE-93
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-383-754-12

Query Match 49.2%; Score 12.8; DB 1; Length 38;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 3 TCTTTCCGAGATCGGTACTCTCAAT 26
Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 21

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US-08-485-978-12/c
: Sequence 12, Application US/08485978
: Patent No. 5814618
:
: GENERAL INFORMATION:
: APPLICANT: Bujard, Hermann
: APPLICANT: Gossen, Manfred
: TITLE OF INVENTION: Methods for Regulating Gene Expression
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street, Suite 510
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109-1875
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,978
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/383,754
: FILING DATE: 03-FEB-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/275,876
: FILING DATE: 15-JULY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/270,637
: FILING DATE: 01-JULY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/260,452
: FILING DATE: 14-JUNE-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/076,327
: FILING DATE: 14-JUNE-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/076,726
: FILING DATE: 14-JUNE-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: DeConti, Giulio A. Jr.
: REGISTRATION NUMBER: 31,503
: REFERENCE/DOCKET NUMBER: BBI-009CP6
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 38 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
:
US-08-485-978-12
Query Match 49.2%; Score 12.8; DB 1; Length 38;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels

Qy 3 TCTTTCCGAGATCGGTACTCAAT 26
Db 36 TCTATCACTGATAGGAACCTCTAT 13

```

RESULT 23

US-08-487-472-12/c
; Sequence 12, Application US/08487472
; Patent No. 5912411
; GENERAL INFORMATION:
; APPLICANT: Bujard, Hermann
; APPLICANT: Gossen, Manfred
; TITLE OF INVENTION: Animal Transgenic for a Tetracycline- Inducible Transcription
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,472
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/383,754
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,876
; FILING DATE: 15-JULY-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/270,637
; FILING DATE: 01-JULY-94
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,452
; FILING DATE: 14-JUNE-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,327
; FILING DATE: 14-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,726
; FILING DATE: 14-JUNE-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-009CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-487-472-12

Query Match 49.2%; Score 12.8; DB 2; Length 38;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGACATCGTACTCAAT 26

Db 36 TCTATCACTGATGGGAACCTCTAT 13

RESULT 24

US-08-485-740-12/c
; Sequence 12, Application US/08485740
; Patent No. 6004941
; GENERAL INFORMATION:
; APPLICANT: Bujard, Hermann
; APPLICANT: Gossen, Manfred
; TITLE OF INVENTION: Methods for Regulating Gene Expression
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,740
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/383,754
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,876
; FILING DATE: 15-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/270,637
; FILING DATE: 01-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,452
; FILING DATE: 14-JUNE-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,327
; FILING DATE: 14-JUNE-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,726
; FILING DATE: 14-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-009CP5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-485-740-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGACATCGTACTCAAT 26

Db 36 TCTATCACTGATGGGAACCTCTAT 13

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 25

US-09-162-184-12/c

; Sequence 12, Application US/09162184A

; Patent No. 6136954

; GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/162,184A

FILING DATE: 28-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/383,754

FILING DATE: 03-FEB-1995

APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-1994

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-1994

APPLICATION NUMBER: US 08/260,452

FILING DATE: 14-JUNE-1994

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

APPLICATION NUMBER: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009C6CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)742-4214

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-162-184-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGAGATCGGTACTCTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 26

US-09-161-902-12/c

; Sequence 12, Application US/09161902

; Patent No. 6242667

; GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/161,902

FILING DATE: 28-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/383,754

FILING DATE: 03-FEB-1995

APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-1994

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-1994

APPLICATION NUMBER: US 08/260,452

FILING DATE: 14-JUNE-1994

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

APPLICATION NUMBER: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009C6CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)742-4214

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-161-902-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGAGATCGGTACTCTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 27

US-09-489-777A-12/c

; Sequence 12, Application US/09489777A

; Patent No. 6271348

; GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/161,902

FILING DATE: 28-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/487,472

FILING DATE: 01-JULY-94

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-94

APPLICATION NUMBER: US 08/260,452

FILING DATE: 14-JUNE-1994

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

APPLICATION NUMBER: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-161-902-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGAGATCGGTACTCTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 28

US-09-489-777A-12/c

; Sequence 12, Application US/09489777A

; Patent No. 6271348

; GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/161,902

FILING DATE: 28-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/487,472

FILING DATE: 01-JULY-94

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-94

APPLICATION NUMBER: US 08/260,452

FILING DATE: 14-JUNE-1994

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

APPLICATION NUMBER: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-161-902-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGAGATCGGTACTCTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13

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/ FILE NUMBER: 2000-04-13
/ FILE REFERENCE: NIH151.001C
/ CURRENT APPLICATION NUMBER: US/09/976,667
/ CURRENT FILING DATE: 2001-10-10
/ PRIOR APPLICATION NUMBER: 60/129,215
/ PRIOR FILING DATE: 1999-04-14
/ PRIOR APPLICATION NUMBER: PCT/US00/10146
/ PRIOR FILING DATE: 2000-04-13
/ NUMBER OF SEQ ID NOS: 15
/

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning Oligonucleotide
US-09-976-667-15

Query Match
Best Local Similarity 48.5%; Score 12.6; DB 4; Length 26;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCTTTCGAGATCGGTACC 21
Db 21 TCTTTCGAGATCGGTACC 3

RESULT 30
RE34606-8
; Patent No. RE34,606
; APPLICANT: ESTELL, DAVID A.; WELLS, JAMES A.; BOTT,
; RICHARD R.
; TITLE OF INVENTION: MODIFIED ENZYMES AND METHODS FOR
; MAKING SAME
; NUMBER OF SEQUENCES: 27
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/556,918
; FILING DATE: 20-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 614,612
; FILING DATE: 29-MAY-1984
; SEQ ID NO: 8
; LENGTH: 48
RE34606-8

Query Match
Best Local Similarity 48.5%; Score 12.6; DB 6; Length 48;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CGCAGATCGGTACTCAAT 26
Db 2 CGTACACGGTACGTCAAT 20

RESULT 31
US-09-672-810-15
; Sequence 15, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide based on Macaca fascicularis
; OTHER INFORMATION: and Homo sapiens
US-09-672-810-15

Query Match
Best Local Similarity 47.7%; Score 12.4; DB 4; Length 28;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGTCTTTCGAGATCGGTACC 22
Db 29 CGTCTTTCGAGATCGGTACC 8

RESULT 34
US-08-641-294-4
; Sequence 4, Application US/08641294
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: Hippenmeyer, Paul J.
; APPLICANT: Highkin, Maureen K.
```

```
Best Local Similarity 72.7%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 CTTTCGAGATCGGTACTCAA 25
Db 1 CTTTCGAGATCGGTAACTGAA 22

RESULT 32
US-09-455-960-28/c
; Sequence 28, Application US/09455960
; Patent No. 6361776
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compositions isolated from M. vaccae and
; TITLE OF INVENTION: their use in modulation of immune responses.
; FILE REFERENCE: 11000.1047
; CURRENT APPLICATION NUMBER: US/09/455,960
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-455-960-28

Query Match
Best Local Similarity 47.7%; Score 12.4; DB 3; Length 35;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTTCGAGATCGGTACT 22
Db 29 CGTCTTTCGAGATCGGTACT 8

RESULT 33
US-10-051-325-28/c
; Sequence 28, Application US/10051325
; Patent No. 6716430
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compositions isolated from M. vaccae and
; TITLE OF INVENTION: their use in modulation of immune responses.
; FILE REFERENCE: 11000.1047/c1
; CURRENT APPLICATION NUMBER: US/10/051,325
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/455,960
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-325-28

Query Match
Best Local Similarity 47.7%; Score 12.4; DB 4; Length 35;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTTCGAGATCGGTACT 22
Db 29 CGTCTTTCGAGATCGGTACT 8

RESULT 34
US-08-641-294-4
; Sequence 4, Application US/08641294
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: Hippenmeyer, Paul J.
; APPLICANT: Highkin, Maureen K.
```


;; TITLE OF INVENTION: Production of Recombinant Proteins Using
;; TITLE OF INVENTION: Herpes Virus Promoters and VP16 Transactivators
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG
;; STREET: 800 N. Lindbergh
;; CITY: St. Louis
;; STATE: Missouri
;; COUNTRY: USA
;; ZIP: 63198
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/641,294
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/290,050
;; FILING DATE:
;; APPLICATION NUMBER: US/07/850,700
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bennett, Dennis A.
;; REGISTRATION NUMBER: 34,547
;; REFERENCE/DOCKET NUMBER: 07-21(690)A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (314)694-5402
;; TELEFAX: (314)694-9009
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 37 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-641-294-4

Query Match 47.7%; Score 12.4; DB 4; Length 37;
Best Local Similarity 92.9%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAA 25
Db 1 GATCGGTACCGCAA 14

RESULT 35
5256558-14/c
; Patent No. 5256558
; APPLICANT: CORUZZI, GLORIA M.; TSAI, FONG-YING
; TITLE OF INVENTION: GENE ENCODING PLANT ASPARAGINE SYNTHETASE
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/514,816
; FILING DATE: 26-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,302
; FILING DATE: 03-MAY-1989
; SEQ ID NO: 14:
; LENGTH: 40
5256558-14

Query Match 47.7%; Score 12.4; DB 6; Length 40;
Best Local Similarity 72.7%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGTCTTTCGACGATCGGTACCT 22
Db 28 GGTCTGTCAGTCTAGATACCT 7

RESULT 36
US-08-879-565-6/c
; Sequence 6; Application US/08879565A
; Patent No. 6093573
; GENERAL INFORMATION:
; APPLICANT: Beamer, Lesa J.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Eisenberg, David
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF
; FILE REFERENCE: 1103/11034US01
; CURRENT APPLICATION NUMBER: US/08/879,565A
; CURRENT FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: Oligonucleotide complementary to SEQ ID NO:5
US-08-879-565-6

Query Match 47.7%; Score 12.4; DB 3; Length 42;
Best Local Similarity 72.7%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACGATCGGTACCTC 23
Db 30 GTCCTTCTCCTTCGTCCTC 9

RESULT 37
US-09-217-228-4
; Sequence 4, Application US/09217228
; Patent No. 6323178
; GENERAL INFORMATION:
; APPLICANT: Butler, Jon P.
; APPLICANT: Hale, John E.
; APPLICANT: Heath Jr., William F.
; APPLICANT: Schoner, Brigitte E.
; APPLICANT: Heiman, Mark L.
; APPLICANT: Becker, Gerald W.
; APPLICANT: Varshavsky, Alexander D.
; TITLE OF INVENTION: Beta-lipotropin and Uses Thereof
; FILE REFERENCE: X-12139
; CURRENT APPLICATION NUMBER: US/09/217,228
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide linker
US-09-217-228-4

Query Match 47.7%; Score 12.4; DB 3; Length 45;
Best Local Similarity 72.7%; Pred. No. 4.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGACGATCGGTACCTCA 24
Db 8 TCTATCGAAGTCTGTGAGCTCA 29

RESULT 38
US-08-363-240A-1102/c
; Sequence 1102, Application US/08363240A
; Patent No. 5705388

GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR PREVENTION, INHIBITION OF PROGRESSION, AND REGRESSION OF VASCULAR DISEASES
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1102:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-1102
Query Match 46.9%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 TTCCGAGATCGGTACCT 22
DB 17 TTTCGAGATCGTCCCT 1
RESULT 39
US-09-165-934-2/c
Sequence 2, Application US/09165934
Patent No. 6284496
GENERAL INFORMATION:
APPLICANT: Litman, Gary W.
APPLICANT: Hawke, Robert N.
APPLICANT: Strong, Scott J.
TITLE OF INVENTION: DNA VECTOR FOR DETERMINING THE PRESENCE OF OUT-OF-READING-FRAME MUTATIONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6284496thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US

ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,934
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 0152.00298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-165-934-2
Query Match 46.9%; Score 12.2; DB 3; Length 24;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 9 GCAGATCGGTACCTCAA 25
DB 23 GCAGATCGATATCTCGA 7
RESULT 40
US-09-343-494-5/c
Sequence 5, Application US/09343494
Patent No. 6413741
GENERAL INFORMATION:
APPLICANT: Jegla, Timothy J.
APPLICANT: Wickenden, Alan
APPLICANT: ICAGEN, Incorporated
TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
FILE REFERENCE: 018512-001320US
CURRENT APPLICATION NUMBER: US/09/343,494
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: US 60/091,469
EARLIER FILING DATE: 1998-07-01
EARLIER APPLICATION NUMBER: US 60/116,621
EARLIER FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: amplification
US-09-343-494-5
Query Match 46.9%; Score 12.2; DB 4; Length 24;
Best Local Similarity 82.4%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGTCTTTCGACAGATCGG 17
DB 18 CGTCTTTCGACAGATCGG 2

Search completed: November 23, 2004, 22:26:50
Job time : 36.0899 secs

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